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OM protein - protein search, using sw model

Run on: April 27, 2006, 17:36:06 ; Search time 165 Seconds
(without alignments)
498.863 Million cell updates/sec

Title: US-09-854-280-3
Perfect score: 1073
Sequence: 1 MTLLPGLLFLTWLHTCLAHH.....FHTEFIHVPVGCTCVLPRSV 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1073	100.0	197	3	US-09-731-816-29 (9/10/98)	Sequence 29, Appl
2	1073	100.0	197	3	US-09-886-404-8 ('01)	Sequence 8, Appli
3	1073	100.0	197	3	US-09-854-280-3	Sequence 3, Appli
4	1073	100.0	197	3	US-09-854-208-3	Sequence 3, Appli
5	1073	100.0	197	3	US-09-874-503-4	Sequence 4, Appli
6	1073	100.0	197	3	US-09-320-713-29	Sequence 29, Appl
7	1073	100.0	197	3	US-09-816-744-4	Sequence 4, Appli
8	1073	100.0	197	3	US-09-747-259-4	Sequence 4, Appli
10	1073	100.0	197	3	US-09-908-827-4	Sequence 4, Appli
13	1073	100.0	197	4	US-10-000-157-4	Sequence 4, Appli
172	1073	100.0	197	4	US-10-036-160-11	Sequence 11, Appl
441	1073	100.0	197	4	US-10-153-770-29	Sequence 29, Appl
469	1073	100.0	197	4	US-10-037-591A-8 ('00)	Sequence 8, Appli
487	1073	100.0	197	4	US-10-174-587-448	Sequence 448, App
522	1073	100.0	197	4	US-10-366-791-23 Gorman	Sequence 23, Appl
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525	1073	100.0	197	4	US-10-410-374-4	Sequence 4, Appli
526	1073	100.0	197	4	US-10-397-282-29	Sequence 29, Appl
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546	1073	100.0	197	4	US-10-408-385-4	Sequence 4, Appli
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552	1073	100.0	197	4	US-10-749-144-24 ('00)	Sequence 24, Appl
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573	459	42.8	87	4	US-10-153-770-2	Sequence 2, Appli
574	459	42.8	87	4	US-10-277-726A-11	Sequence 11, Appl
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587	199	18.5	202	5	US-10-775-204-1758	Sequence 1758, Ap
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697	197	18.4	202	4	US-10-458-442-8	Sequence 8, Appli
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735	192	17.9	160	4	US-10-397-282-4	Sequence 4, Appli

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748	173	16.1	163	3	US-09-747-259-10	Sequence 10, Appl
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883	173	16.1	163	4	US-10-410-374-10	Sequence 10, Appl
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901	173	16.1	163	4	US-10-458-442-10	Sequence 10, Appl
902	173	16.1	163	4	US-10-408-385-10	Sequence 10, Appl
904	173	16.1	163	5	US-10-972-317-160	Sequence 160, App
905	173	16.1	163	5	US-10-491-997-62	Sequence 62, Appl
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909	168.5	15.7	180	3	US-09-774-381-4	Sequence 4, Appli
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914	168.5	15.7	180	4	US-10-772-985-12	Sequence 12, Appl
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1178	154.5	14.4	154	5	US-10-943-594-37	Sequence 37, Appl
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1180	154.5	14.4	157	4	US-10-253-159-43	Sequence 43, Appl
1181	154.5	14.4	157	4	US-10-340-042-43	Sequence 43, Appl
1182	154.5	14.4	157	4	US-10-772-985-43	Sequence 43, Appl
1183	154.5	14.4	157	5	US-10-472-916A-28	Sequence 28, Appl
1184	154.5	14.4	157	5	US-10-943-594-43	Sequence 43, Appl
1185	154.5	14.4	158	3	US-09-794-705A-21	Sequence 21, Appl
1186	154.5	14.4	158	4	US-10-253-159-36	Sequence 36, Appl
1187	154.5	14.4	158	4	US-10-340-042-36	Sequence 36, Appl
1188	154.5	14.4	158	4	US-10-772-985-36	Sequence 36, Appl
1189	154.5	14.4	158	5	US-10-472-916A-21	Sequence 21, Appl
1190	154.5	14.4	158	5	US-10-943-594-36	Sequence 36, Appl
1191	154.5	14.4	160	3	US-09-794-705A-9	Sequence 9, Appli
1192	154.5	14.4	160	3	US-09-794-705A-10	Sequence 10, Appl
1193	154.5	14.4	160	3	US-09-794-705A-11	Sequence 11, Appl
1194	154.5	14.4	160	3	US-09-794-705A-12	Sequence 12, Appl
1195	154.5	14.4	160	3	US-09-794-705A-14	Sequence 14, Appl
1196	154.5	14.4	160	3	US-09-794-705A-15	Sequence 15, Appl
1197	154.5	14.4	160	3	US-09-794-705A-19	Sequence 19, Appl
1198	154.5	14.4	160	3	US-09-794-705A-20	Sequence 20, Appl
1199	154.5	14.4	160	4	US-10-253-159-14	Sequence 14, Appl
1200	154.5	14.4	160	4	US-10-253-159-15	Sequence 15, Appl
1201	154.5	14.4	160	4	US-10-253-159-16	Sequence 16, Appl
1202	154.5	14.4	160	4	US-10-253-159-17	Sequence 17, Appl
1203	154.5	14.4	160	4	US-10-253-159-19	Sequence 19, Appl
1204	154.5	14.4	160	4	US-10-253-159-20	Sequence 20, Appl
1205	154.5	14.4	160	4	US-10-253-159-24	Sequence 24, Appl
1206	154.5	14.4	160	4	US-10-253-159-25	Sequence 25, Appl
1207	154.5	14.4	160	4	US-10-340-042-14	Sequence 14, Appl
1208	154.5	14.4	160	4	US-10-340-042-15	Sequence 15, Appl
1209	154.5	14.4	160	4	US-10-340-042-16	Sequence 16, Appl
1210	154.5	14.4	160	4	US-10-340-042-17	Sequence 17, Appl
1211	154.5	14.4	160	4	US-10-340-042-19	Sequence 19, Appl
1212	154.5	14.4	160	4	US-10-340-042-20	Sequence 20, Appl
1213	154.5	14.4	160	4	US-10-340-042-24	Sequence 24, Appl
1214	154.5	14.4	160	4	US-10-340-042-25	Sequence 25, Appl
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1216	154.5	14.4	160	4	US-10-772-985-15	Sequence 15, Appl
1217	154.5	14.4	160	4	US-10-772-985-16	Sequence 16, Appl
1218	154.5	14.4	160	4	US-10-772-985-17	Sequence 17, Appl
1219	154.5	14.4	160	4	US-10-772-985-19	Sequence 19, Appl
1220	154.5	14.4	160	4	US-10-772-985-20	Sequence 20, Appl
1221	154.5	14.4	160	4	US-10-772-985-24	Sequence 24, Appl
1222	154.5	14.4	160	4	US-10-772-985-25	Sequence 25, Appl
1223	154.5	14.4	160	5	US-10-472-916A-9	Sequence 9, Appli
1224	154.5	14.4	160	5	US-10-472-916A-10	Sequence 10, Appl
1225	154.5	14.4	160	5	US-10-472-916A-11	Sequence 11, Appl
1226	154.5	14.4	160	5	US-10-472-916A-12	Sequence 12, Appl
1227	154.5	14.4	160	5	US-10-472-916A-14	Sequence 14, Appl
1228	154.5	14.4	160	5	US-10-472-916A-15	Sequence 15, Appl
1229	154.5	14.4	160	5	US-10-472-916A-19	Sequence 19, Appl
1230	154.5	14.4	160	5	US-10-472-916A-20	Sequence 20, Appl
1231	154.5	14.4	160	5	US-10-943-594-14	Sequence 14, Appl
1232	154.5	14.4	160	5	US-10-943-594-15	Sequence 15, Appl
1233	154.5	14.4	160	5	US-10-943-594-16	Sequence 16, Appl
1234	154.5	14.4	160	5	US-10-943-594-17	Sequence 17, Appl
1235	154.5	14.4	160	5	US-10-943-594-19	Sequence 19, Appl
1236	154.5	14.4	160	5	US-10-943-594-20	Sequence 20, Appl
1237	154.5	14.4	160	5	US-10-943-594-24	Sequence 24, Appl
1238	154.5	14.4	160	5	US-10-943-594-25	Sequence 25, Appl
1239	154.5	14.4	175	3	US-09-854-280-23	Sequence 23, Appl
1240	154.5	14.4	175	3	US-09-854-208-23	Sequence 23, Appl
1241	154.5	14.4	180	3	US-09-731-816-8	Sequence 8, Appli
1242	154.5	14.4	180	3	US-09-794-705A-2	Sequence 2, Appli
1243	154.5	14.4	180	3	US-09-854-280-1	Sequence 1, Appli
1244	154.5	14.4	180	3	US-09-854-208-1	Sequence 1, Appli
1247	154.5	14.4	180	3	US-09-874-503-2	Sequence 2, Appli
1250	154.5	14.4	180	3	US-09-320-713-8	Sequence 8, Appli
1251	154.5	14.4	180	3	US-09-816-744-2	Sequence 2, Appli
1253	154.5	14.4	180	3	US-09-747-259-2	Sequence 2, Appli
1260	154.5	14.4	180	3	US-09-908-827-2	Sequence 2, Appli
1268	154.5	14.4	180	3	US-09-774-381-2	Sequence 2, Appli
1283	154.5	14.4	180	3	US-09-796-844-35	Sequence 35, Appl
1285	154.5	14.4	180	4	US-10-000-157-2	Sequence 2, Appli
1304	154.5	14.4	180	4	US-10-167-749-470	Sequence 470, App
1426	154.5	14.4	180	4	US-10-153-770-8	Sequence 8, Appli
1433	154.5	14.4	180	4	US-10-253-159-2	Sequence 2, Appli
1483	154.5	14.4	180	4	US-10-340-042-2	Sequence 2, Appli
1500	154.5	14.4	180	5	US-10-931-886-446	Sequence 446, App

Search completed: April 27, 2006, 17:39:54
Job time : 183 secs

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OM protein - protein search, using sw model

Run on: April 27, 2006, 17:18:15 ; Search time 16 Seconds
(without alignments)
1184.669 Million cell updates/sec

Title: US-09-854-280-3
Perfect score: 1073
Sequence: 1 MTLLPGLLFLTWLHTCLAHH.....FHTEFIHVPVGCTCVLPRSV 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160.5	15.0	151	1	B45351	immediate-early pr
2	148.5	13.8	147	2	JC4628	cytotoxic T-lympho
3	148.5	13.8	150	2	I49623	cytotoxic T-lympho
4	110	10.3	148	2	T21334	hypothetical prote
5	93.5	8.7	395	1	KISMG	galactokinase (EC
6	86.5	8.1	389	2	T50809	hypothetical prote
7	86	8.0	297	2	JL0032	hypothetical 31.7K
8	84.5	7.9	1638	2	A42091	transcription acti
9	82.5	7.7	635	2	S76371	hypothetical prote
10	81.5	7.6	325	2	T23218	hypothetical prote
11	81	7.5	553	2	D83640	hypothetical prote
12	80.5	7.5	210	2	B40203	4-alpha-glucanotra
13	80	7.5	411	2	A70509	hypothetical prote
14	79.5	7.4	638	2	JC7753	ring finger B-box
15	79	7.4	549	2	I37386	fas-activated seri
16	79	7.4	837	2	T12514	hypothetical prote
17	79	7.4	885	2	S75894	hypothetical prote
18	78.5	7.3	132	2	E72603	hypothetical prote
19	78	7.3	309	2	T37033	hypothetical prote
20	77.5	7.2	209	2	T30698	hypothetical prote
21	77.5	7.2	323	2	A35909	fra-2 protein - ch
22	77.5	7.2	567	2	E96764	ethylene-insensiti
23	77	7.2	420	2	T14166	fxuD protein - Myc
24	77	7.2	466	2	T36212	replication initia
25	77	7.2	639	2	AC2895	beta-N-acetylhexos
26	77	7.2	639	2	F97670	beta-n-acetylhexos
27	76.5	7.1	405	2	G84338	3-hydroxy-3-methyl
28	76.5	7.1	503	2	S64787	pre-mRNA splicing
29	76.5	7.1	1882	2	T00069	hypothetical prote
30	76	7.1	296	2	T35477	probable oxidoredu
31	75.5	7.0	1044	2	T00342	hypothetical prote
32	75	7.0	744	2	C75276	sensory box sensor
33	74.5	6.9	464	2	T50955	hypothetical prote
34	74.5	6.9	624	2	B49364	protein kinase (EC
35	74	6.9	211	2	G72649	hypothetical prote
36	74	6.9	260	1	A46517	CD27 antigen precu
37	74	6.9	347	2	JH0657	hypothetical 37.5K
38	73.5	6.8	559	2	S33724	transcription fact
39	73.5	6.8	741	2	I48694	probable transcrip
40	73	6.8	329	2	T08262	hypothetical prote
41	73	6.8	373	2	B70673	probable ddlA - My
42	73	6.8	1080	2	T43164	IactA protein - Li
43	72.5	6.8	181	2	T24914	hypothetical prote
44	72.5	6.8	362	2	B87571	hypothetical prote
45	72.5	6.8	466	2	A36389	transcription fact
46	72.5	6.8	514	2	B83360	hypothetical prote
47	72.5	6.8	646	2	JC5583	85K SH3 domain-con
48	72.5	6.8	723	2	G84507	hypothetical prote
49	72.5	6.8	742	2	A49672	transcription fact
50	72.5	6.8	772	2	A55004	transcription fact
51	72	6.7	437	2	T37469	homogentisate 1,2-
52	72	6.7	767	2	T05662	hypothetical prote
53	71.5	6.7	203	2	H85563	hypothetical prote
54	71.5	6.7	203	2	D90713	phosphohistidine p
55	71.5	6.7	203	2	D64798	phosphoglycerate m
56	71.5	6.7	215	2	F72641	hypothetical prote
57	71.5	6.7	245	2	S53867	DNA (cytosine)-met
58	71.5	6.7	330	2	S37595	mucin JUL10 - huma
59	71.5	6.7	336	2	JS0052	37K protein - Myco
60	71.5	6.7	433	2	S70914	pectinesterase (EC
61	71.5	6.7	757	2	T24266	hypothetical prote
62	71.5	6.7	1007	2	T01437	hypothetical prote
63	71.5	6.7	2471	2	A49128	cell-fate determin
64	71	6.6	322	1	TVFVF4	transforming prote
65	71	6.6	325	2	T36495	hypothetical prote
66	71	6.6	329	2	T45200	hypothetical prote
67	71	6.6	367	1	TVCHFS	transforming prote
68	71	6.6	407	2	D87010	probable membrane
69	71	6.6	642	2	T30746	hypothetical prote
70	70.5	6.6	235	2	B71178	hypothetical prote
71	70.5	6.6	256	2	B72777	hypothetical prote
72	70.5	6.6	554	2	T39979	probable zinc fing
73	70.5	6.6	809	2	S67153	probable membrane
74	70.5	6.6	873	2	T50171	hypothetical prote
75	70	6.5	247	2	T49375	hypothetical prote
76	70	6.5	381	1	A47327	selenoprotein P pr
77	70	6.5	411	2	A49127	homeotic protein A
78	70	6.5	420	2	A49642	transcription fact
79	70	6.5	490	2	G85354	hypothetical prote
80	70	6.5	516	2	T49422	RAD57 related prot
81	70	6.5	640	2	AB2251	glucose inhibited
82	70	6.5	704	2	B84530	probable RING zinc
83	70	6.5	750	2	AG3008	polyketide synthet
84	70	6.5	770	2	F98275	saframycin mx1 syn
85	70	6.5	939	2	C70876	hypothetical prote
86	70	6.5	984	1	A34076	protein-tyrosine k
87	70	6.5	1249	2	C83358	probable non-ribos
88	70	6.5	1390	2	T31353	polyprotein - Arab
89	69.5	6.5	146	2	T36476	hypothetical prote
90	69.5	6.5	383	2	AI1028	shufflon-specific
91	69.5	6.5	474	2	T45818	hypothetical prote
92	69.5	6.5	525	1	KGHUGH	histidine-rich gly
93	69.5	6.5	624	2	S41688	DNA-binding protei
94	69.5	6.5	794	2	G84688	hypothetical prote
95	69.5	6.5	1006	2	T42731	atrophin-1 related
96	69.5	6.5	1744	2	A54970	tensin, cardiac mu
97	69	6.4	146	2	S57956	ovine vascular end
98	69	6.4	224	1	A33861	trans-activating t
99	69	6.4	419	1	S70617	homeotic protein g
100	69	6.4	475	2	E84745	probable splicing
101	69	6.4	508	1	JC5713	25-hydroxyvitamin
102	69	6.4	558	2	S57953	C4BP protein alpha

103	69	6.4	583	2	D82672	general secretory
104	69	6.4	610	2	S35049	mucin JER57 - huma
105	69	6.4	671	2	A35912	homeotic protein o
106	69	6.4	954	2	AF2756	glycine cleavage s
107	69	6.4	954	2	E97537	glycine cleavage s
108	69	6.4	1151	2	I38004	M130 antigen precu
109	69	6.4	1156	2	I38005	M130 antigen precu
110	69	6.4	1610	2	D89451	protein T04G9.1 [i
111	69	6.4	1776	1	RRWPYM	genome polyprotein
112	69	6.4	2869	2	T18518	apolipoprotein(a)
113	68.5	6.4	183	2	A75605	hypothetical prote
114	68.5	6.4	189	2	C98167	hypothetical prote
115	68.5	6.4	189	2	AD3120	transcription regu
116	68.5	6.4	367	2	C83553	probable enoyl-CoA
117	68.5	6.4	393	2	E71285	hypothetical prote
118	68.5	6.4	402	2	S05018	beta-N-acetylgluco
119	68.5	6.4	646	1	S15901	chromogranin B pre
120	68.5	6.4	960	2	A41638	chitin synthase (E
121	68.5	6.4	1047	2	T34946	probable isoleucyl
122	68	6.3	190	2	B40080	vascular endotheli
123	68	6.3	239	2	E84232	hypothetical prote
124	68	6.3	295	2	F70692	hypothetical prote
125	68	6.3	312	2	D82690	adenine-specific m
126	68	6.3	359	2	S04570	gene X/C fusion pr
127	68	6.3	426	2	C83212	rhamnosyltransfera
128	68	6.3	426	2	B53652	rhamnosyltransfera
129	68	6.3	482	2	T02739	probable cytochrom
130	68	6.3	857	2	T05352	hypothetical prote
131	68	6.3	915	1	WMBEV3	ribonucleoside-dip
132	68	6.3	1184	2	S50832	atrophin-1 - human
133	68	6.3	1184	2	G01763	atrophin-1 - human
134	68	6.3	1520	2	T00273	hypothetical prote
135	67.5	6.3	127	2	T31206	hypothetical prote
136	67.5	6.3	268	2	T36360	hypothetical prote
137	67.5	6.3	299	2	C75384	conserved hypothet
138	67.5	6.3	314	2	S06967	beta-lactamase (EC
139	67.5	6.3	451	1	GBECAG	alpha-galactosidas
140	67.5	6.3	507	1	KJHUAA	cerebroside-sulfat
141	67.5	6.3	539	2	AF2065	hypothetical prote
142	67.5	6.3	573	2	A84005	transposase (08) B
143	67.5	6.3	574	2	C83828	transposase (08) B
144	67.5	6.3	867	2	T27136	hypothetical prote
145	67.5	6.3	871	2	T27135	hypothetical prote
146	67.5	6.3	901	2	F83781	transposase (08) /
147	67.5	6.3	1189	2	T17088	homeodomain-intera
148	67.5	6.3	1237	2	A31334	phosphorylase kina
149	67.5	6.3	1398	2	T13741	hypothetical prote
150	67	6.2	284	2	A75422	acetyl-CoA carboxy
151	67	6.2	384	2	A46403	transcription fact
152	67	6.2	429	2	S01919	knirps protein - f
153	67	6.2	500	2	S56276	probable membrane
154	67	6.2	572	2	S21325	probable exo-gluca
155	67	6.2	582	2	T34538	hypothetical prote
156	67	6.2	679	2	A83488	hypothetical prote
157	67	6.2	735	2	T45059	hypothetical prote
158	67	6.2	741	2	D83633	conserved hypothet
159	67	6.2	774	2	T39539	alpha-amylase homo
160	67	6.2	775	1	VPXRPG	outer layer protei
161	67	6.2	860	2	B75589	GGDEF family prote
162	67	6.2	919	2	S45889	probable regulator
163	67	6.2	1008	2	T49470	phosphatidic acid-
164	67	6.2	1388	2	T17269	hypothetical prote
165	67	6.2	1812	2	I49350	breast/ovarian can
166	67	6.2	2845	2	I49505	adenomatous polypo
167	66.5	6.2	162	2	T32515	hypothetical prote
168	66.5	6.2	179	2	T36512	probable branched-
169	66.5	6.2	209	2	F96536	hypothetical prote
170	66.5	6.2	231	2	F83186	hypothetical prote
171	66.5	6.2	341	2	S09913	hypothetical prote
172	66.5	6.2	451	2	E91266	alpha-galactosidas
173	66.5	6.2	451	2	B86107	alpha-galactosidas
174	66.5	6.2	471	2	S01052	flavonol 3-O-gluco
175	66.5	6.2	573	2	G75463	O-acetylhomoserine
176	66.5	6.2	608	1	ABRTS	serum albumin prec
177	66.5	6.2	691	2	A25704	synapsin I - rat
178	66.5	6.2	783	2	T30644	hypothetical prote
179	66.5	6.2	893	2	T35014	probable regulator
180	66.5	6.2	4687	1	A39638	plectin - rat
181	66	6.2	262	2	S25655	Spi-B protein - hu
182	66	6.2	317	2	E86264	protein F3F19.7 [i
183	66	6.2	341	2	D72622	hypothetical prote
184	66	6.2	359	2	G81038	3-dehydroquinate s
185	66	6.2	381	2	G75589	hypothetical prote
186	66	6.2	392	2	S11998	finger protein odd
187	66	6.2	397	2	AG3420	phage portal prote
188	66	6.2	403	2	A42149	hydroxymethylgluta
189	66	6.2	481	2	A56346	transcription fact
190	66	6.2	491	2	A27717	cytochrome P450 2B
191	66	6.2	509	2	T02864	probable Zn finger
192	66	6.2	530	2	T30505	hypothetical prote
193	66	6.2	540	2	B57785	zinc finger protei
194	66	6.2	671	2	S51599	Om(2D) protein - f
195	66	6.2	785	2	T37378	probable 90.4K pro
196	66	6.2	891	2	G84693	probable proline-r
197	66	6.2	1090	2	T00533	probable DNA2-NAM7
198	66	6.2	2340	2	I48310	kinase-related pro
199	65.5	6.1	212	2	S51798	gamma-kafirin prec
200	65.5	6.1	274	1	E64065	3',5'-cyclic-nucle
201	65.5	6.1	420	2	I59234	octamer binding tr
202	65.5	6.1	437	2	AB0036	probable coproporp
203	65.5	6.1	506	2	JC7226	endo-1,3(4)-beta-g
204	65.5	6.1	518	2	B83439	hypothetical prote
205	65.5	6.1	522	2	T40520	hypothetical prote
206	65.5	6.1	547	2	S19607	alkaline phosphata
207	65.5	6.1	563	2	B82579	peptide synthase X
208	65.5	6.1	606	2	T11909	NADH2 dehydrogenas
209	65.5	6.1	640	1	QYCHGM	phosphoenolpyruvat
210	65.5	6.1	693	2	T23529	hypothetical prote
211	65.5	6.1	799	2	T48889	serine/threonine p
212	65.5	6.1	837	2	H82970	hypothetical prote
213	65.5	6.1	1079	2	A70972	probable DNA polym
214	65.5	6.1	1360	2	T31674	hypothetical prote
215	65.5	6.1	1442	2	S72441	protein-tyrosine-p
216	65.5	6.1	1516	2	T01055	hypothetical prote
217	65.5	6.1	1553	2	T03301	rab3 effector prot
218	65.5	6.1	2918	2	A54105	fibrillin-2 precur
219	65.5	6.1	4574	2	G02520	plectin - human
220	65.5	6.1	4957	2	T03455	ALR protein - huma
221	65.5	6.1	5262	2	T03454	ALR protein - huma
222	65	6.1	182	2	AF0921	lipopolysaccharide
223	65	6.1	191	2	AG0249	conserved hypothet
224	65	6.1	209	2	G70689	hypothetical prote
225	65	6.1	213	2	T34949	hypothetical prote
226	65	6.1	224	2	AF0838	transcription regu
227	65	6.1	303	2	F98284	3-hydroxybutyryl-C
228	65	6.1	303	2	AC2999	3-hydroxybutyryl-C
229	65	6.1	316	2	T36027	hypothetical prote
230	65	6.1	325	2	AE3575	transcription regu
231	65	6.1	331	2	S78452	POU-domain protein
232	65	6.1	400	2	T41569	hypothetical prote
233	65	6.1	407	2	JN0584	aminoacylase (EC 3
234	65	6.1	470	2	T31465	cell cycle protein
235	65	6.1	485	2	AD0041	rhamnulokinase (EC
236	65	6.1	503	2	S54302	zinc transporter Z
237	65	6.1	518	2	S61920	B-alpha pheromone-
238	65	6.1	533	2	AF0180	hypothetical prote
239	65	6.1	536	2	S06548	finger protein (cl
240	65	6.1	557	1	S34412	transcription fact
241	65	6.1	648	2	A71342	probable DNA misma
242	65	6.1	785	1	QQVZ8	D5 protein - vacci
243	65	6.1	785	2	T28533	hypothetical prote
244	65	6.1	785	2	E72162	F5R protein - vari
245	65	6.1	785	2	B36847	ATP/GTP-binding pr
246	65	6.1	939	2	G75481	sensory box/GGDEF
247	65	6.1	1030	2	A42497	anion exchanger 3,
248	65	6.1	1097	2	S68685	adenylate cyclase

249	65	6.1	1366	2	T35985	probable large Pro
250	65	6.1	1515	2	A40203	4-alpha-glucanotra
251	65	6.1	2325	2	A61208	chondroitin sulfat
252	65	6.1	2813	1	VWHU	von Willebrand fac
253	64.5	6.0	137	2	H82537	TonB protein XF260
254	64.5	6.0	197	2	B70761	probable lipoprote
255	64.5	6.0	198	2	A45067	laminin B1 chain v
256	64.5	6.0	228	2	A72740	hypothetical prote
257	64.5	6.0	242	2	T46543	hypothetical prote
258	64.5	6.0	274	2	F75027	hypothetical prote
259	64.5	6.0	381	2	A54415	transcription fact
260	64.5	6.0	413	2	C83225	conserved hypothet
261	64.5	6.0	450	2	AF0207	probable membrane
262	64.5	6.0	508	2	A30226	thyroid/steroid ho
263	64.5	6.0	543	2	B39369	homeotic protein B
264	64.5	6.0	548	2	H70788	probable peptidetr
265	64.5	6.0	632	2	T45858	hypothetical prote
266	64.5	6.0	752	2	G02273	LIV-1 protein - hu
267	64.5	6.0	758	2	A83121	probable two-compo
268	64.5	6.0	790	2	E83621	probable TonB-depe
269	64.5	6.0	825	2	A26983	regulatory protein
270	64.5	6.0	836	2	T08424	tweety protein - f
271	64.5	6.0	2248	1	D42088	adenylate cyclase
272	64.5	6.0	2715	2	T13049	eyelid - fruit fly
273	64	6.0	162	2	PC4262	cytochrome P450 mo
274	64	6.0	207	2	T03526	blub protein - Rho
275	64	6.0	230	2	T34854	hypothetical prote
276	64	6.0	248	2	T21786	hypothetical prote
277	64	6.0	275	2	S77476	tRNA-pseudouridine
278	64	6.0	301	2	T40402	forkhead nuclear s
279	64	6.0	312	2	S77670	probable transcrip
280	64	6.0	312	2	A86279	F14L17.21 protein
281	64	6.0	353	2	B72468	hypothetical prote
282	64	6.0	380	2	S35785	glycoprotein I - b
283	64	6.0	417	2	T18740	hypothetical prote
284	64	6.0	428	1	TVHUEK	transforming prote
285	64	6.0	476	2	AI0189	exodeoxyribonuclea
286	64	6.0	491	2	S31277	cytochrome P450 2B
287	64	6.0	491	2	JT0676	cytochrome P450 2B
288	64	6.0	492	2	A41907	methyl-CpG-binding
289	64	6.0	563	2	T04359	pectin methylester
290	64	6.0	564	2	H75607	hypothetical prote
291	64	6.0	715	1	TNBE77	77K alpha trans-in
292	64	6.0	787	2	T49614	related to tol pro
293	64	6.0	907	2	T02417	probable C2H2-type
294	64	6.0	921	2	A40597	DNA-directed DNA p
295	64	6.0	1356	1	C45219	N-methyl-D-asparta
296	64	6.0	1616	2	I37183	gene APXL protein
297	64	6.0	1751	1	MMHUMH	laminin alpha-2 ch
298	64	6.0	2599	2	A96616	unknown protein F1
299	64	6.0	3104	2	S20473	fatty-acid synthas
300	63.5	5.9	166	2	C72641	hypothetical prote
301	63.5	5.9	190	2	S52130	vascular endotheli
302	63.5	5.9	231	2	F82577	TonB protein XF228
303	63.5	5.9	238	2	T02118	hypothetical prote
304	63.5	5.9	261	1	WMBEXE	infected cell prot
305	63.5	5.9	269	2	A47008	transcription acti
306	63.5	5.9	284	2	AH0146	probable sulfurtra
307	63.5	5.9	299	2	F97544	high-affinity zinc
308	63.5	5.9	299	2	AG2763	hypothetical prote
309	63.5	5.9	300	2	A41517	meiosis inhibitor
310	63.5	5.9	326	2	I48351	fos-related antige
311	63.5	5.9	440	2	G71522	probable phosphosh
312	63.5	5.9	444	2	T15907	hypothetical prote
313	63.5	5.9	453	2	A05139	serum albumin - mo
314	63.5	5.9	538	1	S12570	homeotic protein b
315	63.5	5.9	608	2	F83397	probable peptidase
316	63.5	5.9	618	2	F83908	transposase (08) B
317	63.5	5.9	752	2	T09082	telomere-associate
318	63.5	5.9	757	2	T09081	telomere-associate
319	63.5	5.9	771	2	T38616	hypothetical prote
320	63.5	5.9	938	2	T39006	related to yeast z
321	63.5	5.9	1015	2	S55474	Human giant larvae
322	63.5	5.9	1241	2	S40528	phosphorylase kina
323	63.5	5.9	1280	2	T00365	hypothetical prote
324	63.5	5.9	1733	2	S27939	tensin - chicken
325	63.5	5.9	2019	2	T27702	hypothetical prote
326	63	5.9	159	2	T48594	hypothetical prote
327	63	5.9	169	2	G96003	hypothetical prote
328	63	5.9	226	2	C70622	probable lipoprote
329	63	5.9	229	2	D69786	glycoprotein endop
330	63	5.9	233	2	AB2107	hypothetical prote
331	63	5.9	253	2	T49820	hypothetical prote
332	63	5.9	261	2	JQ0319	hypothetical 27K p
333	63	5.9	270	2	D72334	sugar kinase, pfkB
334	63	5.9	282	2	AI0721	hydrogenase-1 oper
335	63	5.9	284	2	A82133	conserved hypothet
336	63	5.9	287	2	S71548	homeotic protein p
337	63	5.9	303	2	C84208	proliferating-cell
338	63	5.9	318	2	T33874	hypothetical prote
339	63	5.9	332	2	S46985	indole-3-pyruvate
340	63	5.9	335	2	D38532	hypB protein - Rho
341	63	5.9	349	2	JC5881	myocyte enhancer f
342	63	5.9	352	1	R5HSL0	ribosomal protein
343	63	5.9	352	2	G84266	50S ribosomal prot
344	63	5.9	356	2	B39798	RP2 protein, testo
345	63	5.9	362	2	S22395	fetuin precursor -
346	63	5.9	374	2	G45252	site-specific reco
347	63	5.9	425	2	JC5850	polyketide synthas
348	63	5.9	439	2	T46375	hypothetical prote
349	63	5.9	476	2	E97228	glu-tRNAGln amidot
350	63	5.9	491	1	O4RBPC	cytochrome P450 2B
351	63	5.9	491	2	S31278	cytochrome P450 2B
352	63	5.9	491	2	S35666	cytochrome P450 2B
353	63	5.9	506	2	A40679	transcription enha
354	63	5.9	507	2	S54303	zinc transport pro
355	63	5.9	522	1	GNWVR1	structural polypro
356	63	5.9	523	2	B40679	transcription enha
357	63	5.9	523	2	S67271	hypothetical prote
358	63	5.9	529	2	T45134	hypothetical prote
359	63	5.9	542	1	A54963	transcription fact
360	63	5.9	597	2	AG2430	N-acetylmuramoyl-L
361	63	5.9	638	2	D85435	BEL1-like homeobox
362	63	5.9	653	2	JQ1241	Viral replicase 1
363	63	5.9	710	2	A31641	daughterless (da)
364	63	5.9	718	2	JC5805	transcription fact
365	63	5.9	747	2	D70802	hypothetical prote
366	63	5.9	815	2	T36671	probable helicase
367	63	5.9	947	2	T23107	hypothetical prote
368	63	5.9	948	2	T03225	probable regulator
369	63	5.9	1000	2	T30280	hypothetical prote
370	63	5.9	1068	2	AB1082	B. subtilis YueB p
371	63	5.9	1184	2	A55184	fibulin-2 precurso
372	63	5.9	1554	2	T06370	probable DNA (cyto
373	63	5.9	3712	2	S18253	laminin alpha-1 ch
374	62.5	5.8	125	1	A46315	E4 protein - human
375	62.5	5.8	180	2	T43451	hypothetical prote
376	62.5	5.8	183	2	T29987	hypothetical prote
377	62.5	5.8	250	2	T31836	hypothetical prote
378	62.5	5.8	257	2	A82585	cyclase XF2214 [im
379	62.5	5.8	265	2	C98138	hypothetical prote
380	62.5	5.8	267	2	S27953	Mx protein - pig (
381	62.5	5.8	304	2	D75397	metallo-beta-lacta
382	62.5	5.8	306	2	F72606	probable methanol
383	62.5	5.8	306	2	S50689	hypothetical prote
384	62.5	5.8	309	1	S09257	homeotic protein H
385	62.5	5.8	328	2	AB0435	conserved hypothet
386	62.5	5.8	357	2	E83094	UDP-N-acetylglucos
387	62.5	5.8	372	2	T31060	hypothetical prote
388	62.5	5.8	382	2	S08595	TrfA transcription
389	62.5	5.8	415	2	B83634	hypothetical prote
390	62.5	5.8	416	2	F83010	probable oxidoredu
391	62.5	5.8	437	1	FGRTGA	fibrinogen gamma-A
392	62.5	5.8	445	1	FGRTGB	fibrinogen gamma-B
393	62.5	5.8	450	2	T17234	hypothetical prote
394	62.5	5.8	452	2	C41602	transcription fact

395	62.5	5.8	453	2	C40511	hypothetical prote
396	62.5	5.8	454	2	E70637	hypothetical prote
397	62.5	5.8	459	2	S33424	repSA protein - St
398	62.5	5.8	466	2	A36674	transcription fact
399	62.5	5.8	474	2	S75985	hypothetical prote
400	62.5	5.8	503	2	E82730	peptide synthase X
401	62.5	5.8	519	1	I48966	aldehyde dehydroge
402	62.5	5.8	549	2	C70689	hypothetical prote
403	62.5	5.8	565	2	H69113	glycine-tRNA ligas
404	62.5	5.8	578	2	T21345	hypothetical prote
405	62.5	5.8	618	2	S06446	citrolysin-related
406	62.5	5.8	620	2	S06733	hydroxyproline-ric
407	62.5	5.8	640	2	S62747	homeotic protein A
408	62.5	5.8	651	2	C56653	membrane glycoprot
409	62.5	5.8	653	2	A46362	amyloid precursor-
410	62.5	5.8	658	2	T46359	hypothetical prote
411	62.5	5.8	694	2	A96571	hypothetical prote
412	62.5	5.8	738	2	T00343	hypothetical prote
413	62.5	5.8	851	2	T00374	hypothetical prote
414	62.5	5.8	1017	2	T31354	probable potassium
415	62.5	5.8	1024	2	T46016	hypothetical prote
416	62.5	5.8	1051	1	JW0051	serine/threonine-s
417	62.5	5.8	1737	2	T00209	MEGF8 protein - hu
418	62.5	5.8	1792	2	A57075	tensin - chicken (
419	62.5	5.8	2591	2	T30288	pristinamycin I sy
420	62.5	5.8	3672	2	T23433	hypothetical prote
421	62.5	5.8	3704	2	T37316	probable laminin a
422	62.5	5.8	4485	2	T08044	dynein gamma heavy
423	62.5	5.8	4684	2	A59404	plectin [imported]
424	62	5.8	232	2	D97683	tRNA (guanine-n1)-
425	62	5.8	232	2	AD2908	tRNA-(guanine-N1)-
426	62	5.8	238	2	H70866	hypothetical prote
427	62	5.8	295	2	AF2610	conserved hypothet
428	62	5.8	295	2	D97392	hypothetical prote
429	62	5.8	316	2	E83136	probable transcrip
430	62	5.8	362	2	I65990	G protein-coupled
431	62	5.8	373	2	F87184	conserved hypothet
432	62	5.8	380	2	B70544	probable histidino
433	62	5.8	387	2	F82746	DNA processing cha
434	62	5.8	396	2	A57090	CSA protein - huma
435	62	5.8	429	2	S27793	hypothetical prote
436	62	5.8	429	2	T20387	hypothetical prote
437	62	5.8	456	2	B45728	rdxA 3'-region pro
438	62	5.8	494	2	JC5320	cytochrome P450 mo
439	62	5.8	499	2	T45946	probable protein-k
440	62	5.8	525	2	A85362	leucyl aminopeptid
441	62	5.8	533	2	T00742	ubiquitin-binding
442	62	5.8	557	1	S15342	transcription fact
443	62	5.8	558	1	A39633	transcription fact
444	62	5.8	559	2	AC3373	NAD synthase (glut
445	62	5.8	560	2	A40044	PML-1 protein - hu
446	62	5.8	570	2	C97408	long-chain-fatty-a
447	62	5.8	570	2	AD2626	long-chain-fatty-a
448	62	5.8	572	2	T47219	amino acid transpo
449	62	5.8	589	2	S42517	PML protein, splic
450	62	5.8	589	2	S44381	PML protein, splic
451	62	5.8	590	2	A26638	homeotic protein D
452	62	5.8	593	2	B40045	probable transcrip
453	62	5.8	630	2	D97669	hypothetical prote
454	62	5.8	630	2	AI2893	hypothetical prote
455	62	5.8	633	2	S19244	gene Myl protein -
456	62	5.8	641	2	A39961	choline O-acetyltr
457	62	5.8	641	2	A40045	probable transcrip
458	62	5.8	736	2	S57961	dimethylamine dehy
459	62	5.8	783	1	A38637	Ras interactor RIN
460	62	5.8	784	1	S47270	endopeptidase La (
461	62	5.8	802	2	S42518	PML protein, splic
462	62	5.8	802	2	S44382	PML protein, splic
463	62	5.8	804	2	T05783	hypothetical prote
464	62	5.8	855	2	A48168	proliferating-cell
465	62	5.8	860	2	S44380	PML protein, splic
466	62	5.8	860	2	S42516	PML protein, splic
467	62	5.8	880	2	AD1953	hypothetical prote
468	62	5.8	955	4	C40045	probable transcrip
469	62	5.8	964	2	S06028	gene suppressor-of
470	62	5.8	1043	2	D84900	hypothetical prote
471	62	5.8	1227	2	B34911	band 3-related pro
472	62	5.8	1589	2	T13606	hypothetical prote
473	62	5.8	1723	2	S58880	receptor DEC-205 -
474	62	5.8	1838	2	T18448	pathogenicity fact
475	62	5.8	1851	2	T19964	hypothetical prote
476	62	5.8	2493	2	S72349	nonstructural poly
477	62	5.8	2493	2	S26372	nonstructural poly
478	62	5.8	2629	2	T32735	telomerase-associa
479	61.5	5.7	154	2	JQ1137	rRNA methyltransfe
480	61.5	5.7	154	2	D91285	probable transcrip
481	61.5	5.7	154	2	F86126	hypothetical prote
482	61.5	5.7	271	2	JC6553	transcription fact
483	61.5	5.7	291	2	AF3264	3-hydroxybutyryl-C
484	61.5	5.7	325	2	A83174	probable transcrip
485	61.5	5.7	348	2	T02462	probable AT-hook D
486	61.5	5.7	365	2	S36807	cytochrome P450 71
487	61.5	5.7	367	1	W2WL11	E2 protein - human
488	61.5	5.7	373	2	T25920	hypothetical prote
489	61.5	5.7	431	2	T30755	hypothetical prote
490	61.5	5.7	435	2	A72339	glucose-inhibited
491	61.5	5.7	449	2	T19626	hypothetical prote
492	61.5	5.7	463	2	E70657	hypothetical prote
493	61.5	5.7	465	2	E87591	sensor histidine k
494	61.5	5.7	471	1	S08325	flavonol 3-O-gluco
495	61.5	5.7	471	2	G83561	hypothetical prote
496	61.5	5.7	491	2	JC6197	stromelysin 3 (EC
497	61.5	5.7	497	2	C34469	pulE protein - Kle
498	61.5	5.7	515	2	T23089	hypothetical prote
499	61.5	5.7	576	2	G82792	conserved hypothet
500	61.5	5.7	628	2	I38000	Lutheran blood gro
501	61.5	5.7	638	2	A36929	virulence regulato
502	61.5	5.7	646	2	T35002	probable respirato
503	61.5	5.7	703	2	G75638	nodulation protein
504	61.5	5.7	771	2	S35681	ESG protein - mous
505	61.5	5.7	833	2	AE0564	H+/K+-exchanging A
506	61.5	5.7	883	2	S57653	brevican precursor
507	61.5	5.7	985	2	T29910	hypothetical prote
508	61.5	5.7	1039	2	A85096	hypothetical prote
509	61.5	5.7	1085	2	G72023	transcription-repa
510	61.5	5.7	1085	2	A86602	transcription-repa
511	61.5	5.7	1174	2	I38140	protein-tyrosine-p
512	61.5	5.7	1265	2	S17675	valine-tRNA ligase
513	61.5	5.7	1266	2	AC3154	conjugation protei
514	61.5	5.7	1277	2	G98133	probable traA prot
515	61.5	5.7	1285	2	T14171	ataxin-2 - mouse
516	61.5	5.7	1357	2	T29265	hypothetical prote
517	61.5	5.7	1791	2	T02345	hypothetical prote
518	61.5	5.7	1964	2	T09059	notch4 - mouse
519	61.5	5.7	2504	1	A57788	enoyl-[acyl-carrie
520	61.5	5.7	2509	2	G01880	fatty-acid synthas
521	61.5	5.7	2693	2	A40743	IP3 receptor, XIP3
522	61	5.7	186	2	C87705	transcription regu
523	61	5.7	203	2	T36240	hypothetical prote
524	61	5.7	218	2	T17259	hypothetical prote
525	61	5.7	244	2	JC7299	transformer-2-like
526	61	5.7	244	2	E72099	conserved hypothet
527	61	5.7	244	2	E86523	PP-loop type ATPas
528	61	5.7	245	1	TVCTSS	platelet-derived g
529	61	5.7	247	2	C83296	hypothetical prote
530	61	5.7	262	2	A72469	hypothetical prote
531	61	5.7	291	2	A43674	US2 protein - huma
532	61	5.7	317	2	H70566	hypothetical prote
533	61	5.7	322	2	T36941	probable transcrip
534	61	5.7	324	2	T37931	hypothetical coile
535	61	5.7	329	2	C97560	hypothetical prote
536	61	5.7	329	2	AB2781	amidohydrolase [im
537	61	5.7	340	1	WMBEL1	latency-related pr
538	61	5.7	345	2	B75274	conserved hypothet
539	61	5.7	347	2	AB2358	hypothetical prote
540	61	5.7	387	2	S59390	methionyl aminopep

541	61	5.7	388	2	C70605	probable aspartate
542	61	5.7	418	2	G70775	UDP-N-acetylglucos
543	61	5.7	424	2	A54964	spliceosome-associ
544	61	5.7	429	2	E87261	rRNA methyltransfe
545	61	5.7	429	2	AG2535	DNA polymerase III
546	61	5.7	434	2	S11967	nodule-specific hy
547	61	5.7	440	2	JL0144	interleukin-6 rece
548	61	5.7	472	2	A83331	probable two-compo
549	61	5.7	483	1	TVRTKA	protein kinase (EC
550	61	5.7	488	2	S27652	probable aldehyde
551	61	5.7	491	2	AC2233	hypothetical prote
552	61	5.7	492	1	A32525	steroid 21-monooxy
553	61	5.7	492	2	E75595	conserved hypothet
554	61	5.7	504	2	T13475	hypothetical prote
555	61	5.7	508	2	A82525	carboxyl-terminal
556	61	5.7	570	2	A47266	L-Ornithine N5-oxy
557	61	5.7	576	2	T46385	hypothetical prote
558	61	5.7	587	2	B70884	hypothetical prote
559	61	5.7	604	2	S39885	forked protein - f
560	61	5.7	604	2	A39369	homeotic protein B
561	61	5.7	611	2	A75573	probable oligoendo
562	61	5.7	656	2	D96831	hypothetical prote
563	61	5.7	669	2	S75785	translation elonga
564	61	5.7	712	2	T18195	gag protein - silk
565	61	5.7	769	2	T27550	hypothetical prote
566	61	5.7	803	2	T40475	bromeodomain prote
567	61	5.7	830	2	S56940	factor arrest prot
568	61	5.7	868	1	A45391	mRNA guanylyltrans
569	61	5.7	934	1	H71274	probable ankyrin -
570	61	5.7	1026	1	A40315	maternal effect pr
571	61	5.7	1112	2	T02848	hsp70-related prot
572	61	5.7	1137	2	G70868	probable regulator
573	61	5.7	1138	2	T36406	hypothetical prote
574	61	5.7	1160	2	S32647	parasporal crystal
575	61	5.7	1211	2	T42230	AF4 protein - mous
576	61	5.7	1361	2	T29435	hypothetical prote
577	61	5.7	1401	2	S77657	cyclic peptide syn
578	61	5.7	1645	2	H85554	hypothetical prote
579	61	5.7	1910	2	H88124	protein T12C9.3 [i
580	61	5.7	2100	2	T03223	probable polyketid
581	61	5.7	2222	2	T13924	sdk protein - frui
582	61	5.7	2339	2	A42566	omega-conotoxin-se
583	61	5.7	3436	2	S55659	tegument protein 6
584	61	5.7	8563	2	T30226	polyketide synthas
585	60.5	5.6	151	2	D87663	hypothetical prote
586	60.5	5.6	156	2	H83361	ArsC protein PA227
587	60.5	5.6	184	2	G83591	hypothetical prote
588	60.5	5.6	190	2	A35987	glioma-derived vas
589	60.5	5.6	190	2	B44881	vascular endotheli
590	60.5	5.6	195	2	G75488	hypothetical prote
591	60.5	5.6	202	2	AC0676	hydrogenase 1 matu
592	60.5	5.6	214	2	A44881	vascular endotheli
593	60.5	5.6	230	2	C75552	hypothetical prote
594	60.5	5.6	235	2	T14408	probable zinc-fing
595	60.5	5.6	237	2	T14409	probable zinc-fing
596	60.5	5.6	257	2	I50146	gene 17.5 protein
597	60.5	5.6	265	2	D84654	hypothetical prote
598	60.5	5.6	295	2	AG3240	conserved hypothet
599	60.5	5.6	300	2	D70733	hypothetical prote
600	60.5	5.6	316	2	T12516	hypothetical prote
601	60.5	5.6	337	2	B98041	conserved hypothet
602	60.5	5.6	337	2	D95175	conserved hypothet
603	60.5	5.6	356	2	S45330	thrombopoietin - m
604	60.5	5.6	359	2	A45156	alpha-(1,3)-fucosy
605	60.5	5.6	364	2	I39048	alpha (1,3) fucosy
606	60.5	5.6	366	2	I37527	MHC class I histoc
607	60.5	5.6	374	2	A42270	alpha (1,3) fucosy
608	60.5	5.6	381	2	F75270	cytochrome P450 -
609	60.5	5.6	393	2	T32533	hypothetical prote
610	60.5	5.6	400	2	S58222	PQ-rich protein -
611	60.5	5.6	407	2	A44374	3-carboxy-cis,cis-
612	60.5	5.6	410	2	AD2396	hypothetical prote
613	60.5	5.6	413	2	B82587	D-3-phosphoglycera
614	60.5	5.6	448	2	G70977	hypothetical prote
615	60.5	5.6	467	1	A49377	involucrin - mouse
616	60.5	5.6	473	2	S70357	forkhead transcrip
617	60.5	5.6	491	1	ACBOE	nicotinic acetylch
618	60.5	5.6	491	2	T19635	hypothetical prote
619	60.5	5.6	494	1	WJFFBC	homeotic protein b
620	60.5	5.6	505	1	S05380	transcription fact
621	60.5	5.6	507	2	JC7883	cytochrome P450 4X
622	60.5	5.6	511	2	D70507	hypothetical prote
623	60.5	5.6	522	2	AD1198	peptide chain rele
624	60.5	5.6	525	2	T00459	hypothetical prote
625	60.5	5.6	530	2	H72864	AcOrf-119 protein
626	60.5	5.6	542	2	S42089	Rot(57) protein -
627	60.5	5.6	544	2	D88449	protein F54D8.3 [i
628	60.5	5.6	547	1	S52489	choline oxidase (E
629	60.5	5.6	567	2	A45977	Rab geranylgeranyl
630	60.5	5.6	594	2	JT0766	transcription fact
631	60.5	5.6	595	2	H95899	hypothetical prote
632	60.5	5.6	619	2	AC0816	probable oxidoredu
633	60.5	5.6	628	2	T09785	hydroxymethylgluta
634	60.5	5.6	628	2	H83200	probable acetyl-co
635	60.5	5.6	647	1	I48737	LIM protein kinase
636	60.5	5.6	647	1	I58353	LIM protein kinase
637	60.5	5.6	676	2	T34609	probable helicase
638	60.5	5.6	699	2	A96802	unknown protein [i
639	60.5	5.6	722	2	S57246	ventral nervous sy
640	60.5	5.6	748	2	C82529	conserved hypothet
641	60.5	5.6	762	2	C96653	hypothetical prote
642	60.5	5.6	762	2	H83348	probable acylase P
643	60.5	5.6	778	2	AD2877	conserved hypothet
644	60.5	5.6	778	2	F97653	hypothetical prote
645	60.5	5.6	796	1	JV0107	glucose dehydrogen
646	60.5	5.6	796	2	H85495	glucose dehydrogen
647	60.5	5.6	796	2	H90644	glucose dehydrogen
648	60.5	5.6	806	2	T18840	hypothetical prote
649	60.5	5.6	841	2	C87331	ISCc2, transposase
650	60.5	5.6	868	2	A36878	dynamin 2 - rat
651	60.5	5.6	885	1	VGBESA	glycoprotein B pre
652	60.5	5.6	888	2	S64016	probable regulator
653	60.5	5.6	891	2	H75507	hypothetical prote
654	60.5	5.6	964	2	D59404	plectin isoform pl
655	60.5	5.6	1047	2	G87398	AcrB/AcrD/AcrF fam
656	60.5	5.6	1161	2	T45294	hypothetical prote
657	60.5	5.6	1173	2	I50620	procKr2 - chicken
658	60.5	5.6	1223	2	I38111	phosphorylase kina
659	60.5	5.6	1233	2	T30989	serine/threonine p
660	60.5	5.6	1235	2	S24109	phosphorylase kina
661	60.5	5.6	1300	2	T03166	probable immediate
662	60.5	5.6	1366	2	C85077	probable polyprote
663	60.5	5.6	1597	1	BVFFSL	sol protein, large
664	60.5	5.6	1597	2	T08428	gene small optic l
665	60.5	5.6	1616	2	B90704	Rhs core protein w
666	60.5	5.6	1618	2	S21424	nestin - human
667	60.5	5.6	1774	2	B56101	collagen alpha 1(X
668	60.5	5.6	1819	2	T32008	hypothetical prote
669	60.5	5.6	2767	1	UIHU	thyroglobulin prec
670	60.5	5.6	4391	2	A38096	perlecan precursor
671	60	5.6	116	2	E90716	hypothetical prote
672	60	5.6	157	2	C82121	phosphohistidine p
673	60	5.6	173	2	F70638	hypothetical prote
674	60	5.6	212	2	AB2992	hypothetical prote
675	60	5.6	212	2	H98291	hypothetical prote
676	60	5.6	227	2	I39313	zinc-finger protei
677	60	5.6	237	2	F84687	hypothetical prote
678	60	5.6	245	2	S57550	hypothetical prote
679	60	5.6	245	2	T27780	hypothetical prote
680	60	5.6	246	2	AC3024	transcription regu
681	60	5.6	253	2	AH3106	conserved hypothet
682	60	5.6	256	2	S63588	transcription coac
683	60	5.6	260	2	A75572	conserved hypothet
684	60	5.6	268	2	S71830	transcription coac
685	60	5.6	271	2	G83554	hypothetical prote
686	60	5.6	275	2	D98180	hypothetical prote

687	60	5.6	280	2	A22165	tropomyosin alpha
688	60	5.6	281	2	A87661	conserved hypothet
689	60	5.6	281	2	S49353	protein S2 - Phala
690	60	5.6	285	2	T34836	probable dehydrata
691	60	5.6	318	2	D72283	galactose-1-phosph
692	60	5.6	327	2	F98260	histidine utilizat
693	60	5.6	327	2	S63628	homeotic protein A
694	60	5.6	337	2	H87491	conserved hypothet
695	60	5.6	344	2	A70771	probable hydrolase
696	60	5.6	354	2	S62086	hrpQ protein - Pse
697	60	5.6	367	2	A34436	sex steroid-bindin
698	60	5.6	393	2	S25331	probable methionyl
699	60	5.6	393	2	S48398	outer mitochondria
700	60	5.6	402	2	A45056	osteogenic protein
701	60	5.6	423	2	E82611	conserved hypothet
702	60	5.6	424	2	T14358	transcription init
703	60	5.6	429	2	AH1009	sun protein [impor
704	60	5.6	436	2	T36490	probable transmemb
705	60	5.6	452	2	A82777	anthranilate synth
706	60	5.6	454	2	C64104	gamma-aminobutyrat
707	60	5.6	456	2	S76369	hypothetical prote
708	60	5.6	461	1	A35356	tumor necrosis fac
709	60	5.6	471	2	A81680	conserved hypothet
710	60	5.6	478	1	SGHU1V	vitronectin precur
711	60	5.6	524	2	T44889	probable aminopept
712	60	5.6	529	2	F69989	conserved hypothet
713	60	5.6	537	1	YRHUB6	tyrosinase-related
714	60	5.6	558	2	T50742	protoporphyrin IX
715	60	5.6	568	1	RRNZ73	polymerase-associa
716	60	5.6	574	1	JX0269	5'-nucleotidase (E
717	60	5.6	603	2	G82738	gamma-glutamyltran
718	60	5.6	604	2	S49804	phosphoprotein pho
719	60	5.6	616	2	C75588	conserved hypothet
720	60	5.6	641	2	T44585	acyl-CoA oxidase h
721	60	5.6	679	2	T00636	hypothetical prote
722	60	5.6	698	2	T17261	hypothetical prote
723	60	5.6	733	2	A45301	microtubule-associ
724	60	5.6	734	2	T02820	probable membrane
725	60	5.6	758	2	S60586	glucocorticoid rec
726	60	5.6	782	2	S04047	finger protein zfy
727	60	5.6	783	2	A31491	sex-determining re
728	60	5.6	784	1	SUECLA	endopeptidase La (
729	60	5.6	784	2	AE0558	Lon protease [impo
730	60	5.6	784	2	E90690	endopeptidase La [
731	60	5.6	785	2	G75578	aculeacin A acylas
732	60	5.6	786	2	T49414	related to ahmp1 p
733	60	5.6	799	2	A85541	hypothetical prote
734	60	5.6	806	2	A41341	microbial serine p
735	60	5.6	813	2	E87396	helicase, probable
736	60	5.6	827	2	A41672	glycerol-3-phospha
737	60	5.6	888	2	T31131	pyruvate, phosphat
738	60	5.6	889	2	S51465	hypothetical prote
739	60	5.6	955	2	B87237	conserved integral
740	60	5.6	1141	2	T29104	Tbc1 protein - mou
741	60	5.6	1171	2	T28701	probable polyketid
742	60	5.6	1281	2	JC5368	dynactin 1 - mouse
743	60	5.6	1291	2	T13389	hypothetical prote
744	60	5.6	1311	2	T08986	hypothetical prote
745	60	5.6	1469	2	T09219	basal transcriptio
746	60	5.6	1494	2	T14355	protein-tyrosine-p
747	60	5.6	1555	2	S38758	amylo-alpha-1,6-gl
748	60	5.6	1735	2	A57607	Munc13-1 - rat
749	60	5.6	1773	2	T05128	hypothetical prote
750	60	5.6	1822	2	T14106	probable GTPase-ac
751	60	5.6	2044	2	T13704	still life protein
752	60	5.6	2064	2	T13707	still life protein
753	60	5.6	2104	2	D91286	hypothetical prote
754	60	5.6	2104	2	H86127	hypothetical prote
755	60	5.6	2149	2	C96695	ribulose bisphosph
756	60	5.6	2237	2	T45115	N-type calcium cha
757	60	5.6	2241	2	T02857	conserved hypothet
758	60	5.6	2910	2	T42214	otogelin - mouse
759	59.5	5.5	82	2	S02326	antifreeze protein
760	59.5	5.5	146	1	A48897	aminoglycoside N6'
761	59.5	5.5	146	2	H97788	hypothetical prote
762	59.5	5.5	168	2	E83573	hypothetical prote
763	59.5	5.5	171	2	S72489	hypothetical prote
764	59.5	5.5	212	2	A72648	hypothetical prote
765	59.5	5.5	233	2	E97475	hypothetical prote
766	59.5	5.5	236	2	JQ0606	arylesterase (EC 3
767	59.5	5.5	237	2	G75261	cytidylate kinase
768	59.5	5.5	250	2	T09125	L-ascorbate peroxi
769	59.5	5.5	253	2	T17312	hypothetical prote
770	59.5	5.5	262	2	T17442	ybtT protein - Yer
771	59.5	5.5	267	2	AH0232	yersiniabactin bio
772	59.5	5.5	267	2	T47050	hypothetical prote
773	59.5	5.5	270	2	E87649	hypothetical prote
774	59.5	5.5	271	2	B83027	thiosulfate sulfur
775	59.5	5.5	282	2	S49352	protein S1 - Phala
776	59.5	5.5	294	2	G72706	hypothetical prote
777	59.5	5.5	311	2	T33899	hypothetical prote
778	59.5	5.5	329	2	D96030	hypothetical prote
779	59.5	5.5	338	2	B49642	POU-domain protein
780	59.5	5.5	357	2	A23641	RP2 protein, testo
781	59.5	5.5	359	2	AC0040	alanine racemase (
782	59.5	5.5	364	2	S45346	fructose-bisphosph
783	59.5	5.5	366	2	I37544	MHC class I histoc
784	59.5	5.5	366	2	I37523	MHC class I histoc
785	59.5	5.5	371	2	T36247	probable 4-hydroxy
786	59.5	5.5	376	2	C95988	probable oxidoredu
787	59.5	5.5	381	2	S16506	hypothetical prote
788	59.5	5.5	383	1	A44227	omega-3 fatty acid
789	59.5	5.5	384	2	G75567	conserved hypothet
790	59.5	5.5	386	1	JQ2335	omega-3 fatty acid
791	59.5	5.5	395	2	S75952	hypothetical prote
792	59.5	5.5	395	2	JQ0430	hypothetical 44.4K
793	59.5	5.5	418	2	T09969	UDP-N-acetylglucos
794	59.5	5.5	433	2	AI0891	conserved hypothet
795	59.5	5.5	448	2	A42026	cAMP response elem
796	59.5	5.5	456	2	B42026	cyclic AMP respons
797	59.5	5.5	460	2	JL0145	interleukin-6 rece
798	59.5	5.5	468	1	A54258	transcription fact
799	59.5	5.5	483	2	D87752	protein C18E3.6 [i
800	59.5	5.5	483	2	T15180	hypothetical prote
801	59.5	5.5	489	2	S68280	protein disulfide-
802	59.5	5.5	492	2	C83592	hypothetical prote
803	59.5	5.5	502	1	A34101	cytochrome P450 3A
804	59.5	5.5	503	2	JC7627	cytochrome P450 3A
805	59.5	5.5	519	1	YRHUR2	dopachrome isomera
806	59.5	5.5	522	2	AB1556	peptide chain rele
807	59.5	5.5	544	2	T24913	hypothetical prote
808	59.5	5.5	555	2	H83043	hypothetical prote
809	59.5	5.5	559	2	S54358	transcription fact
810	59.5	5.5	574	2	T30133	hypothetical prote
811	59.5	5.5	583	2	I50518	DNA binding protei
812	59.5	5.5	596	2	A46414	histidine protein
813	59.5	5.5	609	2	JC5838	albumin - Mongolia
814	59.5	5.5	612	2	T40936	probable leukotrie
815	59.5	5.5	615	2	F87599	hypothetical prote
816	59.5	5.5	622	2	A40144	prolactin receptor
817	59.5	5.5	635	1	WMBEW6	capsid protein - h
818	59.5	5.5	647	2	S06450	steroid hormone re
819	59.5	5.5	661	2	T27016	hypothetical prote
820	59.5	5.5	686	2	JC5708	villin-like protei
821	59.5	5.5	720	2	A36526	choline O-acetyltr
822	59.5	5.5	738	2	T27789	hypothetical prote
823	59.5	5.5	748	2	T35818	probable integral
824	59.5	5.5	755	2	D75598	photoreceptor - De
825	59.5	5.5	780	2	S62480	pumilio domain con
826	59.5	5.5	796	2	AG0523	glucose dehydrogen
827	59.5	5.5	902	2	A56823	DNA-directed RNA p
828	59.5	5.5	959	2	D83339	glycine cleavage s
829	59.5	5.5	961	2	A55380	faciogenital dyspl
830	59.5	5.5	966	2	S18955	fix23-3 protein -
831	59.5	5.5	1036	2	T17405	scavenger receptor
832	59.5	5.5	1051	2	A39712	kinase-like protei

833	59.5	5.5	1054	2	A61221	probable calcium t
834	59.5	5.5	1063	2	T34097	probable protein-t
835	59.5	5.5	1121	2	A82809	exodeoxyribonuclea
836	59.5	5.5	1172	2	T00065	hypothetical prote
837	59.5	5.5	1192	2	T17089	homeodomain-intera
838	59.5	5.5	1196	2	H86389	hypothetical prote
839	59.5	5.5	1225	2	F75605	minor tail protein
840	59.5	5.5	1239	2	I49705	glutamate receptor
841	59.5	5.5	1241	2	T18311	hypothetical prote
842	59.5	5.5	1245	2	E83110	exodeoxyribonuclea
843	59.5	5.5	1295	2	T30528	reverse transcript
844	59.5	5.5	1381	2	AF2010	regulatory protein
845	59.5	5.5	1407	2	T28702	probable polyketid
846	59.5	5.5	1584	2	T22674	hypothetical prote
847	59.5	5.5	1638	2	D87749	protein unc-73b [i
848	59.5	5.5	2145	2	JC4747	adenylate cyclase
849	59.5	5.5	2248	2	A35938	profilaggrin - hum
850	59.5	5.5	2488	2	T42739	guanine nucleotide
851	59.5	5.5	3133	2	S52093	hemocytin - silkwo
852	59	5.5	66	2	B83515	hypothetical prote
853	59	5.5	100	2	B83102	conserved hypothet
854	59	5.5	121	2	H87615	conserved hypothet
855	59	5.5	154	2	H83160	hypothetical prote
856	59	5.5	167	2	S76074	hypothetical prote
857	59	5.5	178	2	E95994	hypothetical prote
858	59	5.5	201	2	H70615	hypothetical prote
859	59	5.5	227	2	T50899	hypothetical membr
860	59	5.5	240	2	A39842	insulin-like growt
861	59	5.5	254	2	T35456	hypothetical prote
862	59	5.5	257	2	D70552	hypothetical prote
863	59	5.5	257	2	F72116	conserved hypothet
864	59	5.5	257	2	E86507	hypothetical prote
865	59	5.5	260	2	T18909	hypothetical prote
866	59	5.5	266	2	E84287	hypothetical prote
867	59	5.5	268	2	G70645	hypothetical prote
868	59	5.5	276	2	AF0402	transketolase (EC
869	59	5.5	293	1	B44502	nonstructural prot
870	59	5.5	296	2	B36864	OAC2 protein - Azo
871	59	5.5	310	2	A41776	syndecan 1 precurs
872	59	5.5	313	2	F72575	hypothetical prote
873	59	5.5	313	2	T35935	transcription regu
874	59	5.5	326	2	G84329	hypothetical prote
875	59	5.5	333	2	S51787	D-2-hydroxyisocapr
876	59	5.5	348	1	DEECOO	dihydroorotase (EC
877	59	5.5	348	2	D85668	dihydro-orotase [i
878	59	5.5	348	2	H90808	dihydro-orotase [i
879	59	5.5	350	2	S34136	ribosomal protein
880	59	5.5	352	2	C70578	hypothetical prote
881	59	5.5	354	2	H96021	probable glycosylt
882	59	5.5	363	2	D75423	hypothetical prote
883	59	5.5	377	2	G95923	probable glycosylt
884	59	5.5	384	2	AF2426	histidinol-phospha
885	59	5.5	408	2	A47488	aminoacylase (EC 3
886	59	5.5	412	2	T35514	probable glycosyl
887	59	5.5	416	2	D83386	hypothetical prote
888	59	5.5	417	2	F75303	aminopeptidase - D
889	59	5.5	421	2	I49734	HNF-3/fork-head ho
890	59	5.5	424	2	T14359	transcription init
891	59	5.5	443	1	S29334	transcription fact
892	59	5.5	445	1	A49447	transcription fact
893	59	5.5	445	1	S31224	transcription fact
894	59	5.5	466	2	A88868	protein T23B5.3 [i
895	59	5.5	471	1	B69904	conserved hypothet
896	59	5.5	472	2	G75298	ribosomal protein
897	59	5.5	474	2	S57239	gene forked protei
898	59	5.5	476	2	S57963	methyl CpG binding
899	59	5.5	477	2	T46666	N-ethylammeline ch
900	59	5.5	485	2	AB3042	aldehyde dehydroge
901	59	5.5	490	2	T25147	hypothetical prote
902	59	5.5	492	2	B98244	aldehyde dehydroge
903	59	5.5	494	2	S11305	cytochrome P450 2B
904	59	5.5	504	2	T43496	hypothetical prote
905	59	5.5	512	2	T49797	related to transcr
906	59	5.5	518	2	T13652	hypothetical prote
907	59	5.5	537	2	AF2785	lipoprotein [impor
908	59	5.5	539	2	H84640	probable Rieske ir
909	59	5.5	548	2	S42077	zinc finger protei
910	59	5.5	552	2	T16345	hypothetical prote
911	59	5.5	562	2	H97564	43K antigen (AF157
912	59	5.5	574	1	JC2001	5'-nucleotidase (E
913	59	5.5	574	1	S11032	5'-nucleotidase (E
914	59	5.5	605	1	QQBE29	BRLF1 protein - hu
915	59	5.5	612	2	T34290	hypothetical prote
916	59	5.5	633	2	T24898	hypothetical prote
917	59	5.5	634	2	G86160	protein F10G3.17 [
918	59	5.5	641	2	S57236	forked protein 2.5
919	59	5.5	648	2	A83792	acetyl-CoA synthet
920	59	5.5	655	1	A42420	L-iduronidase (EC
921	59	5.5	655	2	A59430	hypothetical prote
922	59	5.5	657	2	A29454	knob-associated hi
923	59	5.5	666	2	B70803	hypothetical prote
924	59	5.5	688	2	A56360	zinc finger protei
925	59	5.5	701	2	S06475	phenylalanine ammo
926	59	5.5	716	1	A40332	macrophage-stimula
927	59	5.5	724	2	T47149	hypothetical prote
928	59	5.5	759	2	B70585	hypothetical prote
929	59	5.5	775	1	EDBE11	immediate-early pr
930	59	5.5	785	2	D42515	D5R protein - vacc
931	59	5.5	796	1	A32434	abaA protein - Eme
932	59	5.5	837	1	S54429	outer membrane ush
933	59	5.5	846	2	S52418	GTP-binding regula
934	59	5.5	873	2	E83148	leucyl-tRNA synthe
935	59	5.5	923	2	I53280	progesterone recep
936	59	5.5	949	2	D82293	isoleucyl-tRNA syn
937	59	5.5	982	2	T43699	DNA mismatch repai
938	59	5.5	1006	2	AD2195	hypothetical prote
939	59	5.5	1013	2	I50615	receptor-type prot
940	59	5.5	1067	2	T04274	hypothetical prote
941	59	5.5	1106	1	TVHUGL	transforming prote
942	59	5.5	1121	2	JC7329	WD-repeat protein
943	59	5.5	1139	2	B54962	sterol regulatory
944	59	5.5	1141	2	A54962	sterol regulatory
945	59	5.5	1171	2	T35548	hypothetical prote
946	59	5.5	1191	2	T14154	serine/threonine p
947	59	5.5	1227	2	T20370	hypothetical prote
948	59	5.5	1240	2	T30834	nuclear protein SA
949	59	5.5	1248	2	C89874	autolysin [importe
950	59	5.5	1250	1	B45219	N-methyl-D-asparta
951	59	5.5	1275	2	D38164	cobN protein - Pse
952	59	5.5	1341	2	T17285	hypothetical prote
953	59	5.5	1436	2	S57238	forked protein 5.4
954	59	5.5	1447	2	A54100	tumor suppressor p
955	59	5.5	1449	2	S57237	forked protein 5.6
956	59	5.5	2022	2	T48818	glucan 1,4-alpha-g
957	59	5.5	2102	2	T15626	hypothetical prote
958	59	5.5	2110	2	B44110	mycocerosate synth
959	59	5.5	2115	2	S38480	nonstructural prot
960	59	5.5	2410	2	T43731	cell wall alpha-gl
961	59	5.5	3097	2	T00021	DN-cadherin - frui
962	59	5.5	3119	2	T18414	protein g377 - mal
963	59	5.5	3212	2	T24692	hypothetical prote
964	59	5.5	5032	1	A35041	ryanodine receptor
965	58.5	5.5	82	1	FDFLAW	antifreeze protein
966	58.5	5.5	93	2	C86764	hypothetical prote
967	58.5	5.5	102	2	T36634	probable transcrip
968	58.5	5.5	142	2	S62023	probable membrane
969	58.5	5.5	155	2	T30489	apoptosis inhibito
970	58.5	5.5	185	2	AG0577	molybdopterin-cont
971	58.5	5.5	198	2	S53911	ribosomal protein
972	58.5	5.5	199	2	AB2084	phosphonate metabo
973	58.5	5.5	200	1	WZBEA3	gene 4 protein - e
974	58.5	5.5	203	2	E75413	conserved hypothet
975	58.5	5.5	210	2	C75399	hypothetical prote
976	58.5	5.5	227	2	AD0997	probable competenc
977	58.5	5.5	232	2	A41551	vascular endotheli
978	58.5	5.5	237	2	T07820	hypothetical prote

979	58.5	5.5	239	2	T36572	hypothetical prote
980	58.5	5.5	247	2	D75055	hypothetical prote
981	58.5	5.5	248	2	A85747	probable DNA repli
982	58.5	5.5	248	2	A99872	probable DNA repli
983	58.5	5.5	255	2	AB0986	conserved hypothet
984	58.5	5.5	275	2	H83325	hypothetical prote
985	58.5	5.5	280	2	T50583	ABC-type transport
986	58.5	5.5	290	2	AE3519	isochorismatase (E
987	58.5	5.5	292	2	T25374	hypothetical prote
988	58.5	5.5	305	2	H75546	hypothetical prote
989	58.5	5.5	315	2	S74513	hypothetical prote
990	58.5	5.5	315	2	B84654	probable CCCH-type
991	58.5	5.5	316	2	S25843	bifunctional cycla
992	58.5	5.5	326	2	JC4125	thrombopoietin pre
993	58.5	5.5	331	2	T36969	probable phytoene
994	58.5	5.5	337	2	S60520	finger protein ZNF
995	58.5	5.5	352	2	C84199	hypothetical prote
996	58.5	5.5	353	2	B82828	dTDP-glucose 4,6-d
997	58.5	5.5	355	2	T02362	hypothetical prote
998	58.5	5.5	366	2	I61866	MHC HLA-Cw2.2 chai
999	58.5	5.5	373	2	AD0262	probable membrane
1000	58.5	5.5	378	2	H70548	hypothetical prote
1001	58.5	5.5	385	2	A82731	lipid A disacchari
1002	58.5	5.5	394	2	F89822	translational elon
1003	58.5	5.5	416	2	G86268	hypothetical prote
1004	58.5	5.5	422	2	I48305	gene COUP-TF1 prot
1005	58.5	5.5	432	2	T08771	hypothetical prote
1006	58.5	5.5	436	2	I49714	MHC H-2K/t-w5-link
1007	58.5	5.5	438	2	T12494	hypothetical prote
1008	58.5	5.5	439	2	F85189	disease resistance
1009	58.5	5.5	441	2	E86092	response regulator
1010	58.5	5.5	441	2	G91244	response regulator
1011	58.5	5.5	452	2	JC4100	hydroxyindole O-me
1012	58.5	5.5	471	2	S01037	flavonol 3-O-gluco
1013	58.5	5.5	471	2	T33997	hypothetical prote
1014	58.5	5.5	481	2	A56429	I-kappa-B-related
1015	58.5	5.5	483	2	E97255	transcription term
1016	58.5	5.5	489	2	S23410	FUN19 protein - ye
1017	58.5	5.5	491	2	A32969	cytochrome P450 2B
1018	58.5	5.5	494	2	I52658	neurofilament-66 -
1019	58.5	5.5	503	2	T00901	hypothetical prote
1020	58.5	5.5	504	2	A38221	chitinase (EC 3.2.
1021	58.5	5.5	506	2	D82715	competence related
1022	58.5	5.5	513	2	F84371	tryptophanyl-tRNA
1023	58.5	5.5	517	1	S19243	tyrosinase-related
1024	58.5	5.5	517	2	AG0157	probable carbohydr
1025	58.5	5.5	522	2	JC4532	cytochrome P450 4F
1026	58.5	5.5	527	1	SAHUP	saposin precursor
1027	58.5	5.5	530	2	F71445	hypothetical prote
1028	58.5	5.5	534	2	JC5096	transposase - fung
1029	58.5	5.5	540	2	B83121	probable AMP-bindi
1030	58.5	5.5	550	2	G70768	hypothetical prote
1031	58.5	5.5	568	2	AB3341	precorrin-3B C17-m
1032	58.5	5.5	577	2	T16333	hypothetical prote
1033	58.5	5.5	581	2	T04844	probable serine/th
1034	58.5	5.5	597	2	T21883	hypothetical prote
1035	58.5	5.5	600	2	B46642	DNA-directed DNA p
1036	58.5	5.5	605	2	A48115	transcription fact
1037	58.5	5.5	605	2	T01067	transcription fact
1038	58.5	5.5	610	2	T35222	hypothetical prote
1039	58.5	5.5	617	2	T52499	ferredoxin oxidore
1040	58.5	5.5	623	2	I46382	ZP1 precursor - mo
1041	58.5	5.5	644	2	T46277	hypothetical prote
1042	58.5	5.5	660	2	G82672	ATP sulfurylase, l
1043	58.5	5.5	679	2	B75262	conserved hypothet
1044	58.5	5.5	691	2	B85439	hypothetical prote
1045	58.5	5.5	701	2	JC8065	aryl hydrocarbon r
1046	58.5	5.5	717	2	T28829	hypothetical prote
1047	58.5	5.5	718	2	T22329	hypothetical prote
1048	58.5	5.5	720	2	T15756	hypothetical prote
1049	58.5	5.5	734	2	S37998	probable serine/th
1050	58.5	5.5	761	2	S20458	pqqF protein - Kle
1051	58.5	5.5	786	2	G82141	ATP-dependent LA p
1052	58.5	5.5	801	4	TVHURE	transforming prote
1053	58.5	5.5	829	2	A34692	ecdysone-induced p
1054	58.5	5.5	883	2	S04722	puff 74E protein -
1055	58.5	5.5	888	2	JC5399	dual leucine zippe
1056	58.5	5.5	906	2	A71438	probable resistanc
1057	58.5	5.5	925	2	E83529	sensor/response re
1058	58.5	5.5	957	2	T10633	hypothetical prote
1059	58.5	5.5	970	2	T28234	ORF MSV076 probabl
1060	58.5	5.5	1063	2	S18211	hypothetical prote
1061	58.5	5.5	1072	2	T50949	verprolin related
1062	58.5	5.5	1094	2	T00814	RNA-directed DNA p
1063	58.5	5.5	1132	2	T03844	telomerase catalyt
1064	58.5	5.5	1165	2	S11446	parasporal crystal
1065	58.5	5.5	1180	2	T20773	hypothetical prote
1066	58.5	5.5	1184	2	T09484	cartilage intermed
1067	58.5	5.5	1209	2	T14357	homeodomain-intera
1068	58.5	5.5	1297	2	T52065	probable myb-relat
1069	58.5	5.5	1314	2	A85176	hypothetical prote
1070	58.5	5.5	1348	2	AG2558	hypothetical prote
1071	58.5	5.5	1434	2	B36793	hypothetical prote
1072	58.5	5.5	1442	2	T42607	transcription acti
1073	58.5	5.5	1493	2	T10757	MAP kinase kinase
1074	58.5	5.5	1702	2	T14050	protein kinase (EC
1075	58.5	5.5	1892	2	T18314	hypothetical prote
1076	58.5	5.5	2288	2	S41080	calcium channel al
1077	58.5	5.5	3512	2	T17121	CPY protein - midg
1078	58.5	5.5	3635	2	T10053	laminin alpha 5 ch
1079	58.5	5.5	3649	1	S18268	delta-(L-alpha-ami
1080	58.5	5.5	4549	2	T20771	hypothetical prote
1081	58.5	5.5	4667	2	T20774	hypothetical prote
1082	58.5	5.5	7576	2	T17428	FK506 polyketide s
1083	58	5.4	112	2	S67489	cortistatin precur
1084	58	5.4	122	1	D71156	hypothetical prote
1085	58	5.4	131	2	T36958	hypothetical prote
1086	58	5.4	142	2	A71097	hypothetical prote
1087	58	5.4	152	2	A87261	hypothetical prote
1088	58	5.4	162	2	B83287	hypothetical prote
1089	58	5.4	163	2	AG2365	hypothetical prote
1090	58	5.4	176	2	G69163	hypothetical prote
1091	58	5.4	194	2	T00941	hypothetical prote
1092	58	5.4	214	2	D75576	oxidoreductase, ir
1093	58	5.4	221	2	T34554	hypothetical prote
1094	58	5.4	224	2	C48652	transfer protein s
1095	58	5.4	243	2	T13105	minor tail protein
1096	58	5.4	246	2	T37021	probable methyltra
1097	58	5.4	247	2	T27778	hypothetical prote
1098	58	5.4	248	2	AB0615	3-deoxy-manno-octu
1099	58	5.4	255	2	D87355	RNA pseudouridylat
1100	58	5.4	264	2	G86444	probable secretory
1101	58	5.4	269	2	I51708	brain-derived neur
1102	58	5.4	273	2	S37544	H+-transporting tw
1103	58	5.4	284	2	C83738	D-mannonate oxidor
1104	58	5.4	285	2	E75507	hypothetical prote
1105	58	5.4	289	2	T08176	glucose-1-phosphat
1106	58	5.4	295	2	G83638	hypothetical prote
1107	58	5.4	296	2	T00559	hypothetical prote
1108	58	5.4	302	2	A87369	copper-binding pro
1109	58	5.4	316	2	T44749	hypothetical prote
1110	58	5.4	318	2	H75490	proline iminopepti
1111	58	5.4	330	2	T01016	hypothetical prote
1112	58	5.4	340	2	JC7505	brain link protein
1113	58	5.4	346	2	G70448	transcription regu
1114	58	5.4	348	2	AF0193	dihydroorotase (EC
1115	58	5.4	357	2	T02785	probable homeotic
1116	58	5.4	363	2	S48697	probable G protein
1117	58	5.4	363	2	S74814	hypothetical prote
1118	58	5.4	374	2	F86632	pyruvate dehydroge
1119	58	5.4	374	2	T06276	benzothiadiazole-i
1120	58	5.4	381	2	T46884	3-methyl-2-oxobuta
1121	58	5.4	415	2	C70695	probable hydrolase
1122	58	5.4	439	2	G98073	beta-fructofuranos
1123	58	5.4	448	2	D71477	hypothetical prote
1124	58	5.4	458	2	B87647	hypothetical prote

1125	58	5.4	460	2	C84750	probable tyrosyl-t
1126	58	5.4	463	2	T33992	hypothetical prote
1127	58	5.4	478	2	T38014	hypothetical zinc
1128	58	5.4	482	2	E70554	hypothetical prote
1129	58	5.4	494	1	O4HUC2	steroid 21-monooxy
1130	58	5.4	494	2	T14729	betaine-aldehyde d
1131	58	5.4	494	2	AD3255	l-sorbose dehydrog
1132	58	5.4	498	2	S11246	LAG-3 protein prec
1133	58	5.4	521	1	ACFFNN	nicotinic acetylch
1134	58	5.4	524	2	E75574	aldehyde dehydroge
1135	58	5.4	527	2	JE0373	low density lipopr
1136	58	5.4	532	2	T35119	probable aminotran
1137	58	5.4	533	2	E86207	hypothetical prote
1138	58	5.4	537	2	D86299	hypothetical prote
1139	58	5.4	564	2	I53106	gene gli protein -
1140	58	5.4	594	2	D96015	probable tartronat
1141	58	5.4	595	2	T41007	atp dependent heli
1142	58	5.4	604	2	T35793	probable ATP/GTP b
1143	58	5.4	631	2	B86251	hypothetical prote
1144	58	5.4	634	1	S35574	transcription fact
1145	58	5.4	635	2	D64835	ABC-type transport
1146	58	5.4	651	2	B32891	finger protein 2,
1147	58	5.4	717	2	F82613	VacB protein XF198
1148	58	5.4	756	2	S47656	tMDC II protein -
1149	58	5.4	776	1	VPXRB3	outer layer protei
1150	58	5.4	776	2	I48317	cyclin F - mouse
1151	58	5.4	784	2	AC0383	endopeptidase La (
1152	58	5.4	819	2	A82549	phage-related prot
1153	58	5.4	852	2	T28790	hypothetical prote
1154	58	5.4	858	2	E72419	flagellar hook-ass
1155	58	5.4	870	2	B53165	dynamin II isoform
1156	58	5.4	870	2	A53165	dynamin II isoform
1157	58	5.4	943	2	T03306	PSD-95/SAP90-assoc
1158	58	5.4	1003	2	F81731	glycyl-tRNA synthe
1159	58	5.4	1019	2	T00117	dve protein - frui
1160	58	5.4	1027	2	T46481	hypothetical prote
1161	58	5.4	1097	1	S47220	protein kinase C (
1162	58	5.4	1118	2	A48292	mucin, tracheobron
1163	58	5.4	1203	2	T17415	mycelial surface a
1164	58	5.4	1227	2	A33638	erythrocyte anion
1165	58	5.4	1232	2	I38496	anion exchanger 3
1166	58	5.4	1346	2	A57376	probable regulator
1167	58	5.4	1438	2	AI0093	conserved hypothet
1168	58	5.4	1460	1	EDBEIF	immediate-early pr
1169	58	5.4	1770	2	T18551	saframycin Mx1 syn
1170	58	5.4	1959	1	AGRT	agrin - rat
1171	58	5.4	2231	2	S53416	SEN1 protein - yea
1172	58	5.4	2761	2	T21064	hypothetical prote
1173	58	5.4	2843	1	RBHUAP	adenomatous polypo
1174	58	5.4	3305	2	T18358	apolipophorin prec
1175	58	5.4	3491	2	T43231	probable 6-deoxyer
1176	58	5.4	4162	2	T42633	connectin/titin -
1177	58	5.4	4180	2	G83559	hypothetical prote
1178	58	5.4	4613	2	T17409	polyketide synthas
1179	58	5.4	4767	2	T31345	hypothetical prote
1180	58	5.4	4836	2	T14346	herc2 protein - mo
1181	57.5	5.4	82	2	JS0706	antifreeze protein
1182	57.5	5.4	83	2	AB2558	hypothetical prote
1183	57.5	5.4	123	2	T23448	hypothetical prote
1184	57.5	5.4	133	2	D87593	hypothetical prote
1185	57.5	5.4	155	2	T42422	hypothetical prote
1186	57.5	5.4	155	2	T41556	hypothetical prote
1187	57.5	5.4	160	2	E82710	conserved hypothet
1188	57.5	5.4	168	2	A71184	probable ferredoxi
1189	57.5	5.4	194	2	S70990	hypothetical prote
1190	57.5	5.4	199	2	D95378	conserved hypothet
1191	57.5	5.4	202	2	E72466	hypothetical prote
1192	57.5	5.4	210	2	AB3420	hypothetical phage
1193	57.5	5.4	221	2	S49374	conserved hypothet
1194	57.5	5.4	222	2	T16381	hypothetical prote
1195	57.5	5.4	228	2	C70623	hypothetical prote
1196	57.5	5.4	231	2	D72532	hypothetical prote
1197	57.5	5.4	241	2	D83584	probable phosphori
1198	57.5	5.4	244	1	TVMVFB	transforming prote
1199	57.5	5.4	244	2	E83098	hypothetical prote
1200	57.5	5.4	254	1	S39876	gufA protein - Myx
1201	57.5	5.4	255	2	AD0463	high-affinity bran
1202	57.5	5.4	261	2	S72895	hypothetical prote
1203	57.5	5.4	273	2	T34672	probable gntR fami
1204	57.5	5.4	282	2	F83063	isopentenyl monoph
1205	57.5	5.4	293	2	G82282	vibriobactin-speci
1206	57.5	5.4	293	2	D86602	AMP nucleosidase [
1207	57.5	5.4	293	2	A72021	AMP nucleosidase-r
1208	57.5	5.4	312	2	T37922	hypothetical prote
1209	57.5	5.4	318	2	JC4963	metalloproteinase
1210	57.5	5.4	321	2	T50875	hypothetical elect
1211	57.5	5.4	326	2	G83261	conserved hypothet
1212	57.5	5.4	334	2	G75344	probable polyferre
1213	57.5	5.4	351	2	T12728	structural protein
1214	57.5	5.4	357	2	E70696	hypothetical prote
1215	57.5	5.4	361	2	A36669	3-alpha-galactosyl
1216	57.5	5.4	366	2	T21454	hypothetical prote
1217	57.5	5.4	371	2	A53908	brevican precursor
1218	57.5	5.4	373	2	T23372	hypothetical prote
1219	57.5	5.4	375	2	S35941	homeotic protein H
1220	57.5	5.4	375	2	I50589	transcription fact
1221	57.5	5.4	385	2	T25492	hypothetical prote
1222	57.5	5.4	387	2	AG3218	acetylornithine de
1223	57.5	5.4	397	2	T09579	nuclear protein EM
1224	57.5	5.4	398	2	B75448	hypothetical prote
1225	57.5	5.4	398	2	A69101	conserved hypothet
1226	57.5	5.4	400	2	T25889	hypothetical prote
1227	57.5	5.4	401	2	C71483	probable nifS-rela
1228	57.5	5.4	418	2	JX0129	contrapsin precurs
1229	57.5	5.4	419	2	A57000	orphan receptor CO
1230	57.5	5.4	423	2	S02710	transcription fact
1231	57.5	5.4	428	2	T32952	hypothetical prote
1232	57.5	5.4	430	2	T36892	hypothetical prote
1233	57.5	5.4	430	2	T12541	hypothetical prote
1234	57.5	5.4	432	2	F83883	hypothetical prote
1235	57.5	5.4	439	2	C95209	sucrose-6-phosphat
1236	57.5	5.4	441	1	B33862	transcription regu
1237	57.5	5.4	446	2	S32871	regulatory protein
1238	57.5	5.4	450	2	AB1023	alpha-galactosidas
1239	57.5	5.4	452	2	F71826	ATP-dependent prot
1240	57.5	5.4	455	2	S50725	hypothetical prote
1241	57.5	5.4	461	1	JX0210	protein C (activat
1242	57.5	5.4	492	2	S32951	regulatory protein
1243	57.5	5.4	505	2	S57672	hypothetical prote
1244	57.5	5.4	511	2	T00868	probable cytochrom
1245	57.5	5.4	529	2	T10388	hypothetical prote
1246	57.5	5.4	574	2	T29747	hypothetical prote
1247	57.5	5.4	576	2	A42236	protein-tyrosine-p
1248	57.5	5.4	579	2	T04378	peptide transport
1249	57.5	5.4	592	2	T32402	hypothetical prote
1250	57.5	5.4	597	2	JQ0107	hypothetical 66K p
1251	57.5	5.4	600	2	H75516	probable maltoolig
1252	57.5	5.4	602	1	A35385	hydrogen dehydroge
1253	57.5	5.4	616	2	T46292	hypothetical prote
1254	57.5	5.4	633	2	C84475	hypothetical prote
1255	57.5	5.4	659	2	A36664	S59/2 homeotic pro
1256	57.5	5.4	662	1	TQBPU	transposase - phag
1257	57.5	5.4	665	2	JC7191	85K c-Cbl-interact
1258	57.5	5.4	729	2	A45716	leukemia virus cel
1259	57.5	5.4	760	2	D87553	exoribonuclease, V
1260	57.5	5.4	764	2	I51302	myosin heavy chain
1261	57.5	5.4	769	2	B87681	tyrosine kinase Di
1262	57.5	5.4	792	2	T21276	hypothetical prote
1263	57.5	5.4	837	2	T12531	hypothetical prote
1264	57.5	5.4	838	2	T08423	Axin homolog Axil
1265	57.5	5.4	855	2	S56948	HAL5 protein - yea
1266	57.5	5.4	877	2	T43449	hypothetical prote
1267	57.5	5.4	883	2	S49126	brevican precursor
1268	57.5	5.4	939	2	AE2275	hypothetical prote
1269	57.5	5.4	941	2	A70722	probable gcvB prot
1270	57.5	5.4	982	2	T15967	hypothetical prote

1271	57.5	5.4	1015	1	TQECT	transposase - Esch
1272	57.5	5.4	1028	2	AF3286	ATP-dependent DNA
1273	57.5	5.4	1106	2	JQ0405	hypothetical 119.5
1274	57.5	5.4	1114	1	S05582	protein-tyrosine k
1275	57.5	5.4	1152	2	F86363	hypothetical prote
1276	57.5	5.4	1216	2	T34101	hypothetical prote
1277	57.5	5.4	1296	2	T13936	collar protein iso
1278	57.5	5.4	1321	2	JE0352	mucin MUC5B, trach
1279	57.5	5.4	1321	2	T29308	hypothetical prote
1280	57.5	5.4	1372	2	T29309	hypothetical prote
1281	57.5	5.4	1487	1	EDBEE1	immediate-early pr
1282	57.5	5.4	1487	1	EDBEF6	155K transcription
1283	57.5	5.4	1496	2	T00499	probable retroelem
1284	57.5	5.4	1931	2	A59234	slow myosin heavy
1285	57.5	5.4	1957	2	S68453	sodium channel pro
1286	57.5	5.4	1958	2	B40505	hypothetical prote
1287	57.5	5.4	2225	2	T26063	hypothetical prote
1288	57.5	5.4	2364	2	A56577	microtubule-associ
1289	57.5	5.4	2500	2	G88493	protein F57B9.2 [i
1290	57.5	5.4	2774	2	A43359	microtubule-associ
1291	57.5	5.4	3075	2	S14458	laminin alpha-1 ch
1292	57.5	5.4	3227	2	T37964	probable ubiquitin
1293	57.5	5.4	4548	1	S00657	apoprotein(a) (EC
1294	57.5	5.4	13055	2	T16580	hypothetical prote
1295	57	5.3	113	2	E72648	hypothetical prote
1296	57	5.3	123	2	T34746	hypothetical prote
1297	57	5.3	152	2	AG0067	conserved hypothet
1298	57	5.3	153	2	S48998	hypothetical prote
1299	57	5.3	185	2	A83156	molybdopterin bios
1300	57	5.3	223	2	T37004	probable hydrolase
1301	57	5.3	227	2	B70790	hypothetical prote
1302	57	5.3	237	2	A84720	hypothetical prote
1303	57	5.3	245	2	T24565	hypothetical prote
1304	57	5.3	248	2	A71106	hypothetical prote
1305	57	5.3	248	2	S16417	homeotic protein H
1306	57	5.3	250	2	T31835	hypothetical prote
1307	57	5.3	265	2	S34668	nodulation protein
1308	57	5.3	267	2	G83206	hypothetical prote
1309	57	5.3	268	1	PKSMR	kanamycin kinase (
1310	57	5.3	269	2	T42919	protein tio - atel
1311	57	5.3	270	1	A64367	pyruvate synthase
1312	57	5.3	275	2	F83243	probable hydrolase
1313	57	5.3	289	2	T35950	hypothetical prote
1314	57	5.3	296	2	S21306	hypothetical prote
1315	57	5.3	299	2	T18563	hypothetical prote
1316	57	5.3	303	2	G70756	hypothetical prote
1317	57	5.3	311	2	G83249	probable arginase
1318	57	5.3	316	2	T36909	probable dihydropi
1319	57	5.3	325	2	B72475	probable transcrip
1320	57	5.3	331	2	A42482	cathepsin S (EC 3.
1321	57	5.3	337	2	A53041	effector cell prot
1322	57	5.3	354	2	A82544	translation initia
1323	57	5.3	354	2	S39406	homeotic protein o
1324	57	5.3	355	2	S35345	otx1 protein - mou
1325	57	5.3	355	2	I56547	homeodomain protei
1326	57	5.3	359	2	G81984	3-dehydroquinate s
1327	57	5.3	360	1	E64130	alanine racemase (
1328	57	5.3	369	2	AF0966	probable transfera
1329	57	5.3	382	2	C84050	thiamin biosynthes
1330	57	5.3	383	2	AF0141	8-amino-7-oxononan
1331	57	5.3	384	2	S03815	probable integrase
1332	57	5.3	385	2	H95413	probable integrase
1333	57	5.3	386	2	T35438	probable secreted
1334	57	5.3	388	2	D75496	aspartate transami
1335	57	5.3	401	2	T42374	conserved hypothet
1336	57	5.3	405	2	T32274	hypothetical prote
1337	57	5.3	409	2	C83607	D-3-phosphoglycera
1338	57	5.3	416	2	S75321	serine/threonine-s
1339	57	5.3	421	2	B86973	probable membrane
1340	57	5.3	423	1	XXPS2M	dihydrolipoamide S
1341	57	5.3	426	2	S54812	probable ketoacyl
1342	57	5.3	441	2	H70632	hypothetical prote
1343	57	5.3	452	2	T30082	hypothetical prote
1344	57	5.3	455	2	C83494	probable 2-isoprop
1345	57	5.3	461	2	T05979	hypothetical prote
1346	57	5.3	469	2	G69825	transcription regu
1347	57	5.3	479	2	A75353	mocR protein - Dei
1348	57	5.3	482	2	JC5092	E-selectin - pig
1349	57	5.3	483	2	F75360	hypothetical prote
1350	57	5.3	484	2	T51070	hypothetical prote
1351	57	5.3	510	2	S10724	surface protein pr
1352	57	5.3	515	2	F70786	probable pepA - My
1353	57	5.3	519	2	D70695	hypothetical prote
1354	57	5.3	527	2	T41856	AcMNPV orf119 - Bo
1355	57	5.3	552	1	S35703	colony-stimulating
1356	57	5.3	552	1	A31401	macrophage colony-
1357	57	5.3	563	2	E85855	PTS system, fructo
1358	57	5.3	563	2	C91011	fructose-specific
1359	57	5.3	563	2	A34962	phosphotransferase
1360	57	5.3	566	1	HMIVSA	hemagglutinin prec
1361	57	5.3	569	2	AB0005	probable exported
1362	57	5.3	572	1	B43675	64K protein - infe
1363	57	5.3	578	2	B71431	hypothetical prote
1364	57	5.3	602	1	JQ0806	hydrogenase (EC 1.
1365	57	5.3	604	2	B84221	hypothetical prote
1366	57	5.3	627	2	E71353	hypothetical prote
1367	57	5.3	628	2	S19150	hypothetical prote
1368	57	5.3	631	2	T00925	hypothetical prote
1369	57	5.3	660	1	QQBE3	BHLF1 protein - hu
1370	57	5.3	662	2	T04856	hypothetical prote
1371	57	5.3	671	2	A65023	hypothetical prote
1372	57	5.3	703	1	WMBET7	UL17 protein - hum
1373	57	5.3	763	2	T24367	hypothetical prote
1374	57	5.3	765	2	H91238	formate acetyltran
1375	57	5.3	765	2	E86086	formate acetyltran
1376	57	5.3	800	2	AF3262	hypothetical prote
1377	57	5.3	837	2	A42112	mucin-like peptide
1378	57	5.3	857	2	JC4169	phosphoenolpyruvat
1379	57	5.3	866	1	JC4305	dynamin II - human
1380	57	5.3	885	2	S76357	penicillin-binding
1381	57	5.3	955	2	A60990	alpha-amylase (EC
1382	57	5.3	955	2	T00247	zinc finger protei
1383	57	5.3	964	2	JC5545	integrin beta-4 pr
1384	57	5.3	986	2	A87590	hypothetical prote
1385	57	5.3	1006	2	JC5526	kinase-defective E
1386	57	5.3	1040	2	T29092	TSC-22 protein hom
1387	57	5.3	1067	2	T30061	hypothetical prote
1388	57	5.3	1136	1	S57845	protein-tyrosine k
1389	57	5.3	1160	2	A27868	lethal (2) giant l
1390	57	5.3	1161	2	A27069	lethal (2) giant l
1391	57	5.3	1199	2	T18348	probable pol polyp
1392	57	5.3	1206	2	D84542	probable chloropla
1393	57	5.3	1221	2	A49457	fibulin-2 precurso
1394	57	5.3	1245	1	MMMSND	nidogen precursor
1395	57	5.3	1265	2	F88886	protein F52G2.2 [i
1396	57	5.3	1323	2	S27224	N-methyl-D-asparta
1397	57	5.3	1323	2	T30253	spalt protein - mo
1398	57	5.3	1373	2	JE0095	gastric mucin MUC5
1399	57	5.3	1417	2	T21012	hypothetical prote
1400	57	5.3	1561	2	T00248	zinc finger protei
1401	57	5.3	1621	2	T30200	protein-tyrosine k
1402	57	5.3	1626	2	A75613	hypothetical prote
1403	57	5.3	1682	1	C70588	probable mbtE prot
1404	57	5.3	1762	2	T03222	probable polyketid
1405	57	5.3	1802	2	T00020	bacterial blight-r
1406	57	5.3	1844	2	S01956	hypothetical prote
1407	57	5.3	1944	2	A55117	tsg24 protein - mo
1408	57	5.3	1985	2	S19151	hypothetical prote
1409	57	5.3	2025	2	T21588	hypothetical prote
1410	57	5.3	2073	1	BWASBE	bimE protein - Eme
1411	57	5.3	2215	2	T00348	LR11 protein - mou
1412	57	5.3	2215	2	T16871	hypothetical prote
1413	57	5.3	2295	2	C88369	protein unc-52 [im
1414	57	5.3	2517	2	S58380	probable RNA-direc
1415	57	5.3	2944	2	A54849	collagen alpha 1(V
1416	57	5.3	3375	2	T19821	hypothetical prote

1417	57	5.3	3498	2	T22330	hypothetical prote
1418	57	5.3	5035	1	I46646	ryanodine receptor
1419	57	5.3	5037	2	B35041	ryanodine receptor
1420	57	5.3	5376	2	T42215	zonadhesin - mouse
1421	56.5	5.3	117	2	H72706	hypothetical prote
1422	56.5	5.3	119	2	T46478	hypothetical prote
1423	56.5	5.3	126	2	H95331	hypothetical prote
1424	56.5	5.3	135	2	F72688	hypothetical prote
1425	56.5	5.3	135	2	H72531	hypothetical prote
1426	56.5	5.3	151	2	B45696	23-29K immunoreact
1427	56.5	5.3	164	2	F87438	hypothetical prote
1428	56.5	5.3	173	2	A75512	hypothetical prote
1429	56.5	5.3	184	2	G87480	hypothetical prote
1430	56.5	5.3	194	2	T17381	vrlB protein - Dic
1431	56.5	5.3	200	2	E83539	hypothetical prote
1432	56.5	5.3	204	2	T28939	hypothetical prote
1433	56.5	5.3	219	2	F69341	conserved hypothet
1434	56.5	5.3	230	2	H75343	SUA5-related prote
1435	56.5	5.3	238	2	T34710	hypothetical prote
1436	56.5	5.3	243	2	D83504	probable transcrip
1437	56.5	5.3	248	1	LNHUPS	pulmonary surfacta
1438	56.5	5.3	263	2	T25665	hypothetical prote
1439	56.5	5.3	267	2	T30344	irp4 protein - Yer
1440	56.5	5.3	283	2	B75263	thiosulfate sulfur
1441	56.5	5.3	283	2	C87346	hypothetical prote
1442	56.5	5.3	313	2	A46233	FLAT element-bindi
1443	56.5	5.3	324	2	S44956	lmbI protein - Str
1444	56.5	5.3	328	2	AB0905	conserved hypothet
1445	56.5	5.3	328	2	H87359	transcription regu
1446	56.5	5.3	352	2	JC7781	hematopoietic Src
1447	56.5	5.3	355	2	F87213	conserved membrane
1448	56.5	5.3	355	2	B96499	hypothetical prote
1449	56.5	5.3	357	2	A39798	RP2 protein, testo
1450	56.5	5.3	358	1	A55973	transcription fact
1451	56.5	5.3	359	2	S14283	transcription fact
1452	56.5	5.3	366	2	I81231	lymphocyte antigen
1453	56.5	5.3	368	2	C70809	hypothetical prote
1454	56.5	5.3	377	1	JQ2337	omega-3 fatty acid
1455	56.5	5.3	380	1	TVMSF	transforming prote
1456	56.5	5.3	401	2	T18568	hypothetical prote
1457	56.5	5.3	413	2	A82726	conserved hypothet
1458	56.5	5.3	416	2	F75434	hypothetical prote
1459	56.5	5.3	421	2	A60058	neural cell adhesi
1460	56.5	5.3	423	2	C84024	hypothetical prote
1461	56.5	5.3	430	2	AB0811	probable transcrip
1462	56.5	5.3	434	2	G83133	probable two-compo
1463	56.5	5.3	435	2	E86515	oligopeptide bindi
1464	56.5	5.3	435	2	C72107	peptide ABC transp
1465	56.5	5.3	440	1	XXHUN	phosphatidylcholin
1466	56.5	5.3	442	2	A45529	heat shock protein
1467	56.5	5.3	444	2	C75509	probable integrase
1468	56.5	5.3	444	2	AE0646	hypothetical prote
1469	56.5	5.3	452	2	B69229	conserved hypothet
1470	56.5	5.3	458	2	T36455	probable deoxyribo
1471	56.5	5.3	463	2	D87201	conserved hypothet
1472	56.5	5.3	464	2	T50734	regulatory protein
1473	56.5	5.3	470	2	T46814	gamma-aminobutyrat
1474	56.5	5.3	470	2	B95419	diaminobutyrate-py
1475	56.5	5.3	473	2	A48949	beta-glucosidase,
1476	56.5	5.3	493	2	T07374	fumarate hydratase
1477	56.5	5.3	493	2	T48219	hypothetical prote
1478	56.5	5.3	500	1	JT0482	glucokinase (EC 2.
1479	56.5	5.3	503	2	T05347	hypothetical prote
1480	56.5	5.3	516	2	H70935	hypothetical prote
1481	56.5	5.3	524	2	C86299	F3O9.20 protein -
1482	56.5	5.3	526	2	T13687	hypothetical prote
1483	56.5	5.3	529	2	C75453	GMC oxidoreductase
1484	56.5	5.3	552	1	TVMVT3	transforming prote
1485	56.5	5.3	555	2	A87458	sensor histidine k
1486	56.5	5.3	564	2	AD1550	heat shock protein
1487	56.5	5.3	576	2	T22461	hypothetical prote
1488	56.5	5.3	578	2	B37852	phosphotransferase
1489	56.5	5.3	580	2	H86189	hypothetical prote
1490	56.5	5.3	580	2	A37107	spermatogenesis pr
1491	56.5	5.3	581	2	B84715	hypothetical prote
1492	56.5	5.3	586	2	S19381	hypothetical prote
1493	56.5	5.3	607	2	A83726	sulfite reductase
1494	56.5	5.3	629	1	BVECQA	glucose inhibited
1495	56.5	5.3	629	2	C91214	glucose-inhibited
1496	56.5	5.3	629	2	D86060	glucose-inhibited
1497	56.5	5.3	642	2	S18667	deoxyribodipyrimid
1498	56.5	5.3	644	2	C86747	topoisomerase IV s
1499	56.5	5.3	645	2	G01205	TYL protein - huma
1500	56.5	5.3	648	2	H85056	probable receptor-

ALIGNMENTS

RESULT 1
B45351
immediate-early protein 2 - saimiriine herpesvirus 1 (strain 11)
N;Alternate names: hypothetical protein ORF13
C;Species: saimiriine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: B45351; D36807
R;Nicholas, J.; Smith, E.P.; Coles, L.; Honess, R.
Virology 179, 189-200, 1990
A;Title: Gene expression in cells infected with gammaherpesvirus saimiri: properties of
A;Reference number: A45351; MUID:91021021; PMID:1699352
A;Accession: B45351
A;Molecule type: mRNA
A;Residues: 1-151 <NIC>
A;Cross-references: UNIPARC:UPI00001384DB; GB:M60286; NID:g331040; PIDN:AAA46156.1; PID:
R;Albrecht, J.
submitted to the EMBL Data Library, January 1992
A;Description: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A36806
A;Accession: D36807
A;Molecule type: DNA
A;Residues: 1-151 <ALB>
A;Cross-references: UNIPARC:UPI00001384DB; GB:X64346; NID:g60320; PIDN:CAA45636.1; PID:g
R;Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; Wi
J. Virol. 66, 5047-5058, 1992
A;Title: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A37309; MUID:92333688; PMID:1321287
A;Contents: annotation; protein-coding frames
A;Note: neither protein nor nucleotide sequence is given
C;Genetics:
A;Gene: 13
C;Superfamily: saimiri herpesvirus immediate-early protein 2
C;Keywords: early protein

Query Match 15.0%; Score 160.5; DB 1; Length 151;
Best Local Similarity 28.6%; Pred. No. 1.1e-07;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

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Qy         36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEE 95
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Db         18 CIVKSEITSAQTPRCLAA-----NNSFPRSVMVTLSIRNWNTSSKRAS------------ 60

Qy         96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSL 155
                 | : || |||     : |:|||  :  |:|   ||::|  |     :||| : | :
Db         61 ----DYYNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQQEI 115

Qy        156 LVLRR--RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                ||:|:  :||            :|  | : | ||||| |
Db        116 LVVRKGHQPCPN----------SFRLEKMLVTVGCTCVTP 145
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RESULT 2
JC4628
cytotoxic T-lymphocyte-associated antigen 8 precursor - mouse
N;Alternate names: CTLA8 protein
C;Species: Mus musculus (house mouse)

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C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4628
R;Yao, Z.; Timour, M.; Painter, S.; Fanslow, W.; Spriggs, M.
Gene 168, 223-225, 1996
A;Title: Complete nucleotide sequence of the mouse CTLA8 gene.
A;Reference number: JC4628; MUID:96194901; PMID:8654948
A;Accession: JC4628
A;Molecule type: DNA
A;Residues: 1-147 <YAO>
A;Cross-references: UNIPROT:Q62386; UNIPARC:UPI000016CB50; GB:U35108; NID:g1244499; PIDN
C;Genetics:
A;Gene: ctla8
A;Introns: 69/2
C;Superfamily: saimiri herpesvirus immediate-early protein 2
C;Keywords: cytokine; glycoprotein; lymphocyte
F;1-14/Domain: signal sequence #status predicted <SIG>
F;15-147/Product: cytotoxic T-lymphocyte-associated antigen 8 #status predicted <MAT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             13.8%;  Score 148.5;  DB 2;  Length 147;
  Best Local Similarity   37.6%;  Pred. No. 1.4e-06;
  Matches   38;  Conservative   13;  Mismatches   35;  Indels   15;  Gaps    3;

Qy          92 RPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRL 151
               || : |      || |||    : | ||||  :  |:|  : |::|  |:    :||| :
Db          54 RPSDYL-----NRSTSPWTLHRNEDPDRYPSVIWEAQCRHQRCVNAE-GKLDHHMNSVLI 107

Qy         152 LQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
               | :|||:| | |           | |  | : | ||||||
Db         108 QQEILVLKREPES---------CPFTFRVEKMLVGVGCTCV 139


RESULT 3
I49623
cytotoxic T-lymphocyte-associated antigen 8 precursor - mouse
N;Alternate names: immediate-early protein 2 (ORF13) homolog
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 26-Aug-1999
C;Accession: I49623
R;Rouvier, E.; Luciani, M.
J. Immunol. 150, 5445-5456, 1993
A;Title: CTLA-8, cloned from an activated T cell, bearing AU-rich messenger RNA instabil
A;Reference number: I49623; MUID:93294300; PMID:8390535
A;Accession: I49623
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-150 <RES>
A;Cross-references: UNIPARC:UPI000012D484; GB:L13839; NID:g293329; PIDN:AAA37490.1; PID:
C;Genetics:
A;Gene: Ctla-8
C;Superfamily: saimiri herpesvirus immediate-early protein 2

  Query Match             13.8%;  Score 148.5;  DB 2;  Length 150;
  Best Local Similarity   29.4%;  Pred. No. 1.4e-06;
  Matches   45;  Conservative   20;  Mismatches   55;  Indels   33;  Gaps    5;

Qy          42 LPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADT 101
               :|      |:  |         : : :::||    | :    |||                 |
Db          21 IPQSSVCPNAEANNFLQNVKVNLKVINSL---SSKASSRRPS----------------DY 61

Qy         102 HQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRR 161
               || |||    : | ||||  :  |:|  : |::|  |:    :||| : | :|||:|
Db          62 LNRSTSPWTLSRNEDPDRYPSVIWEAQCRHQRCVNAE-GKLDHHMNSVLIQQEILVLKRE 120

Qy         162 P--CSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
               |  |           | |  | : | ||||||
Db         121 PEKC----------PFTFRVEKMLVGVGCTCV 142


RESULT 4
T21334
hypothetical protein F25D1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21334
R;Kelly, P.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19408
A;Accession: T21334
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-148 <WIL>
A;Cross-references: UNIPROT:Q19778; UNIPARC:UPI0000164258; EMBL:Z73973; PIDN:CAA98268.1;
A;Experimental source: clone F25D1
C;Genetics:
A;Gene: CESP:F25D1.3
A;Map position: 5
A;Introns: 60/2

  Query Match             10.3%;  Score 110;  DB 2;  Length 148;
  Best Local Similarity   33.0%;  Pred. No. 0.0051;
  Matches   31;  Conservative   17;  Mismatches   34;  Indels   12;  Gaps    4;

Qy         103 QRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRP 162
               :|:: ||  ||:  | | |: :| : |||       |  | :     : ::: : :|||
Db          51 ERALCPWDSRVNYQESREPKLIAESVCLC------RKSRGSTGAFCMPIVRKVPILRRVS 104

Qy         163 CSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRS 196
               | |  :||     :   || |   |||  ||||:
Db         105 CDR-STGL---WNYVRSTELI--TVGCHSVLPRT 132


RESULT 5
KISMG
galactokinase (EC 2.7.1.6) - Streptomyces sp.
C;Species: Streptomyces sp.
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-Oct-2004
C;Accession: C28669
R;Adams, C.W.; Fornwald, J.A.; Schmidt, F.J.; Rosenberg, M.; Brawner, M.E.
J. Bacteriol. 170, 203-212, 1988
A;Title: Gene organization and structure of the Streptomyces lividans gal operon.
A;Reference number: A28669; MUID:88086869; PMID:3335481
A;Accession: C28669
A;Molecule type: DNA
A;Residues: 1-395 <ADA>
A;Cross-references: UNIPROT:P13227; UNIPARC:UPI00001427A8; GB:M18953; NID:g153259; PIDN:
A;Note: the source is designated as Streptomyces lividans
C;Genetics:
A;Gene: galK
C;Superfamily: galactokinase
C;Keywords: ATP; galactose metabolism; phosphotransferase

  Query Match              8.7%;  Score 93.5;  DB 1;  Length 395;
  Best Local Similarity   29.5%;  Pred. No. 0.51;
  Matches   44;  Conservative   15;  Mismatches   79;  Indels   11;  Gaps    5;

Qy          32 GTPHCYSAEELPLGQAPPHLLARG-AKW----GQALPVALVSSLEAASHRGRHERPSATT 86
               |||   :    | |::|     || | |    | : | |  |:  ||    |  |  |:|
Db         183 GTPSSSTPATSPSGRSPSTSPPRGCACWSSTPGSSTPTARASTASAARAARRAPRCWAST 242

Qy          87 QC--PVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETA 144
               :|  |     :  ||    :  :       | |:::|  : :|  |    |       | |
Db         243 RCDVPYADLDAALERLGDEEEVRRLVRHVVTEDERVERVVALLESATPGASAPSWSRATP 302

Qy         145 ALNSVRLLQSLLVLRRRPCSRDGSGLPTP 173
               |    | |  ||  |  |  | | ||  |
Db         303 A---ARRLPHLLP-RAGPGRRHGPGLRGP 327


RESULT 6
T50809
hypothetical protein T30N20_270 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50809
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
```

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submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25240
A;Accession: T50809
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <BEV>
A;Cross-references: UNIPROT:Q9LEU1; UNIPARC:UPI00000A3D68; EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
C;Genetics:
A;Map position: 5
A;Note: T30N20_270

  Query Match             8.1%;  Score 86.5;  DB 2;  Length 389;
  Best Local Similarity   23.0%;  Pred. No. 2.2;
  Matches   56;  Conservative   25;  Mismatches   83;  Indels   79;  Gaps   10;

Qy          6 GLLFLTWLHTCLAHHDPSLRGHP---HSHGTPHCYSAEELPLGQAPP-HL----LA---- 53
              |: :|||  | |  |  :|  |    ::| :|  :|: :| |  |   ||    ||
Db         44 GVFYLTWSRTFLGGHSVNLFLHSQDYYNHSSPLSFSSADLSLSSAVSFHLNLNTLAFWKK 103

Qy         54 RGAK---------WG-------------QALPVALV----------SSLEAASHRGRHER 81
              ||::          |                  :|:|          |:: |  | :  :
Db        104 RGSRFVSPKIQVFWDLSKAKFDSGSEPRSGFYIAVVVDGEMGLLVGDSVKEAYARAKSAK 163

Qy         82 PSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDAR--- 138
              |    | :|| | |  |              || | : |:  |        ||   ||:
Db        164 PPTNPQALLLRKEHVFGA-----------RVFTTKARFGGKNREISIDCRVDEDAKLCF 211

Qy        139 -----------------TGRETAALNSVRLLQSLLV---LRRRPCSRDGSGLPTPGAFAF 178
                              | |   :: | :  |  |   | :   | || |      | |
Db        212 SVDSKQVLQIKRLRWKFRGNEKVEIDGVHVQISWDVYNWLFQSKSSGDGGGGGGHAVFMF 271

Qy        179 HTE 181
                |
Db        272 RFE 274


RESULT 7
JL0032
hypothetical 31.7K protein (aphE region) - Streptomyces griseus
C;Species: Streptomyces griseus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL0032
R;Heinzel, P.; Werbitzky, O.; Distler, J.; Piepersberg, W.
Arch. Microbiol. 150, 184-192, 1988
A;Title: A second streptomycin resistance gene from Streptomyces griseus codes for strep
A;Reference number: JL0031; MUID:88339496; PMID:2844130
A;Accession: JL0032
A;Molecule type: DNA
A;Residues: 1-297 <HEI>
A;Cross-references: UNIPROT:Q99391; UNIPARC:UPI00000AFA54; GB:M37378; GB:X56876; NID:g15
A;Experimental source: strain N2-3-11
A;Note: the function of the protein is unknown; the orf1 gene and aphE (streptomyces-3"-
C;Genetics:
A;Gene: orf1
C;Superfamily: Streptomyces griseus hypothetical 31.7K protein (aphE region)

  Query Match             8.0%;  Score 86;  DB 2;  Length 297;
  Best Local Similarity   27.4%;  Pred. No. 1.8;
  Matches   40;  Conservative   15;  Mismatches   55;  Indels   36;  Gaps    7;

Qy         48 PPHLLARGAKWGQALPVAL---------VSSLEAASH------RGRHERPSA-----TTQ 87
              |  ||  |  | :  |: |           ||:|  :       ||  :|  |       |
Db         28 PSRLLLLG--WNRRAPLVLDQLRSTARTGSSVEVVADSAVPGPRGTEDRQPAGRDVRFRQ 85

Qy         88 CPVLRPEEVLEADTHQRS----ISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRET 143
              |: ||| :|  |  :      : | |      |   :|         |    :| ||||||
Db         86 APLSRPETLLGLDLDRYDAVVVLGPDR----GDGPDHPDDWTLVALLAVRLLDGRTGRET 141

Qy        144 AALNSVRLLQSLLVLRRRPCSRDGSG 169
                 |::  |:  | || :   ||
Db        142 ------RVVTELVDDRNRPLAPVNSG 161


RESULT 8
A42091
transcription activator SNF2/SWI2 homolog brm - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42091
R;Tamkun, J.W.; Deuring, R.; Scott, M.P.; Kissinger, M.; Pattatucci, A.M.; Kaufman, T.C.
Cell 68, 561-572, 1992
A;Title: brahma: a regulator of Drosophila homeotic genes structurally related to the ye
A;Reference number: A42091; MUID:92154670; PMID:1346755
A;Accession: A42091
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1638 <TAM>
A;Cross-references: UNIPROT:P25439; UNIPARC:UPI000016BB03; GB:M85049; NID:g157011; PIDN:
A;Experimental source: iso-1
A;Note: sequence extracted from NCBI backbone (NCBIN:82354, NCBIP:82360)
C;Genetics:
A;Gene: FlyBase:brm
A;Cross-references: FlyBase:FBgn0000212
C;Superfamily: human SNF2alpha protein; bromodomain homology
C;Keywords: transcription regulation
F;1451-1506/Domain: bromodomain homology <BRO>

  Query Match             7.9%;  Score 84.5;  DB 2;  Length 1638;
  Best Local Similarity   22.2%;  Pred. No. 17;
  Matches   42;  Conservative   26;  Mismatches   70;  Indels   51;  Gaps    8;

Qy         22 PSLRGHPHSHGTPHCYSAEELPLGQAPPH----LLARGAKWGQALPVALVSSLEAASHRG 77
              |   |||  || |      :  |    |||    : ::|    |  :|    :    : ::
Db         52 PGAYGHPMQHGPP----GQGPPGHHMPPHHQGMIFSKGPHMGMQMP---PTGPNMSPYQT 104

Qy         78 RHERPSATTQCPVLR----------PEEVLEADTH--QRSISPWRYRVDTDEDRYPQKLA 125
                 |:| ||  ::           ||   : : |  ||:|      :   :: || | ||
Db        105 HGMPPNAPTQPCIVSPGGPPGGPPPPERSSQENLHALQRAIDSMEEKGLQEDPRYSQLLA 164

Qy        126 FAECLCRGCIDARTGRETAALNSVRLLQS-----LLVLRRRPCSRD-------------- 166
                    : | :  :    | | ||::      |: | :| |
Db        165 ---------MRATSKHQHLNGNQVNLLRTQITAYRLLARNKPISMQMQQALQAAQQQPPP 215

Qy        167 GSGLPTPGA 175
                |  :  |||
Db        216 GPPIGPPGA 224


RESULT 9
S76371
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76371
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76371
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-635 <KAN>
A;Cross-references: UNIPROT:Q55694; UNIPARC:UPI000012B455; EMBL:D64000; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: gidA protein

  Query Match             7.7%;  Score 82.5;  DB 2;  Length 635;
  Best Local Similarity   24.2%;  Pred. No. 9;
  Matches   44;  Conservative   21;  Mismatches   60;  Indels   57;  Gaps    8;

Qy         19 HHDPSLRGHPHSHGTPHCYSAEEL--------------PLGQAPPHLLARGAKWG--QA 61
              |  |   |  | |  :| | |:                | |:  | |  :|   |  :
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```
Db        267 HLSPIYGGFIDSKGPRYCPSIEDKIVRFADKESHQIFIEPEGRDIPELYIQGFSTGLPEN 326

Qy         62 LPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYP 121

Db        327 VQLAMLQTLPGLEN-----------CVMLRPAYAVEYDFLPAT-----------QCYP 362

Qy        122 QKLA--FAECLCRGCIDARTGRETAA-------LNSVRLLQ--SLLVLRRRPCSRDGSGL 170

Db        363 SLMTKKVAGLFCAGQINGTTGYEEAAAQGLVAGINAARHCQGKSLIIF-----SREGSYL 417

Qy        171 PT 172

Db        418 GT 419


RESULT 10
T23218
hypothetical protein K02B12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Feb-2000
C;Accession: T23218
R;Harris, B.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19710
A;Accession: T23218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-325 <WIL>
A;Cross-references: UNIPARC:UPI0000177DB7; EMBL:Z75711; PIDN:CAB00031.1; GSPDB:GN00019;
A;Experimental source: clone K02B12
C;Genetics:
A;Gene: CESP:K02B12.1
A;Map position: 1
A;Introns: 155/2; 189/3; 234/3; 268/3
C;Superfamily: transcription factor Pit-1; homeobox homology; POU domain homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

  Query Match             7.6%;  Score 81.5;  DB 2;  Length 325;
  Best Local Similarity   25.9%;  Pred. No. 5.3;
  Matches   29;  Conservative   14;  Mismatches   54;  Indels   15;  Gaps    4;

Qy          9 FLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVS 68

Db         12 FQDWPHTPMLYQQPQLHFMLPQHDWAYPHLAQSLP----PPHHLTPS--------TAAVA 59

Qy         69 SLEAASHRGRHERPSATTQCPVLR-PEEVLEADTHQRSISPW--RYRVDTDE 117

Db         60 AATIASQSSIINQTSVVTSTPSCQIKQEVERPEIIQRLMPPWPPAYQFSCDD 111


RESULT 11
D83640
hypothetical protein PA0049 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83640
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83640
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-553 <STO>
A;Cross-references: UNIPROT:Q9I783; UNIPARC:UPI00000C4F03; GB:AE004444; GB:AE004091; NID
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0049

  Query Match             7.5%;  Score 81;  DB 2;  Length 553;
  Best Local Similarity   24.2%;  Pred. No. 11;
  Matches   55;  Conservative   16;  Mismatches   72;  Indels   84;  Gaps   13;

Qy         12 WLHTCLAHHDPSLRGHPHSHGTPHCYSAEELP-----------LGQAPPHLLARG----- 55

Db        305 WLEAWNGRFHGSSAG---NDGIVYCPADSALPNYVLPLGSVTNPGTAPISLRGSGCNINP 361

Qy         56 ----------AKWGQALPVALVSS-------LEAASHRGRHERPSATTQCPVLRPEEVLE 98

Db        362 PRRWLGYDSASRWRQNLPAQFSKASLPVRQLLAADTWRGIERPPGATSQA-----AEGFD 416

Qy         99 ADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSV--RLLQSLL 156

Db        417 VTWH-----------TNYDFFPD-----------CANPRT--ENVPTNGVMNAMPDPSL 451

Qy        157 VL--RRRPCSRDGSG---LPTPGAF-------AFHTEF----IHVPV 187

Db        452 VLPPNRRICARNGGGGDYLSNESAYRNTVLRDAFRLEIPAGHIHVPV 498


RESULT 12
B40203
4-alpha-glucanotransferase (EC 2.4.1.25) / amylo-1,6-glucosidase (EC 3.2.1.33) - pig (fra
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 16-Aug-2002
C;Accession: B40203
R;Yang, B.Z.; Ding, J.H.; Enghild, J.J.; Bao, Y.; Chen, Y.T.
J. Biol. Chem. 267, 9294-9299, 1992
A;Title: Molecular cloning and nucleotide sequence of cDNA encoding human muscle glycoger
A;Reference number: A40203; MUID:92250533; PMID:1374391
A;Accession: B40203
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-210 <YAN>
A;Cross-references: UNIPARC:UPI0000178DB6
C;Superfamily: 4-alpha-glucanotransferase / amylo-1,6-glucosidase
C;Keywords: glycosidase; glycosyltransferase; hexosyltransferase; hydrolase; polysacchari

  Query Match             7.5%;  Score 80.5;  DB 2;  Length 210;
  Best Local Similarity   25.3%;  Pred. No. 4.1;
  Matches   50;  Conservative   17;  Mismatches   76;  Indels   55;  Gaps   10;

Qy         22 PSLRGHPHSHGT--PHCYS-AEELPLG---QAPPHLLARGAKWGQALPVALVSSLEAASH 75

Db          3 PTLQGKPVTVYTNYPSCYSLADQLELNPDFSRPPK-----KEWNMLCITDVVYNHTAANS 57

Qy         76 RGRHERPSAT--------------TQCPVLRPEEV---LEADTHQRSISPWRYRVDTDED 118

Db         58 RWLHEHPECAYNLVNSPHHKALWHLSCDVAEGRGVPALIENDHHMNSI-----RLIIWED 112

Qy        119 RYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTP----- 173

Db        113 IFPKELIQWGDQVKQAYDA------------LPSSTIV--SMACCASGSTKWNPAASPS 157

Qy        174 --GAFAFHTEFIHVPVGC 189

Db        158 DTGEVNFQSGIIEVPQVC 175


RESULT 13
A70509
hypothetical protein Rv1230c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: A70509
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome s
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70509
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
```

```
A;Molecule type: DNA
A;Residues: 1-411 <COL>
A;Cross-references: UNIPROT:O86313; UNIPARC:UPI00000CCBBB; GB:Z98260; GB:AL123456; NID:g
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1230c

  Query Match             7.5%;  Score 80;  DB 2;  Length 411;
  Best Local Similarity   23.7%;  Pred. No. 9.5;
  Matches   45;  Conservative   23;  Mismatches   78;  Indels   44;  Gaps   10;

Qy          5 PGLLFLTWLHTCLAHHDPSLRGHPHSHGTP----HCYSAEELPLGQAPPHLLARGAKWGQ 60
              |    |  : |  |    | :   | : | |       |   || :  | |     |  |
Db         85 PPTSFRVAVATISAPPPPMIVNSPGALGIPAMALSAYRNAELKMAAAAP---GCGVSWNL 141

Qy         61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRP---------EEVLEAD-----THQRSI 106
                 :  : |: |    |        |   |:  |          | ::::      |: |::
Db        142 LAGIGRIESMHA---NGGATDARGTAIQPIYGPTLDGTLPGNEIIIQSSVGNRVTYARAM 198

Qy        107 SP-------W-RYRVDTDED-------RYPQKLAFAECLCRGCIDARTGRET-AAL---- 146
               |       | ||  | |:|       :   || |  || | :: |   :  |||
Db        199 GPMQFLPGTWARYATDGDDDGVADPQNLFDSTLAAARYLCSGGLNLRDPAQVMAALLRYN 258

Qy        147 NSVRLLQSLL 156
              ||:   |::|
Db        259 NSMPYAQNVL 268


RESULT 14
JC7753
ring finger B-box coiled-coil protein, GOA - human
C;Species: Homo sapiens (man)
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: JC7753
R;Vandeputte, D.A.A.; Meije, C.B.; van Dartel, M.; Leenstra, S.; IJlst-Keizers, H.; Das,
Biochem. Biophys. Res. Commun. 286, 574-579, 2001
A;Title: GOA, a novel gene encoding a ring finger B-box coiled-coil protein, is overexpr
A;Reference number: JC7753; MUID:21402356; PMID:11511098
A;Accession: JC7753
A;Molecule type: DNA
A;Residues: 1-638 <VAN>
A;Cross-references: UNIPROT:Q96LD4; UNIPARC:UPI000013CE62; GB:AY026763
C;Comment: This protein, a member of the subfamily of the ring finger proteins, has an i
as well.
C;Genetics:
A;Gene: goa
A;Map position: 17q24-25

  Query Match             7.4%;  Score 79.5;  DB 2;  Length 638;
  Best Local Similarity   30.3%;  Pred. No. 17;
  Matches   36;  Conservative   10;  Mismatches   56;  Indels   17;  Gaps    6;

Qy         40 EELPLGQAPPHLLARGAKWGQALPVAL--VSSLEA--ASHRGRHERPSATTQCPVLRPEE 95
              |  | |: |  :       | ||| ||  :| | :   :| | |||  |     :: |
Db        118 EPWPAGEEP--VRCDACPEGAALPAALSCLSCLASFCPAHLGPHERSPALRGHRLVPPLR 175

Qy         96 VLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGC-IDARTGRETAALNSVRLLQ 153
               ||     | : |         :|| :  |   |||  |       | |   |   | ||
Db        176 RLEESLCPRHLRPL--------ERYCR--AERVCLCEACAAQEHRGHELVPLEQERALQ 224


RESULT 15
I37386
fas-activated serine/threonine kinase - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I37386
R;Tian, Q.; Taupin, J.; Elledge, S.; Robertson, M.; Anderson, P.
J. Exp. Med. 182, 865-874, 1995
A;Title: Fas-activated serine/threonine kinase (FAST) phosphorylates TIA-1 during Fas-me
A;Reference number: I37386; MUID:95378805; PMID:7544399
A;Accession: I37386
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-549 <RES>
A;Cross-references: UNIPROT:Q14296; UNIPARC:UPI0000000CBA; EMBL:X86779; NID:g1006658; PI
C;Genetics:
A;Gene: fast
C;Superfamily: human fas-activated serine/threonine kinase

  Query Match             7.4%;  Score 79;  DB 2;  Length 549;
  Best Local Similarity   28.6%;  Pred. No. 16;
  Matches   56;  Conservative   12;  Mismatches   58;  Indels   70;  Gaps   12;

Qy         13 LHTCLAHHDPSLRGHPHSHGTPHCYSAEE--LPLGQAPPHLLARGAKWGQALPVA----- 65
              :| ||  |    | | | | |    |   :|  | |   ||  |    : ||| |  |
Db        158 IHVCL--HLAVLLGFP-SDGPLVCALEQERRLRLPPKPPPPLQPLLRGGQGLEAALSCPR 214

Qy         66 --------LVSSL-EA-------------ASHRGRHERPSATTQCPVLRPEEVLEADTH- 102
                     |:||| ||             | |  ||           ||  ::|||  |
Db        215 FLRYPRQHLISSLAEARPEELTPHVMVLLAQHLARHR----------LREPQLLEAIAHF 264

Qy        103 ------------QRSISPW---RYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAAL 146
                         |: : |:    |         | :  |  || |  | ||     | |
Db        265 LVVQETQLSSKVVQKLVLPFGRLNY--------LPLEQQFMPCLER--ILAREA-GVAPL 313

Qy        147 NSVRLLQSLLVLRRRP 162
               :| :| ||  ||  |
Db        314 ATVNILMSLCQLRCLP 329


Search completed: April 27, 2006, 17:19:23
Job time : 46 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 27, 2006, 17:18:50 ; Search time 226 Seconds
(without alignments)
614.996 Million cell updates/sec

Title: US-09-854-280-3
Perfect score: 1073
Sequence: 1 MTLLPGLLFLTWLHTCLAHH.....FHTEFIHVPVGCTCVLPRSV 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1073	100.0	197	1	IL17C_HUMAN	Q9p0m4 homo sapien
2	788	73.4	194	2	Q8K4C5_MOUSE	Q8k4c5 mus musculu
3	199	18.5	202	1	IL17D_HUMAN	Q8tad2 homo sapien
4	199	18.5	202	2	Q5VUZ7_HUMAN	Q5vuz7 homo sapien
5	197.5	18.4	153	2	Q5BJ95_RAT	Q5bj95 rattus norv
6	193	18.0	169	2	Q8VHH8_MOUSE	Q8vhh8 mus musculu
7	186	17.3	153	2	Q8VHC9_MOUSE	Q8vhc9 mus musculu
8	184	17.1	153	2	Q8K4C3_MOUSE	Q8k4c3 mus musculu
9	184	17.1	161	2	Q7TNI7_MOUSE	Q7tni7 mus musculu
10	183	17.1	205	2	Q8K4C4_MOUSE	Q8k4c4 mus musculu
11	182	17.0	212	2	Q5TKT1_BRARE	Q5tkt1 brachydanio
12	179	16.7	171	2	Q6L5M6_CIOIN	Q6l5m6 ciona intes
13	177.5	16.5	167	2	Q5TKT2_BRARE	Q5tkt2 brachydanio
14	177.5	16.5	203	2	Q6DIY0_XENTR	Q6diy0 xenopus tro
15	173	16.1	153	1	IL17F_HUMAN	Q96pd4 homo sapien
16	173	16.1	163	2	Q6NSI0_HUMAN	Q6nsi0 homo sapien
17	168.5	15.7	180	1	IL17B_MOUSE	Q9qxt6 mus musculu
18	165.5	15.4	177	1	IL17B_HUMAN	Q9h293 homo sapien
19	165	15.4	169	2	Q5XP68_CHICK	Q5xp68 gallus gall
20	165	15.4	169	2	Q7T1P7_CHICK	Q7t1p7 gallus gall
21	163.5	15.2	162	2	Q4RTP8_TETNG	Q4rtp8 tetraodon n
22	163.5	15.2	206	2	Q70I20_ONCMY	Q70i20 oncorhynchu
23	160.5	15.0	151	1	VG13_SHV21	P24916 saimiriine
24	158	14.7	155	1	IL17_HUMAN	Q16552 homo sapien
25	158	14.7	155	2	Q5T2P0_HUMAN	Q5t2p0 homo sapien
26	157.5	14.7	151	1	VG13_SHV2C	O40633 saimiriine
27	157.5	14.7	151	2	Q778B0_9GAMA	Q778b0 saimiriine
28	157.5	14.7	153	2	Q60I29_PIG	Q60i29 sus scrofa
29	157.5	14.7	178	1	IL17B_MESAU	Q9eqi6 mesocricetu
30	157	14.6	141	2	Q95L56_BOVIN	Q95l56 bos taurus
31	157	14.6	153	2	Q687Y7_BOVIN	Q687y7 bos taurus
32	154.5	14.4	180	1	IL17B_HUMAN	Q9uhf5 homo sapien
33	151.5	14.1	171	2	Q6L5M5_CIOIN	Q6l5m5 ciona intes
34	151	14.1	155	2	Q6NZ94_HUMAN	Q6nz94 homo sapien
35	150.5	14.0	180	2	Q6IAG3_HUMAN	Q6iag3 homo sapien
36	148.5	13.8	150	1	IL17_RAT	Q61453 rattus norv
37	148.5	13.8	158	1	IL17_MOUSE	Q62386 mus musculu
38	148.5	13.8	158	2	Q544E6_MOUSE	Q544e6 mus musculu
39	142	13.2	162	2	Q5TKT0_BRARE	Q5tkt0 brachydanio
40	141	13.1	186	2	Q6L5M4_CIOIN	Q6l5m4 ciona intes
41	141	13.1	196	2	Q8K599_MOUSE	Q8k599 mus musculu
42	129.5	12.1	111	2	Q9EQI7_RAT	Q9eqi7 rattus norv
43	124	11.6	153	2	Q5TKT4_BRARE	Q5tkt4 brachydanio
44	121.5	11.3	146	2	Q70I21_ONCMY	Q70i21 oncorhynchu
45	119	11.1	189	2	Q19778_CAEEL	Q19778 caenorhabdi
46	118.5	11.0	82	2	Q5U4M4_XENLA	Q5u4m4 xenopus lae
47	113	10.5	145	2	Q61JV0_CAEBR	Q61jv0 caenorhabdi
48	110	10.3	140	2	Q5TKT3_BRARE	Q5tkt3 brachydanio
49	97.5	9.1	539	2	Q4RFD4_TETNG	Q4rfd4 tetraodon n
50	95.5	8.9	93	2	Q9BEH5_HORSE	Q9beh5 equus cabal
51	91.5	8.5	898	2	Q4SPV1_TETNG	Q4spv1 tetraodon n
52	89.5	8.3	168	2	Q9XDC3_HERSE	Q9xdc3 herbaspiril
53	89.5	8.3	521	2	Q9DPS2_9ALPH	Q9dps2 meleagrid h
54	88.5	8.2	314	2	Q6NX20_XENTR	Q6nx20 xenopus tro
55	88.5	8.2	521	2	Q9E1H8_9ALPH	Q9e1h8 meleagrid h
56	88	8.2	266	2	Q6AGG8_LEIXX	Q6agg8 leifsonia x
57	88	8.2	2161	1	SHAN1_HUMAN	Q9y566 homo sapien
58	87.5	8.2	345	2	Q6ZH77_ORYSA	Q6zh77 oryza sativ
59	87.5	8.2	1755	2	Q80WC3_MOUSE	Q80wc3 mus musculu
60	87	8.1	306	2	Q5GYT2_XANOR	Q5gyt2 xanthomonas
61	87	8.1	1084	2	Q4P4N5_USTMA	Q4p4n5 ustilago ma
62	86.5	8.1	296	2	Q8NBR1_HUMAN	Q8nbr1 homo sapien
63	86.5	8.1	363	2	Q4RQA9_TETNG	Q4rqa9 tetraodon n
64	86.5	8.1	389	2	Q9LEU1_ARATH	Q9leu1 arabidopsis
65	86.5	8.1	1280	2	Q5B3K4_EMENI	Q5b3k4 aspergillus
66	86	8.0	297	2	Q99391_STRGR	Q99391 streptomyce
67	86	8.0	1098	2	Q9JL71_MOUSE	Q9jl71 mus musculu
68	86	8.0	2126	2	Q6P4S8_MOUSE	Q6p4s8 mus musculu
69	85.5	8.0	458	2	Q7NCB6_GLOVI	Q7ncb6 gloeobacter
70	85.5	8.0	465	1	HNF6_HUMAN	Q9ubc0 homo sapien
71	85.5	8.0	465	1	HNF6_MOUSE	O08755 mus musculu
72	85.5	8.0	465	1	HNF6_RAT	P70512 rattus norv
73	85.5	8.0	486	2	Q4SQ55_TETNG	Q4sq55 tetraodon n
74	84.5	7.9	225	2	Q86UU4_HUMAN	Q86uu4 homo sapien
75	84.5	7.9	317	2	Q9BTV9_HUMAN	Q9btv9 homo sapien
76	84.5	7.9	341	2	Q86W42_HUMAN	Q86w42 homo sapien
77	84.5	7.9	1344	2	Q670Z5_FUGRU	Q670z5 fugu rubrip
78	84.5	7.9	1638	1	BRM_DROME	P25439 drosophila
79	84	7.8	341	2	Q6AY87_RAT	Q6ay87 rattus norv
80	84	7.8	354	2	Q9SE51_ARATH	Q9se51 arabidopsis
81	84	7.8	382	2	Q7VW62_BORPE	Q7vw62 bordetella
82	84	7.8	402	2	Q4TND2_9SPHN	Q4tnd2 erythrobact
83	84	7.8	422	2	Q4RKC0_TETNG	Q4rkc0 tetraodon n
84	84	7.8	719	2	Q4TAY1_TETNG	Q4tay1 tetraodon n
85	83.5	7.8	532	2	Q4Q0P4_LEIMA	Q4q0p4 leishmania
86	83	7.7	306	2	Q8PLD8_XANAC	Q8pld8 xanthomonas
87	83	7.7	371	2	Q82RU9_STRAW	Q82ru9 streptomyce
88	83	7.7	708	2	Q4WTE2_ASPFU	Q4wte2 aspergillus
89	83	7.7	961	2	Q6AXH5_MOUSE	Q6axh5 mus musculu
90	83	7.7	1030	2	Q68FE9_MOUSE	Q68fe9 mus musculu
91	83	7.7	1059	2	Q5DTF1_MOUSE	Q5dtf1 mus musculu
92	83	7.7	1147	2	Q4NXG9_9DELT	Q4nxg9 anaeromyxob
93	83	7.7	1214	2	Q4QED7_LEIMA	Q4qed7 leishmania
94	83	7.7	1792	2	Q4PCP7_USTMA	Q4pcp7 ustilago ma
95	83	7.7	2429	2	Q4HZ37_GIBZE	Q4hz37 gibberella
96	82.5	7.7	635	1	GIDA_SYNY3	Q55694 synechocyst
97	82.5	7.7	656	2	Q7NM86_GLOVI	Q7nm86 gloeobacter
98	82.5	7.7	806	2	Q4RZ79_TETNG	Q4rz79 tetraodon n
99	82	7.6	313	2	Q9P795_SCHPO	Q9p795 schizosacch
100	82	7.6	319	2	Q520D4_MAGGR	Q520d4 magnaporthe
101	82	7.6	331	2	Q8P3U5_XANCP	Q8p3u5 xanthomonas
102	82	7.6	359	2	Q7NQ73_CHRVO	Q7nq73 chromobacte
103	82	7.6	363	2	Q6TMP4_STRCL	Q6tmp4 streptomyce
104	82	7.6	370	2	Q4IRC3_GIBZE	Q4irc3 gibberella

105	82	7.6	415	2	Q9LGI3_ORYSA	Q9lgi3	oryza sativ
106	82	7.6	547	2	Q7R5I5_GIALA	Q7r5i5	giardia lam
107	82	7.6	982	2	Q4K8V1_PSEF5	Q4k8v1	pseudomonas
108	81.5	7.6	243	2	Q5NXI9_AZOSE	Q5nxi9	azoarcus sp
109	81.5	7.6	306	2	Q9L4D4_XANCA	Q9l4d4	xanthomonas
110	81.5	7.6	306	2	Q4UU76_XANCP	Q4uu76	xanthomonas
111	81.5	7.6	306	2	Q7CLS7_XANCP	Q7cls7	xanthomonas
112	81.5	7.6	316	2	Q6PTA6_AZOCA	Q6pta6	azorhizobiu
113	81.5	7.6	341	2	Q5U4D9_MOUSE	Q5u4d9	mus musculu
114	81.5	7.6	380	1	HM06_CAEEL	P20268	caenorhabdi
115	81.5	7.6	964	2	Q6CDQ6_YARLI	Q6cdq6	yarrowia li
116	81	7.5	172	2	Q6XD76_HUMAN	Q6xd76	homo sapien
117	81	7.5	186	2	Q7RTS2_HUMAN	Q7rts2	homo sapien
118	81	7.5	333	2	Q4UPC0_XANCP	Q4upc0	xanthomonas
119	81	7.5	380	1	AROB_TROW8	Q83hu4	tropheryma
120	81	7.5	553	2	Q9I783_PSEAE	Q9i783	pseudomonas
121	81	7.5	1022	2	Q4S3R8_TETNG	Q4s3r8	tetraodon n
122	80.5	7.5	214	2	Q6ZHB1_ORYSA	Q6zhb1	oryza sativ
123	80.5	7.5	285	2	Q9W4E1_DROME	Q9w4e1	drosophila
124	80.5	7.5	290	2	Q8JID4_BRARE	Q8jid4	brachydanio
125	80.5	7.5	296	2	Q6WEE0_BRARE	Q6wee0	brachydanio
126	80.5	7.5	297	2	Q6WEE1_BRARE	Q6wee1	brachydanio
127	80.5	7.5	304	2	Q8MS32_DROME	Q8ms32	drosophila
128	80.5	7.5	638	1	TRI47_HUMAN	Q96ld4	homo sapien
129	80.5	7.5	858	2	Q8K058_MOUSE	Q8k058	mus musculu
130	80.5	7.5	909	2	Q6ZPL5_MOUSE	Q6zpl5	mus musculu
131	80.5	7.5	1739	2	Q8LH63_ORYSA	Q8lh63	oryza sativ
132	80	7.5	113	2	Q6XYE2_HUMAN	Q6xye2	homo sapien
133	80	7.5	258	2	Q6ZIQ3_ORYSA	Q6ziq3	oryza sativ
134	80	7.5	380	1	AROB_TROWT	Q83gd7	tropheryma
135	80	7.5	408	2	Q96H86_HUMAN	Q96h86	homo sapien
136	80	7.5	411	2	Q7D8K4_MYCTU	Q7d8k4	mycobacteri
137	80	7.5	411	2	O86313_MYCTU	O86313	mycobacteri
138	80	7.5	527	2	Q84JU8_ORYSA	Q84ju8	oryza sativ
139	80	7.5	641	1	TRI47_MOUSE	Q8c0e3	mus musculu
140	80	7.5	1307	2	Q4SE51_TETNG	Q4se51	tetraodon n
141	80	7.5	1578	2	Q4SV81_TETNG	Q4sv81	tetraodon n
142	80	7.5	1901	2	Q4I1B9_GIBZE	Q4i1b9	gibberella
143	80	7.5	1955	2	Q7S893_NEUCR	Q7s893	neurospora
144	79.5	7.4	243	2	Q8N4B2_HUMAN	Q8n4b2	homo sapien
145	79.5	7.4	308	2	Q5TWV6_ANOGA	Q5twv6	anopheles g
146	79.5	7.4	355	2	Q8DJ00_SYNEL	Q8dj00	synechococc
147	79.5	7.4	433	2	Q8X0I2_NEUCR	Q8x0i2	neurospora
148	79.5	7.4	528	2	Q4N135_THEPA	Q4n135	theileria p
149	79.5	7.4	604	2	Q7XTB7_ORYSA	Q7xtb7	oryza sativ
150	79.5	7.4	643	2	Q4IBU9_GIBZE	Q4ibu9	gibberella
151	79.5	7.4	681	2	Q95RM4_DROME	Q95rm4	drosophila
152	79.5	7.4	745	2	Q98SJ5_BRARE	Q98sj5	brachydanio
153	79.5	7.4	787	2	Q7XP98_ORYSA	Q7xp98	oryza sativ
154	79.5	7.4	880	2	Q6PLP7_CHLRE	Q6plp7	chlamydomon
155	79.5	7.4	1352	2	Q68DU2_HUMAN	Q68du2	homo sapien
156	79.5	7.4	1406	2	Q9V4D4_DROME	Q9v4d4	drosophila
157	79.5	7.4	1406	2	Q9U1I0_DROME	Q9u1i0	drosophila
158	79.5	7.4	1408	2	Q9XZU7_DROME	Q9xzu7	drosophila
159	79	7.4	241	2	Q8VPR4_9MICC	Q8vpr4	micrococcus
160	79	7.4	355	2	Q7QL91_ANOGA	Q7ql91	anopheles g
161	79	7.4	382	2	Q8DHE0_SYNEL	Q8dhe0	synechococc
162	79	7.4	406	2	Q4R4K3_MACFA	Q4r4k3	macaca fasc
163	79	7.4	411	2	Q7U0C2_MYCBO	Q7u0c2	mycobacteri
164	79	7.4	463	2	Q5RG24_BRARE	Q5rg24	brachydanio
165	79	7.4	465	2	Q9BWD7_HUMAN	Q9bwd7	homo sapien
166	79	7.4	549	1	FASTK_HUMAN	Q14296	homo sapien
167	79	7.4	549	2	Q53FZ9_HUMAN	Q53fz9	homo sapien
168	79	7.4	696	2	Q51W67_MAGGR	Q51w67	magnaporthe
169	79	7.4	837	2	Q9Y4R8_HUMAN	Q9y4r8	homo sapien
170	79	7.4	837	2	Q7LDV4_HUMAN	Q7ldv4	homo sapien
171	79	7.4	844	2	O75168_HUMAN	O75168	homo sapien
172	79	7.4	885	2	P74259_SYNY3	P74259	synechocyst
173	79	7.4	1279	2	Q4RJ85_TETNG	Q4rj85	tetraodon n
174	79	7.4	1308	2	Q5TSZ3_ANOGA	Q5tsz3	anopheles g
175	78.5	7.3	132	2	Q9YCG5_AERPE	Q9ycg5	aeropyrum p
176	78.5	7.3	260	2	Q6H5Y3_ORYSA	Q6h5y3	oryza sativ
177	78.5	7.3	298	2	Q9D0U1_MOUSE	Q9d0u1	mus musculu
178	78.5	7.3	501	2	Q7MT41_PORGI	Q7mt41	porphyromon
179	78.5	7.3	745	2	Q4QDF9_LEIMA	Q4qdf9	leishmania
180	78.5	7.3	1150	2	Q4I0I4_GIBZE	Q4i0i4	gibberella
181	78.5	7.3	1385	2	Q7R003_GIALA	Q7r003	giardia lam
182	78.5	7.3	2006	2	Q8XYE7_RALSO	Q8xye7	ralstonia s
183	78	7.3	273	2	Q4FTW8_9GAMM	Q4ftw8	psychrobact
184	78	7.3	309	2	Q9RI44_STRCO	Q9ri44	streptomyce
185	78	7.3	402	2	Q6DRG1_BRARE	Q6drg1	brachydanio
186	78	7.3	519	2	Q4I9W3_GIBZE	Q4i9w3	gibberella
187	78	7.3	687	2	Q4Q3T8_LEIMA	Q4q3t8	leishmania
188	78	7.3	785	2	Q60PV7_CAEBR	Q60pv7	caenorhabdi
189	78	7.3	992	2	Q4FZ22_LEIMA	Q4fz22	leishmania
190	78	7.3	1181	2	Q4FZ26_LEIMA	Q4fz26	leishmania
191	78	7.3	1292	2	Q4P1N8_USTMA	Q4p1n8	ustilago ma
192	78	7.3	1462	2	Q4TBB7_TETNG	Q4tbb7	tetraodon n
193	78	7.3	1885	2	Q5K8J1_CRYNE	Q5k8j1	cryptococcu
194	77.5	7.2	197	2	Q4SAP6_TETNG	Q4sap6	tetraodon n
195	77.5	7.2	204	2	Q8FJZ2_ECOL6	Q8fjz2	escherichia
196	77.5	7.2	209	2	Q98263_MCV1	Q98263	molluscum c
197	77.5	7.2	231	2	Q6B6N7_ORNAN	Q6b6n7	ornithorhyn
198	77.5	7.2	287	2	Q5B7S1_EMENI	Q5b7s1	aspergillus
199	77.5	7.2	323	1	FOSL2_CHICK	P18625	gallus gall
200	77.5	7.2	325	2	Q4QAQ8_LEIMA	Q4qaq8	leishmania
201	77.5	7.2	355	2	Q8C9U5_MOUSE	Q8c9u5	mus musculu
202	77.5	7.2	357	2	Q95XT2_CAEEL	Q95xt2	caenorhabdi
203	77.5	7.2	385	2	Q7WD57_BORBR	Q7wd57	bordetella
204	77.5	7.2	385	2	Q7W5M1_BORPA	Q7w5m1	bordetella
205	77.5	7.2	520	2	Q4NAE4_9MICC	Q4nae4	arthrobacte
206	77.5	7.2	531	2	Q4VA54_MOUSE	Q4va54	mus musculu
207	77.5	7.2	555	2	Q5ASE2_EMENI	Q5ase2	aspergillus
208	77.5	7.2	567	1	EIL3_ARATH	O23116	arabidopsis
209	77.5	7.2	569	2	Q4NXI0_9DELT	Q4nx10	anaeromyxob
210	77.5	7.2	572	2	Q8BR38_MOUSE	Q8br38	mus musculu
211	77.5	7.2	775	2	Q9W233_DROME	Q9w233	drosophila
212	77.5	7.2	802	2	Q8BWA8_MOUSE	Q8bwa8	m mus muscu
213	77.5	7.2	802	2	Q6PAC2_MOUSE	Q6pac2	mus musculu
214	77.5	7.2	1231	2	Q51PT3_MAGGR	Q51pt3	magnaporthe
215	77.5	7.2	1452	2	Q7XVC7_ORYSA	Q7xvc7	oryza sativ
216	77	7.2	335	2	Q68KL4_NASVI	Q68kl4	nasonia vit
217	77	7.2	420	2	O87315_MYCSM	O87315	mycobacteri
218	77	7.2	466	2	Q9X8C5_STRCO	Q9x8c5	streptomyce
219	77	7.2	623	2	P90533_DICDI	P90533	dictyosteli
220	77	7.2	639	2	Q8UCA2_AGRT5	Q8uca2	agrobacteri
221	77	7.2	749	2	Q4FWB5_LEIMA	Q4fwb5	leishmania
222	77	7.2	798	2	Q6L4G1_ORYSA	Q6l4g1	oryza sativ
223	77	7.2	894	2	Q52BM3_MAGGR	Q52bm3	magnaporthe
224	77	7.2	1021	2	Q4Q0P2_LEIMA	Q4q0p2	leishmania
225	77	7.2	1183	2	Q54QR1_DICDI	Q54qr1	dictyosteli
226	77	7.2	1183	2	Q6T9C1_BRARE	Q6t9c1	brachydanio
227	77	7.2	1289	2	Q4FW63_LEIMA	Q4fw63	leishmania
228	77	7.2	1387	2	Q6T9C2_BRARE	Q6t9c2	brachydanio
229	77	7.2	1540	2	Q6T9C3_BRARE	Q6t9c3	brachydanio
230	77	7.2	2104	2	Q5AVV8_EMENI	Q5avv8	aspergillus
231	76.5	7.1	179	2	Q9D7A2_MOUSE	Q9d7a2	mus musculu
232	76.5	7.1	304	2	Q72HA3_THET2	Q72ha3	thermus the
233	76.5	7.1	349	2	Q5LWI3_SILPO	Q5lwi3	silicibacte
234	76.5	7.1	367	2	Q4NU74_9DELT	Q4nu74	anaeromyxob
235	76.5	7.1	399	2	Q52AE5_MAGGR	Q52ae5	magnaporthe
236	76.5	7.1	404	2	Q89FS4_BRAJA	Q89fs4	bradyrhizob
237	76.5	7.1	405	2	Q9HNZ5_HALSA	Q9hnz5	halobacteri
238	76.5	7.1	435	2	Q6N3Z7_RHOPA	Q6n3z7	rhodopseudo
239	76.5	7.1	481	2	Q5VNE6_ORYSA	Q5vne6	oryza sativ
240	76.5	7.1	503	1	PRP19_YEAST	P32523	saccharomyc
241	76.5	7.1	503	2	Q8NJV2_YEAST	Q8njv2	saccharomyc
242	76.5	7.1	506	2	Q7XW06_ORYSA	Q7xw06	oryza sativ
243	76.5	7.1	594	2	Q6XN74_RHOER	Q6xn74	rhodococcus
244	76.5	7.1	833	2	Q4QJJ7_LEIMA	Q4qjj7	leishmania
245	76.5	7.1	1075	1	DNAE2_RALSO	Q8xrn1	ralstonia s
246	76.5	7.1	1141	2	Q52FA1_MAGGR	Q52fa1	magnaporthe
247	76.5	7.1	1204	2	Q7QBG5_ANOGA	Q7qbg5	anopheles g
248	76.5	7.1	1876	2	Q4P456_USTMA	Q4p456	ustilago ma
249	76.5	7.1	2346	2	Q5VU43_HUMAN	Q5vu43	homo sapien
250	76.5	7.1	2362	2	Q5VU44_HUMAN	Q5vu44	homo sapien

251	76.5	7.1	4796	2	Q4Q363_LEIMA	Q4q363	leishmania
252	76	7.1	93	2	Q9VBC1_DROME	Q9vbc1	drosophila
253	76	7.1	246	2	Q5YPJ3_NOCFA	Q5ypj3	nocardia fa
254	76	7.1	264	2	Q99L79_MOUSE	Q99l79	mus musculu
255	76	7.1	296	2	Q9ZBN9_STRCO	Q9zbn9	streptomyce
256	76	7.1	384	2	Q6REJ3_9NOCA	Q6rej3	rhodococcus
257	76	7.1	396	2	Q62MT6_BURMA	Q62mt6	burkholderi
258	76	7.1	396	2	Q63YR8_BURPS	Q63yr8	burkholderi
259	76	7.1	402	2	Q504F4_BRARE	Q504f4	brachydanio
260	76	7.1	429	2	Q6K5L3_ORYSA	Q6k513	oryza sativ
261	76	7.1	457	2	Q82F29_STRAW	Q82f29	streptomyce
262	76	7.1	463	2	Q5RG28_BRARE	Q5rg28	brachydanio
263	76	7.1	478	2	Q5BJY5_RAT	Q5bjy5	rattus norv
264	76	7.1	524	2	Q4T4D3_TETNG	Q4t4d3	tetraodon n
265	76	7.1	549	2	Q5RF17_PONPY	Q5rf17	pongo pygma
266	76	7.1	561	2	Q8BG36_MOUSE	Q8bg36	mus musculu
267	76	7.1	584	2	Q9BR22_HUMAN	Q9br22	homo sapien
268	76	7.1	606	2	Q4Q661_LEIMA	Q4q661	leishmania
269	76	7.1	641	2	Q62DI1_BURMA	Q62di1	burkholderi
270	76	7.1	641	2	Q63MU7_BURPS	Q63mu7	burkholderi
271	76	7.1	699	2	Q55Q95_CRYNE	Q55q95	cryptococcu
272	76	7.1	724	2	Q6P1R6_HUMAN	Q6p1r6	homo sapien
273	76	7.1	978	2	Q93H70_STRAW	Q93h70	streptomyce
274	76	7.1	1295	2	Q4Q968_LEIMA	Q4q968	leishmania
275	76	7.1	1482	2	Q4P0T3_USTMA	Q4p0t3	ustilago ma
276	76	7.1	2028	1	TRPM6_MOUSE	Q8cir4	mus musculu
277	76	7.1	2602	2	Q9VZ45_DROME	Q9vz45	drosophila
278	75.5	7.0	150	2	Q9XSS7_CANFA	Q9xss7	canis famil
279	75.5	7.0	192	2	Q6IJ70_DROME	Q6ij70	drosophila
280	75.5	7.0	244	2	Q4LJJ5_9BURK	Q4ljj5	burkholderi
281	75.5	7.0	257	2	Q4NXW1_9DELT	Q4nxw1	anaeromyxob
282	75.5	7.0	277	2	Q90XE3_COTJA	Q90xe3	coturnix co
283	75.5	7.0	352	2	Q9K3V0_STRCO	Q9k3v0	streptomyce
284	75.5	7.0	407	2	Q5GTU6_XANOR	Q5gtu6	xanthomonas
285	75.5	7.0	422	2	Q9D8T1_MOUSE	Q9d8t1	mus musculu
286	75.5	7.0	494	2	Q4Q0J7_LEIMA	Q4q0j7	leishmania
287	75.5	7.0	495	2	Q6FUU4_CANGA	Q6fuu4	candida gla
288	75.5	7.0	521	2	Q4SGD1_TETNG	Q4sgd1	tetraodon n
289	75.5	7.0	652	2	Q86UU5_HUMAN	Q86uu5	homo sapien
290	75.5	7.0	783	2	Q4WLT7_ASPFU	Q4wlt7	aspergillus
291	75.5	7.0	792	2	Q4ITQ5_AZOVI	Q4itq5	azotobacter
292	75.5	7.0	918	2	Q4SK19_TETNG	Q4sk19	tetraodon n
293	75.5	7.0	931	2	Q7S500_NEUCR	Q7s500	neurospora
294	75.5	7.0	1078	2	Q6NRQ4_XENLA	Q6nrq4	xenopus lae
295	75.5	7.0	1614	2	Q4WQM3_ASPFU	Q4wqm3	aspergillus
296	75.5	7.0	1704	1	CEND1_HUMAN	Q8wz64	homo sapien
297	75.5	7.0	1745	2	Q4QE94_LEIMA	Q4qe94	leishmania
298	75	7.0	284	2	Q6W8X0_PSEFL	Q6w8x0	pseudomonas
299	75	7.0	366	2	Q6ATF0_ORYSA	Q6atf0	oryza sativ
300	75	7.0	415	2	Q4FE78_MAIZE	Q4fe78	zea mays (m
301	75	7.0	433	2	Q4UY84_XANCP	Q4uy84	xanthomonas
302	75	7.0	433	2	Q8P5X8_XANCP	Q8p5x8	xanthomonas
303	75	7.0	452	2	Q93IX7_STRCO	Q93ix7	streptomyce
304	75	7.0	505	2	Q27692_MUSDO	Q27692	musca domes
305	75	7.0	564	2	Q55S00_CRYNE	Q55s00	cryptococcu
306	75	7.0	564	2	Q5KGF2_CRYNE	Q5kgf2	cryptococcu
307	75	7.0	575	2	Q9BW81_HUMAN	Q9bw81	homo sapien
308	75	7.0	744	2	Q9RRR7_DEIRA	Q9rrr7	deinococcus
309	75	7.0	764	2	Q60QM4_CAEBR	Q60qm4	caenorhabdi
310	75	7.0	773	2	Q992Z7_MHV68	Q992z7	murid herpe
311	75	7.0	799	2	Q4P8F7_USTMA	Q4p8f7	ustilago ma
312	75	7.0	866	2	Q4S657_TETNG	Q4s657	tetraodon n
313	75	7.0	1146	2	Q4UV95_XANCP	Q4uv95	xanthomonas
314	75	7.0	1146	2	Q8P8T6_XANCP	Q8p8t6	xanthomonas
315	75	7.0	1222	2	Q4T4E0_TETNG	Q4t4e0	tetraodon n
316	75	7.0	1291	2	O41978_MHV68	O41978	murid herpe
317	75	7.0	1454	1	PTPRT_MOUSE	Q99m80	mus musculu
318	75	7.0	1482	2	Q5BG68_EMENI	Q5bg68	aspergillus
319	75	7.0	2634	2	Q4QCB9_LEIMA	Q4qcb9	leishmania
320	75	7.0	5095	2	Q4Q3Q7_LEIMA	Q4q3q7	leishmania
321	74.5	6.9	126	2	Q84ER5_9BURK	Q84er5	cupriavidus
322	74.5	6.9	137	2	Q87A50_XYLFT	Q87a50	xylella fas
323	74.5	6.9	192	2	Q5TQW5_ANOGA	Q5tqw5	anopheles g
324	74.5	6.9	218	2	Q6ZN89_HUMAN	Q6zn89	homo sapien
325	74.5	6.9	218	2	Q6AKM9_DESPS	Q6akm9	desulfotale
326	74.5	6.9	222	2	Q9F370_STRCO	Q9f370	streptomyce
327	74.5	6.9	319	2	Q91639_XENLA	Q91639	xenopus lae
328	74.5	6.9	363	2	O01353_DROPI	O01353	drosophila
329	74.5	6.9	414	2	Q6BVG0_DEBHA	Q6bvg0	debaryomyce
330	74.5	6.9	435	2	Q4IKR0_GIBZE	Q4ikr0	gibberella
331	74.5	6.9	447	2	Q5FVJ1_RAT	Q5fvj1	rattus norv
332	74.5	6.9	520	2	Q5NDL4_DROYA	Q5ndl4	drosophila
333	74.5	6.9	523	2	Q59EM8_HUMAN	Q59em8	homo sapien
334	74.5	6.9	531	2	Q8KCF8_CHLTE	Q8kcf8	chlorobium
335	74.5	6.9	563	2	Q9N634_LEIMA	Q9n634	leishmania
336	74.5	6.9	612	2	Q804W7_FUGRU	Q804w7	fugu rubrip
337	74.5	6.9	629	2	Q6P5Z6_HUMAN	Q6p5z6	homo sapien
338	74.5	6.9	639	1	DMPK_HUMAN	Q09013	homo sapien
339	74.5	6.9	655	2	Q4G186_HUMAN	Q4g186	homo sapien
340	74.5	6.9	668	2	Q4H2H8_CIOIN	Q4h2h8	ciona intes
341	74.5	6.9	668	2	Q4H5Y9_9DEIO	Q4h5y9	deinococcus
342	74.5	6.9	672	2	Q59FU6_HUMAN	Q59fu6	homo sapien
343	74.5	6.9	695	1	FBX34_MOUSE	Q80xi1	mus musculu
344	74.5	6.9	704	2	Q6NHK1_CORDI	Q6nhk1	corynebacte
345	74.5	6.9	728	2	Q5P3R0_AZOSE	Q5p3r0	azoarcus sp
346	74.5	6.9	796	2	Q4P0F3_USTMA	Q4p0f3	ustilago ma
347	74.5	6.9	1130	2	Q6CAD9_YARLI	Q6cad9	yarrowia li
348	74.5	6.9	1370	2	Q7XQL3_ORYSA	Q7xql3	oryza sativ
349	74.5	6.9	1807	2	Q6ATI6_ORYSA	Q6ati6	oryza sativ
350	74.5	6.9	1928	2	Q4PE06_USTMA	Q4pe06	ustilago ma
351	74.5	6.9	2027	2	Q65WT8_ORYSA	Q65wt8	oryza sativ
352	74.5	6.9	2072	2	Q4SA09_TETNG	Q4sa09	tetraodon n
353	74.5	6.9	2135	1	PLXB1_HUMAN	O43157	homo sapien
354	74.5	6.9	2240	2	Q5VU48_HUMAN	Q5vu48	homo sapien
355	74.5	6.9	2296	2	O75042_HUMAN	O75042	homo sapien
356	74.5	6.9	2306	2	Q4SEE4_TETNG	Q4see4	tetraodon n
357	74.5	6.9	2490	2	Q7PQ16_ANOGA	Q7pq16	anopheles g
358	74	6.9	189	2	Q7XW17_ORYSA	Q7xw17	oryza sativ
359	74	6.9	201	2	Q6ZT56_HUMAN	Q6zt56	homo sapien
360	74	6.9	211	2	Q9YEE7_AERPE	Q9yee7	aeropyrum p
361	74	6.9	260	1	TNR7_HUMAN	P26842	homo sapien
362	74	6.9	267	1	SPIB_MOUSE	O35906	mus musculu
363	74	6.9	317	2	Q9XDF3_STRGR	Q9xdf3	streptomyce
364	74	6.9	347	2	Q54229_STRGR	Q54229	streptomyce
365	74	6.9	367	2	Q8JIB3_COTCO	Q8jib3	coturnix co
366	74	6.9	373	2	Q4IEJ6_GIBZE	Q4iej6	gibberella
367	74	6.9	404	2	Q96DL6_HUMAN	Q96dl6	homo sapien
368	74	6.9	435	2	Q19059_CAEEL	Q19059	caenorhabdi
369	74	6.9	457	2	Q7RTU6_HUMAN	Q7rtu6	homo sapien
370	74	6.9	482	2	Q9C0H3_HUMAN	Q9c0h3	homo sapien
371	74	6.9	504	2	Q8DIR1_SYNEL	Q8dir1	synechococc
372	74	6.9	517	2	Q5RE20_PONPY	Q5re20	pongo pygma
373	74	6.9	518	2	Q5NXW9_AZOSE	Q5nxw9	azoarcus sp
374	74	6.9	652	2	Q8NAA1_HUMAN	Q8naa1	homo sapien
375	74	6.9	670	2	Q4Q919_LEIMA	Q4q919	leishmania
376	74	6.9	679	2	Q5N2R4_SYNP6	Q5n2r4	synechococc
377	74	6.9	699	2	Q5KFX2_CRYNE	Q5kfx2	cryptococcu
378	74	6.9	907	2	Q7QST2_GIALA	Q7qst2	giardia lam
379	74	6.9	960	2	Q4Q480_LEIMA	Q4q480	leishmania
380	74	6.9	1076	2	Q727F9_DESVH	Q727f9	desulfovibr
381	74	6.9	1084	2	Q4S8L1_TETNG	Q4s8l1	tetraodon n
382	74	6.9	1146	2	Q5U263_XENTR	Q5u263	xenopus tro
383	74	6.9	1400	2	Q4SAD4_TETNG	Q4sad4	tetraodon n
384	74	6.9	1405	2	Q9P3S5_NEUCR	Q9p3s5	neurospora
385	74	6.9	1812	2	Q9Z1D2_MOUSE	Q9z1d2	mus musculu
386	74	6.9	2289	2	Q4PBD1_USTMA	Q4pbd1	ustilago ma
387	74	6.9	2289	2	Q9HFW4_USTMA	Q9hfw4	ustilago ma
388	74	6.9	2358	2	Q9L1V8_STRCO	Q9l1v8	streptomyce
389	74	6.9	2368	2	Q4S4K5_TETNG	Q4s4k5	tetraodon n
390	74	6.9	2842	1	APC_RAT	P70478	rattus norv
391	74	6.9	4196	2	Q7VV06_BORPE	Q7vv06	bordetella
392	74	6.9	4218	2	Q7WL14_BORBR	Q7wl14	bordetella
393	73.5	6.8	184	2	Q8HY70_MUSVI	Q8hy70	mustela vis
394	73.5	6.8	186	2	Q9FRD0_ORYSA	Q9frd0	oryza sativ
395	73.5	6.8	212	2	Q4G0L6_HUMAN	Q4g0l6	homo sapien
396	73.5	6.8	249	2	Q5P8T4_AZOSE	Q5p8t4	azoarcus sp

397	73.5	6.8	258	2	Q4SR10_TETNG	Q4sr10	tetraodon n
398	73.5	6.8	276	2	Q6D5U0_ERWCT	Q6d5u0	erwinia car
399	73.5	6.8	320	2	Q4LJZ7_9BURK	Q4ljz7	burkholderi
400	73.5	6.8	331	2	Q9CW60_MOUSE	Q9cw60	mus musculu
401	73.5	6.8	384	2	Q9FSQ3_ORYSA	Q9fsq3	oryza sativ
402	73.5	6.8	396	2	Q9K3Z5_STRCO	Q9k3z5	streptomyce
403	73.5	6.8	440	2	Q69YS8_HUMAN	Q69ys8	homo sapien
404	73.5	6.8	443	2	Q72IQ5_THET2	Q72iq5	thermus the
405	73.5	6.8	451	2	Q9F1K2_CITFR	Q9f1k2	citrobacter
406	73.5	6.8	545	2	Q4ILA6_GIBZE	Q4ila6	gibberella
407	73.5	6.8	559	1	HNF1B_PIG	Q03365	sus scrofa
408	73.5	6.8	571	2	Q4Q2S6_LEIMA	Q4q2s6	leishmania
409	73.5	6.8	573	2	Q4WGZ0_ASPFU	Q4wgz0	aspergillus
410	73.5	6.8	580	2	Q6NCE3_RHOPA	Q6nce3	rhodopseudo
411	73.5	6.8	681	2	Q4PBC8_USTMA	Q4pbc8	ustilago ma
412	73.5	6.8	714	2	Q7PMQ2_ANOGA	Q7pmq2	anopheles g
413	73.5	6.8	714	2	Q9PU31_OREAU	Q9pu31	oreochromis
414	73.5	6.8	741	1	NF2L1_MOUSE	Q61985	mus musculu
415	73.5	6.8	741	2	Q6GTN8_MOUSE	Q6gtn8	mus musculu
416	73.5	6.8	767	2	Q6KAM4_MOUSE	Q6kam4	mus musculu
417	73.5	6.8	979	2	Q6UUD4_ORYSA	Q6uud4	oryza sativ
418	73.5	6.8	998	2	Q52V61_9ACTO	Q52v61	streptomyce
419	73.5	6.8	1011	2	Q55YK2_CRYNE	Q55yk2	cryptococcu
420	73.5	6.8	1011	2	Q5KLD6_CRYNE	Q5kld6	cryptococcu
421	73.5	6.8	1047	2	Q82AC9_STRAW	Q82ac9	streptomyce
422	73.5	6.8	1056	2	Q4RMW5_TETNG	Q4rmw5	tetraodon n
423	73.5	6.8	1106	2	Q9YH35_TETFL	Q9yh35	tetraodon f
424	73.5	6.8	1148	2	Q93GZ6_STRAW	Q93gz6	streptomyce
425	73.5	6.8	1310	2	Q4Q2H5_LEIMA	Q4q2h5	leishmania
426	73.5	6.8	1508	2	Q51VU8_MAGGR	Q51vu8	magnaporthe
427	73.5	6.8	1541	2	Q94I61_ORYSA	Q94i61	oryza sativ
428	73.5	6.8	1615	1	RIMS1_RAT	Q9jir4	rattus norv
429	73.5	6.8	1615	2	Q7XS76_ORYSA	Q7xs76	oryza sativ
430	73.5	6.8	1957	2	Q4SKB4_TETNG	Q4skb4	tetraodon n
431	73.5	6.8	2026	2	Q84T73_ORYSA	Q84t73	oryza sativ
432	73.5	6.8	2027	2	Q65WY4_ORYSA	Q65wy4	oryza sativ
433	73.5	6.8	2027	2	Q6UU84_ORYSA	Q6uu84	oryza sativ
434	73.5	6.8	2148	2	Q8IR53_DROME	Q8ir53	drosophila
435	73.5	6.8	2196	2	Q9VY40_DROME	Q9vy40	drosophila
436	73	6.8	103	2	Q9T463_NEPOL	Q9t463	nephroselmi
437	73	6.8	170	2	Q5H2Q5_XANOR	Q5h2q5	xanthomonas
438	73	6.8	245	2	Q6B6N8_DIDMA	Q6b6n8	didelphis m
439	73	6.8	310	2	Q6Z436_ORYSA	Q6z436	oryza sativ
440	73	6.8	311	2	Q7XVJ7_ORYSA	Q7xvj7	oryza sativ
441	73	6.8	321	2	Q654E7_ORYSA	Q654e7	oryza sativ
442	73	6.8	329	2	O54633_HALSA	O54633	halobacteri
443	73	6.8	344	2	Q8PHX8_XANAC	Q8phx8	xanthomonas
444	73	6.8	370	1	DDL_MYCBO	Q7txh9	mycobacteri
445	73	6.8	373	1	DDL_MYCTU	P95114	mycobacteri
446	73	6.8	398	2	Q4JVZ8_CORJK	Q4jvz8	corynebacte
447	73	6.8	491	2	Q7LDW0_HUMAN	Q7ldw0	homo sapien
448	73	6.8	499	2	Q5QT31_ORYSA	Q5qt31	oryza sativ
449	73	6.8	531	2	Q5TKQ7_ORYSA	Q5tkq7	oryza sativ
450	73	6.8	532	2	Q4IK92_GIBZE	Q4ik92	gibberella
451	73	6.8	548	2	Q96NZ8_HUMAN	Q96nz8	homo sapien
452	73	6.8	565	2	Q8JT92_9INFA	Q8jt92	influenza a
453	73	6.8	565	2	Q8JT93_9INFA	Q8jt93	influenza a
454	73	6.8	575	2	Q6UXF1_HUMAN	Q6uxf1	homo sapien
455	73	6.8	581	2	Q4QCP7_LEIMA	Q4qcp7	leishmania
456	73	6.8	584	2	Q6IM06_DROME	Q6im06	drosophila
457	73	6.8	584	2	Q8C0B1_MOUSE	Q8c0b1	mus musculu
458	73	6.8	584	2	Q8R3Y8_MOUSE	Q8r3y8	mus musculu
459	73	6.8	585	2	Q4WCQ9_ASPFU	Q4wcq9	aspergillus
460	73	6.8	615	2	Q4IBL6_GIBZE	Q4ibl6	gibberella
461	73	6.8	664	2	Q5ZL14_CHICK	Q5zl14	gallus gall
462	73	6.8	667	2	Q4IC96_GIBZE	Q4ic96	gibberella
463	73	6.8	711	2	Q51UB4_MAGGR	Q51ub4	magnaporthe
464	73	6.8	772	2	Q6MVM6_NEUCR	Q6mvm6	neurospora
465	73	6.8	773	2	Q4SEP7_TETNG	Q4sep7	tetraodon n
466	73	6.8	853	2	Q4NS34_9DELT	Q4ns34	anaeromyxob
467	73	6.8	868	2	Q8SX72_DROME	Q8sx72	drosophila
468	73	6.8	1058	2	Q6BPG5_DEBHA	Q6bpg5	debaryomyce
469	73	6.8	1080	2	Q48579_LISIV	Q48579	listeria iv
470	73	6.8	1173	2	Q9VHC2_DROME	Q9vhc2	drosophila
471	73	6.8	1215	1	HIPK3_HUMAN	Q9h422	homo sapien
472	73	6.8	1265	2	Q7UX59_RHOBA	Q7ux59	rhodopirell
473	73	6.8	1426	2	Q5RE74_PONPY	Q5re74	pongo pygma
474	73	6.8	1431	2	Q5W0Y4_HUMAN	Q5w0y4	homo sapien
475	73	6.8	1440	2	Q5W0Y3_HUMAN	Q5w0y3	homo sapien
476	73	6.8	1441	2	Q5W0Y0_HUMAN	Q5w0y0	homo sapien
477	73	6.8	1444	2	Q5W0X9_HUMAN	Q5w0x9	homo sapien
478	73	6.8	1450	2	Q5W0Y2_HUMAN	Q5w0y2	homo sapien
479	73	6.8	1451	2	Q5W0Y5_HUMAN	Q5w0y5	homo sapien
480	73	6.8	1463	1	PTPRT_HUMAN	O14522	homo sapien
481	73	6.8	1463	2	Q5W0Y1_HUMAN	Q5w0y1	homo sapien
482	73	6.8	1518	1	HR4_DROME	Q9w539	drosophila
483	73	6.8	1518	2	Q56AW0_DROME	Q56aw0	drosophila
484	73	6.8	1862	2	Q83X88_STRRO	Q83x88	streptomyce
485	73	6.8	1969	2	Q7XW75_ORYSA	Q7xw75	oryza sativ
486	72.5	6.8	101	2	Q7MDN5_VIBVY	Q7mdn5	vibrio vuln
487	72.5	6.8	181	2	Q22497_CAEEL	Q22497	caenorhabdi
488	72.5	6.8	194	2	Q4H1D5_LEIMA	Q4h1d5	leishmania
489	72.5	6.8	209	2	Q4PIQ1_USTMA	Q4piq1	ustilago ma
490	72.5	6.8	308	2	Q8PQK8_XANAC	Q8pqk8	xanthomonas
491	72.5	6.8	309	2	Q4H6D8_9DEIO	Q4h6d8	deinococcus
492	72.5	6.8	329	2	Q7PXT4_ANOGA	Q7pxt4	anopheles g
493	72.5	6.8	341	2	Q4Q797_LEIMA	Q4q797	leishmania
494	72.5	6.8	341	2	Q6SH20_9BACT	Q6sh20	uncultured
495	72.5	6.8	351	2	Q6FB56_ACIAD	Q6fb56	acinetobact
496	72.5	6.8	362	2	Q9A567_CAUCR	Q9a567	caulobacter
497	72.5	6.8	377	2	Q4NZA5_9DELT	Q4nza5	anaeromyxob
498	72.5	6.8	382	2	Q4TSG7_9SPHN	Q4tsg7	erythrobact
499	72.5	6.8	420	2	Q4QGD1_LEIMA	Q4qgd1	leishmania
500	72.5	6.8	423	2	Q872X2_NEUCR	Q872x2	neurospora
501	72.5	6.8	451	2	Q4Q4A6_LEIMA	Q4q4a6	leishmania
502	72.5	6.8	466	1	GATA2_CHICK	P23824	gallus gall
503	72.5	6.8	467	2	Q4SQZ8_TETNG	Q4sqz8	tetraodon n
504	72.5	6.8	480	2	Q7NF80_GLOVI	Q7nf80	gloeobacter
505	72.5	6.8	503	2	Q9I7K2_DROME	Q9i7k2	drosophila
506	72.5	6.8	503	2	Q4UZS2_XANCP	Q4uzs2	xanthomonas
507	72.5	6.8	503	2	Q8PDI4_XANCP	Q8pdi4	xanthomonas
508	72.5	6.8	509	2	Q5GH58_RAT	Q5gh58	rattus norv
509	72.5	6.8	513	2	Q8W4P1_ARATH	Q8w4p1	arabidopsis
510	72.5	6.8	514	2	Q9I1I9_PSEAE	Q9ili9	pseudomonas
511	72.5	6.8	528	1	CP1A5_CHICK	P79761	gallus gall
512	72.5	6.8	532	2	Q6ZD77_ORYSA	Q6zd77	oryza sativ
513	72.5	6.8	561	2	Q9U1T0_CAEEL	Q9u1t0	caenorhabdi
514	72.5	6.8	580	2	Q9FU86_ORYSA	Q9fu86	oryza sativ
515	72.5	6.8	581	1	TRIP4_HUMAN	Q15650	homo sapien
516	72.5	6.8	659	2	Q4SWJ2_TETNG	Q4swj2	tetraodon n
517	72.5	6.8	661	2	Q69MP6_ORYSA	Q69mp6	oryza sativ
518	72.5	6.8	697	2	Q5GYP9_XANOR	Q5gyp9	xanthomonas
519	72.5	6.8	723	2	Q9SHS2_ARATH	Q9shs2	arabidopsis
520	72.5	6.8	736	2	Q4IX80_AZOVI	Q4ix80	azotobacter
521	72.5	6.8	771	2	Q98TH2_BRARE	Q98th2	brachydanio
522	72.5	6.8	772	1	NF2L1_HUMAN	Q14494	h nuclear f
523	72.5	6.8	772	2	Q5RA25_PONPY	Q5ra25	pongo pygma
524	72.5	6.8	791	2	Q8NF22_HUMAN	Q8nf22	homo sapien
525	72.5	6.8	854	2	Q4RTJ3_TETNG	Q4rtj3	tetraodon n
526	72.5	6.8	899	2	Q5PB98_ANAMM	Q5pb98	anaplasma m
527	72.5	6.8	940	2	Q4P744_USTMA	Q4p744	ustilago ma
528	72.5	6.8	1130	2	Q60UW9_CAEBR	Q60uw9	caenorhabdi
529	72.5	6.8	1157	1	ZN516_MOUSE	Q7tsh3	mus musculu
530	72.5	6.8	1259	2	Q6YIQ9_HUMAN	Q6yiq9	homo sapien
531	72.5	6.8	1309	2	Q5AS95_EMENI	Q5as95	aspergillus
532	72.5	6.8	1373	2	Q63HU3_BURPS	Q63hu3	burkholderi
533	72.5	6.8	1373	2	Q629N7_BURMA	Q629n7	burkholderi
534	72.5	6.8	1489	2	Q9W0I1_DROME	Q9w0i1	drosophila
535	72.5	6.8	1539	2	Q4FZ12_LEIMA	Q4fz12	leishmania
536	72.5	6.8	1827	2	Q7XR55_ORYSA	Q7xr55	oryza sativ
537	72.5	6.8	1886	2	Q4SLF6_TETNG	Q4slf6	tetraodon n
538	72.5	6.8	2027	2	Q53L26_ORYSA	Q53l26	oryza sativ
539	72.5	6.8	2229	2	Q4RWM8_TETNG	Q4rwm8	tetraodon n
540	72.5	6.8	2297	2	Q7QXM5_GIALA	Q7qxm5	giardia lam
541	72.5	6.8	2345	2	Q4QHI8_LEIMA	Q4qhi8	leishmania
542	72.5	6.8	2398	2	Q4Q3E5_LEIMA	Q4q3e5	leishmania

543	72.5	6.8	4437	2	Q8GGP3_STRAZ	Q8ggp3	streptomyce
544	72	6.7	147	2	Q8C7Q1_MOUSE	Q8c7q1	mus musculu
545	72	6.7	198	2	Q60DT1_ORYSA	Q60dt1	oryza sativ
546	72	6.7	206	2	Q9H6I6_HUMAN	Q9h6i6	homo sapien
547	72	6.7	213	2	Q6K7Q2_ORYSA	Q6k7q2	oryza sativ
548	72	6.7	236	2	Q71AJ2_9NUCL	Q71aj2	mamestra co
549	72	6.7	236	2	Q8QLL5_NPVMC	Q8qll5	mamestra co
550	72	6.7	294	2	Q86GS9_OXYTR	Q86gs9	oxytricha t
551	72	6.7	319	2	Q53R79_ORYSA	Q53r79	oryza sativ
552	72	6.7	406	2	Q96AI3_HUMAN	Q96ai3	homo sapien
553	72	6.7	426	2	Q6YX78_ORYSA	Q6yx78	oryza sativ
554	72	6.7	444	2	Q7X7C3_ORYSA	Q7x7c3	oryza sativ
555	72	6.7	448	2	Q67TH3_SYMTH	Q67th3	symbiobacte
556	72	6.7	463	2	Q6IQ96_BRARE	Q6iq96	brachydanio
557	72	6.7	473	2	Q6P1R4_HUMAN	Q6p1r4	homo sapien
558	72	6.7	475	2	Q4LL27_9BURK	Q4ll27	burkholderi
559	72	6.7	502	2	Q8PF80_XANAC	Q8pf80	xanthomonas
560	72	6.7	509	2	Q7XVP4_ORYSA	Q7xvp4	oryza sativ
561	72	6.7	546	2	Q9FVZ0_ORYSA	Q9fvz0	oryza sativ
562	72	6.7	553	2	Q7VTR1_BORPE	Q7vtr1	bordetella
563	72	6.7	553	2	Q7WNW2_BORBR	Q7wnw2	bordetella
564	72	6.7	565	2	Q7W169_BORPA	Q7w169	bordetella
565	72	6.7	576	2	Q5AZF3_EMENI	Q5azf3	aspergillus
566	72	6.7	639	2	Q6SWY6_HCMV	Q6swy6	human cytom
567	72	6.7	648	2	Q8F6A9_LEPIN	Q8f6a9	leptospira
568	72	6.7	661	2	Q5BFB4_EMENI	Q5bfb4	aspergillus
569	72	6.7	665	2	Q59E69_DROME	Q59e69	drosophila
570	72	6.7	720	1	GLGB2_XANOR	Q5h6q3	xanthomonas
571	72	6.7	767	2	Q9SVF1_ARATH	Q9svf1	arabidopsis
572	72	6.7	908	2	Q75IJ5_ORYSA	Q75ij5	oryza sativ
573	72	6.7	957	2	Q53RK9_ORYSA	Q53rk9	oryza sativ
574	72	6.7	958	1	ATG13_ASPFU	Q4whn5	aspergillus
575	72	6.7	965	2	Q5AQL7_EMENI	Q5aql7	aspergillus
576	72	6.7	1059	2	Q659F1_HUMAN	Q659f1	homo sapien
577	72	6.7	1064	2	Q89K68_BRAJA	Q89k68	bradyrhizob
578	72	6.7	1139	2	Q51LL1_MAGGR	Q51ll1	magnaporthe
579	72	6.7	1140	2	Q62AE2_BURMA	Q62ae2	burkholderi
580	72	6.7	1144	2	Q80T84_MOUSE	Q80t84	mus musculu
581	72	6.7	1170	2	Q95TI5_DROME	Q95ti5	drosophila
582	72	6.7	1236	2	Q51P93_MAGGR	Q51p93	magnaporthe
583	72	6.7	1649	2	Q746C7_THET2	Q746c7	thermus the
584	72	6.7	1945	2	Q7XFX1_ORYSA	Q7xfx1	oryza sativ
585	72	6.7	1945	2	Q8S844_ORYSA	Q8s844	oryza sativ
586	72	6.7	1950	2	Q7X8E7_ORYSA	Q7x8e7	oryza sativ
587	72	6.7	1986	2	Q7X6L5_ORYSA	Q7x6l5	oryza sativ
588	72	6.7	1990	2	Q9U8Q0_DROME	Q9u8q0	drosophila
589	72	6.7	1991	2	Q7XNV9_ORYSA	Q7xnv9	oryza sativ
590	72	6.7	1995	2	Q9W244_DROME	Q9w244	drosophila
591	72	6.7	2000	2	Q75KG3_ORYSA	Q75kg3	oryza sativ
592	72	6.7	2008	2	Q7XWE4_ORYSA	Q7xwe4	oryza sativ
593	71.5	6.7	140	2	Q6ZVP1_HUMAN	Q6zvp1	homo sapien
594	71.5	6.7	172	2	Q98ST9_CHICK	Q98st9	gallus gall
595	71.5	6.7	189	2	Q95LQ4_FELCA	Q95lq4	felis silve
596	71.5	6.7	203	1	COBC_ECOLI	P52086	escherichia
597	71.5	6.7	203	2	Q7AGP4_ECO57	Q7agp4	escherichia
598	71.5	6.7	203	2	Q83S68_SHIFL	Q83s68	shigella fl
599	71.5	6.7	203	2	Q8XBP1_ECO57	Q8xbp1	escherichia
600	71.5	6.7	214	1	VEGFA_CANFA	Q9myv3	canis famil
601	71.5	6.7	214	2	Q8CG83_MOUSE	Q8cg83	mus musculu
602	71.5	6.7	215	2	Q9YEL2_AERPE	Q9yel2	aeropyrum p
603	71.5	6.7	220	2	Q6PHV7_BRARE	Q6phv7	brachydanio
604	71.5	6.7	223	2	Q5V7I4_HALMA	Q5v7i4	haloarcula
605	71.5	6.7	245	2	Q38204_BPPHH	Q38204	bacteriopha
606	71.5	6.7	265	2	Q8AW41_BRARE	Q8aw41	brachydanio
607	71.5	6.7	292	2	Q89S78_BRAJA	Q89s78	bradyrhizob
608	71.5	6.7	296	2	Q78AM8_BRARE	Q78am8	brachydanio
609	71.5	6.7	297	1	HXA11_CHICK	P31258	gallus gall
610	71.5	6.7	307	2	Q4KB04_PSEF5	Q4kb04	pseudomonas
611	71.5	6.7	318	2	Q8GUB6_MUSAC	Q8gub6	musa acumin
612	71.5	6.7	330	2	Q14882_HUMAN	Q14882	homo sapien
613	71.5	6.7	331	2	Q4T8T1_TETNG	Q4t8t1	tetraodon n
614	71.5	6.7	336	2	Q52148_9ZZZZ	Q52148	plasmid pal
615	71.5	6.7	377	2	Q5YPH9_NOCFA	Q5yph9	nocardia fa
616	71.5	6.7	399	2	Q9IB63_XENLA	Q9ib63	xenopus lae
617	71.5	6.7	402	2	Q96S07_HUMAN	Q96s07	homo sapien
618	71.5	6.7	433	1	PMEB_ERWCH	Q47474	erwinia chr
619	71.5	6.7	458	2	Q8PMN0_XANAC	Q8pmn0	xanthomonas
620	71.5	6.7	486	1	GALT_LACCA	O84904	lactobacill
621	71.5	6.7	487	2	Q5J4D5_MOUSE	Q5j4d5	mus musculu
622	71.5	6.7	501	2	Q8KRH6_9XANT	Q8krh6	xanthomonas
623	71.5	6.7	516	2	Q4T9I8_TETNG	Q4t9i8	tetraodon n
624	71.5	6.7	538	2	Q5PQM8_RAT	Q5pqm8	rattus norv
625	71.5	6.7	540	2	Q936X7_PSESD	Q936x7	pseudomonas
626	71.5	6.7	556	2	Q642B9_RAT	Q642b9	rattus norv
627	71.5	6.7	608	2	Q55TX3_CRYNE	Q55tx3	cryptococcu
628	71.5	6.7	608	2	Q5KIG5_CRYNE	Q5kig5	cryptococcu
629	71.5	6.7	649	2	Q6JWU4_9BACT	Q6jwu4	uncultured
630	71.5	6.7	653	2	Q659D7_HUMAN	Q659d7	homo sapien
631	71.5	6.7	656	2	Q52GH0_MAGGR	Q52gh0	magnaporthe
632	71.5	6.7	667	2	Q70IK3_CHICK	Q70ik3	gallus gall
633	71.5	6.7	678	2	Q5P401_AZOSE	Q5p401	azoarcus sp
634	71.5	6.7	718	2	Q4Q5P3_LEIMA	Q4q5p3	leishmania
635	71.5	6.7	757	2	Q22043_CAEEL	Q22043	caenorhabdi
636	71.5	6.7	770	1	TLE1_MOUSE	Q62440	mus musculu
637	71.5	6.7	778	2	Q965D9_DROME	Q965d9	drosophila
638	71.5	6.7	907	2	Q4QJ40_LEIMA	Q4qj40	leishmania
639	71.5	6.7	928	2	Q89FD0_BRAJA	Q89fd0	bradyrhizob
640	71.5	6.7	939	2	Q6AUM2_ORYSA	Q6aum2	oryza sativ
641	71.5	6.7	971	1	GMIP_MOUSE	Q6pgg2	mus musculu
642	71.5	6.7	976	2	Q63NS5_BURPS	Q63ns5	burkholderi
643	71.5	6.7	993	2	Q8MQZ3_DROME	Q8mqz3	drosophila
644	71.5	6.7	993	2	Q9VSF2_DROME	Q9vsf2	drosophila
645	71.5	6.7	1007	2	O43379_HUMAN	O43379	homo sapien
646	71.5	6.7	1017	1	KCNH4_HUMAN	Q9uq05	homo sapien
647	71.5	6.7	1034	2	Q6N003_HUMAN	Q6n003	homo sapien
648	71.5	6.7	1034	2	Q8N260_HUMAN	Q8n260	homo sapien
649	71.5	6.7	1034	2	Q4VXM4_HUMAN	Q4vxm4	homo sapien
650	71.5	6.7	1061	2	Q62A81_BURMA	Q62a81	burkholderi
651	71.5	6.7	1129	2	Q5BD93_EMENI	Q5bd93	aspergillus
652	71.5	6.7	1156	2	Q4LJ64_9BURK	Q4lj64	burkholderi
653	71.5	6.7	1178	1	DSRAD_MOUSE	Q99mu3	mus musculu
654	71.5	6.7	1201	2	Q8XT74_RALSO	Q8xt74	ralstonia s
655	71.5	6.7	1248	2	Q5B480_EMENI	Q5b480	aspergillus
656	71.5	6.7	1255	1	TBCD1_MOUSE	Q60949	mus musculu
657	71.5	6.7	1335	2	Q7NCX8_GLOVI	Q7ncx8	gloeobacter
658	71.5	6.7	1377	2	Q5VPC8_ORYSA	Q5vpc8	oryza sativ
659	71.5	6.7	1560	2	Q4SJ00_TETNG	Q4sj00	tetraodon n
660	71.5	6.7	1980	2	Q6F3A3_ORYSA	Q6f3a3	oryza sativ
661	71.5	6.7	2471	1	NOTC2_RAT	Q9qw30	rattus norv
662	71.5	6.7	2577	2	Q4WM65_ASPFU	Q4wm65	aspergillus
663	71.5	6.7	4535	2	Q5YV27_NOCFA	Q5yv27	nocardia fa
664	71	6.6	68	2	Q6Q7E1_ORYSA	Q6q7e1	oryza sativ
665	71	6.6	206	2	Q6IA03_HUMAN	Q6ia03	homo sapien
666	71	6.6	220	2	Q6NIR0_CORDI	Q6nir0	corynebacte
667	71	6.6	285	2	Q8PLZ9_XANAC	Q8plz9	xanthomonas
668	71	6.6	292	2	Q8GRL4_ORYSA	Q8grl4	oryza sativ
669	71	6.6	320	2	Q8WYY1_HUMAN	Q8wyy1	homo sapien
670	71	6.6	322	1	FOS_AVINK	P23050	avian retro
671	71	6.6	325	2	Q9XA63_STRCO	Q9xa63	streptomyce
672	71	6.6	329	2	Q49974_MYCLE	Q49974	mycobacteri
673	71	6.6	332	2	Q4HA73_9DEIO	Q4ha73	deinococcus
674	71	6.6	337	2	Q4RNI3_TETNG	Q4rni3	tetraodon n
675	71	6.6	342	1	CRTB_STRGR	P54977	streptomyce
676	71	6.6	350	2	Q7NCN9_GLOVI	Q7ncn9	gloeobacter
677	71	6.6	367	1	FOS_CHICK	P11939	gallus gall
678	71	6.6	377	2	Q14097_HUMAN	Q14097	homo sapien
679	71	6.6	382	2	Q8LPU3_MAIZE	Q8lpu3	zea mays (m
680	71	6.6	406	2	Q8VPN0_9MICC	Q8vpn0	micrococcus
681	71	6.6	406	2	O11374_MCV1	O11374	molluscum c
682	71	6.6	407	2	Q9CCH4_MYCLE	Q9cch4	mycobacteri
683	71	6.6	420	2	Q9KWX1_STRAM	Q9kwx1	streptomyce
684	71	6.6	428	2	Q6DCG5_XENLA	Q6dcg5	xenopus lae
685	71	6.6	440	2	Q9F2E4_STRTE	Q9f2e4	streptomyce
686	71	6.6	448	2	Q7QBL0_ANOGA	Q7qbl0	anopheles g
687	71	6.6	483	2	Q8N6K9_HUMAN	Q8n6k9	homo sapien
688	71	6.6	533	2	Q4U0D3_ORYSA	Q4u0d3	oryza sativ

689	71	6.6	553	2	Q6YUK1_ORYSA	Q6yuk1	oryza sativ
690	71	6.6	553	2	Q6ZXE0_PASPI	Q6zxe0	pasteurella
691	71	6.6	555	2	Q9RL02_STRCO	Q9rl02	streptomyce
692	71	6.6	565	2	Q8JT94_9INFA	Q8jt94	influenza a
693	71	6.6	565	2	Q8JT95_9INFA	Q8jt95	influenza a
694	71	6.6	604	1	ENR1_HUMAN	Q14264	h herv-r_7q
695	71	6.6	607	2	Q9L8D4_POLCB	Q9l8d4	polyangium
696	71	6.6	630	2	Q96AD9_HUMAN	Q96ad9	homo sapien
697	71	6.6	639	2	Q6SWQ1_HCMV	Q6swq1	human cytom
698	71	6.6	642	2	Q98310_MCV1	Q98310	molluscum c
699	71	6.6	649	2	Q6P7P7_RAT	Q6p7p7	rattus norv
700	71	6.6	655	2	Q7T1J7_ORYLA	Q7t1j7	oryzias lat
701	71	6.6	697	2	Q8S6A1_ORYSA	Q8s6a1	oryza sativ
702	71	6.6	756	2	Q4WKE4_ASPFU	Q4wke4	aspergillus
703	71	6.6	758	2	Q8N1P1_HUMAN	Q8n1p1	homo sapien
704	71	6.6	790	2	Q9NVK9_HUMAN	Q9nvk9	homo sapien
705	71	6.6	824	2	Q7XSS3_ORYSA	Q7xss3	oryza sativ
706	71	6.6	847	2	Q6PEH9_BRARE	Q6peh9	brachydanio
707	71	6.6	851	2	Q6V1P4_9ACTO	Q6v1p4	streptomyce
708	71	6.6	879	2	Q90ZT8_CHICK	Q90zt8	gallus gall
709	71	6.6	995	2	Q51JE4_MAGGR	Q51je4	magnaporthe
710	71	6.6	1028	2	Q4N321_THEPA	Q4n321	theileria p
711	71	6.6	1065	2	Q4TBD4_TETNG	Q4tbd4	tetraodon n
712	71	6.6	1077	2	O97217_LEIMA	O97217	leishmania
713	71	6.6	1104	2	Q4T9Q1_TETNG	Q4t9q1	tetraodon n
714	71	6.6	1248	2	Q6NR70_DROME	Q6nr70	drosophila
715	71	6.6	1248	2	Q9NGK5_DROME	Q9ngk5	drosophila
716	71	6.6	1248	2	Q8K3T2_SPAJD	Q8k3t2	spalax juda
717	71	6.6	1256	2	Q6AWE3_DROME	Q6awe3	drosophila
718	71	6.6	1256	2	Q9VGI6_DROME	Q9vgi6	drosophila
719	71	6.6	1463	2	Q5J8K4_MOUSE	Q5j8k4	mus musculu
720	71	6.6	1496	2	Q4WIA6_ASPFU	Q4wia6	aspergillus
721	71	6.6	1594	2	Q4RJJ1_TETNG	Q4rjj1	tetraodon n
722	71	6.6	1599	2	Q6V1P0_9ACTO	Q6v1p0	streptomyce
723	71	6.6	1964	2	Q8RUA5_ORYSA	Q8rua5	oryza sativ
724	71	6.6	2002	2	Q71S06_HUMAN	Q71s06	homo sapien
725	71	6.6	2028	2	Q4QHD9_LEIMA	Q4qhd9	leishmania
726	71	6.6	2104	1	YCF2_ADICA	Q85b60	adiantum ca
727	71	6.6	2483	2	Q4PHC5_USTMA	Q4phc5	ustilago ma
728	71	6.6	2564	1	SPTN4_HUMAN	Q9h254	homo sapien
729	71	6.6	2564	2	Q71S07_HUMAN	Q71s07	homo sapien
730	70.5	6.6	167	2	Q4H7Y8_9DEIO	Q4h7y8	deinococcus
731	70.5	6.6	219	2	Q5DAC0_SCHJA	Q5dac0	schistosoma
732	70.5	6.6	220	1	KPTA_AERPE	Q9yfp5	aeropyrum p
733	70.5	6.6	235	2	O59414_PYRHO	O59414	pyrococcus
734	70.5	6.6	273	2	Q8LNC0_ORYSA	Q8lnc0	oryza sativ
735	70.5	6.6	277	2	Q8C5Z1_MOUSE	Q8c5z1	mus musculu
736	70.5	6.6	288	2	Q9ATW7_MAIZE	Q9atw7	zea mays (m
737	70.5	6.6	299	2	Q93LB1_BIFAN	Q93lb1	bifidobacte
738	70.5	6.6	304	2	Q5SGX4_THET8	Q5sgx4	thermus the
739	70.5	6.6	313	1	HXA11_MOUSE	P31311	mus musculu
740	70.5	6.6	332	2	Q84CX2_9BACT	Q84cx2	uncultured
741	70.5	6.6	338	2	Q827A7_STRAW	Q827a7	streptomyce
742	70.5	6.6	340	2	Q5ZB44_ORYSA	Q5zb44	oryza sativ
743	70.5	6.6	364	2	Q7XMQ5_ORYSA	Q7xmq5	oryza sativ
744	70.5	6.6	376	2	Q852V8_9CAUD	Q852v8	mycobacteri
745	70.5	6.6	384	2	Q73SL9_MYCPA	Q73sl9	mycobacteri
746	70.5	6.6	389	2	Q9F8T4_9ACTO	Q9f8t4	streptomyce
747	70.5	6.6	393	2	Q8PQY5_XANAC	Q8pqy5	xanthomonas
748	70.5	6.6	414	2	Q9W2B8_DROME	Q9w2b8	drosophila
749	70.5	6.6	429	2	Q69JZ6_ORYSA	Q69jz6	oryza sativ
750	70.5	6.6	451	2	Q9FB34_9ACTO	Q9fb34	streptomyce
751	70.5	6.6	466	2	Q87XC9_PSESM	Q87xc9	pseudomonas
752	70.5	6.6	470	2	Q6MWN9_NEUCR	Q6mwn9	neurospora
753	70.5	6.6	501	2	Q5GUP5_XANOR	Q5gup5	xanthomonas
754	70.5	6.6	504	2	Q6XP41_DROSI	Q6xp41	drosophila
755	70.5	6.6	507	2	Q9RMT5_9ACTO	Q9rmt5	streptomyce
756	70.5	6.6	518	2	Q6NBU5_RHOPA	Q6nbu5	rhodopseudo
757	70.5	6.6	523	2	Q7SC11_NEUCR	Q7sc11	neurospora
758	70.5	6.6	525	2	Q6K663_ORYSA	Q6k663	oryza sativ
759	70.5	6.6	528	2	Q56D25_MELGA	Q56d25	meleagris g
760	70.5	6.6	533	2	Q93NX3_9ACTO	Q93nx3	streptomyce
761	70.5	6.6	554	2	O74775_SCHPO	O74775	schizosacch
762	70.5	6.6	562	2	Q885Q6_PSESM	Q885q6	pseudomonas
763	70.5	6.6	579	2	Q4RLQ1_TETNG	Q4rlq1	tetraodon n
764	70.5	6.6	625	2	Q96GX6_HUMAN	Q96gx6	homo sapien
765	70.5	6.6	635	2	Q7S7P2_NEUCR	Q7s7p2	neurospora
766	70.5	6.6	642	2	Q9C260_NEUCR	Q9c260	neurospora
767	70.5	6.6	656	1	GTR1_DROME	Q8iri6	drosophila
768	70.5	6.6	702	2	Q553Q2_DICDI	Q553q2	dictyosteli
769	70.5	6.6	705	1	ARHG7_MOUSE	Q9es28	mus musculu
770	70.5	6.6	738	2	Q5U1A7_DROME	Q5u1a7	drosophila
771	70.5	6.6	743	2	Q83111_ADEM1	Q83111	murine aden
772	70.5	6.6	756	2	Q96RZ1_HUMAN	Q96rz1	homo sapien
773	70.5	6.6	779	2	Q6FTP1_CANGA	Q6ftp1	candida gla
774	70.5	6.6	809	2	Q08693_YEAST	Q08693	saccharomyc
775	70.5	6.6	810	2	Q6XPA5_MOUSE	Q6xpa5	mus musculu
776	70.5	6.6	828	1	US6NL_HUMAN	Q92738	homo sapien
777	70.5	6.6	828	2	Q5VV10_HUMAN	Q5vv10	homo sapien
778	70.5	6.6	829	1	SYL_DESVH	Q72ct7	desulfovibr
779	70.5	6.6	835	2	Q82EK1_STRAW	Q82ek1	streptomyce
780	70.5	6.6	837	2	Q7ULU5_RHOBA	Q7ulu5	rhodopirell
781	70.5	6.6	873	2	Q9UTC4_SCHPO	Q9utc4	schizosacch
782	70.5	6.6	961	2	Q4V9K7_BRARE	Q4v9k7	brachydanio
783	70.5	6.6	986	2	Q7Z346_HUMAN	Q7z346	homo sapien
784	70.5	6.6	1039	2	Q52G03_MAGGR	Q52g03	magnaporthe
785	70.5	6.6	1050	2	Q7S1N5_NEUCR	Q7s1n5	neurospora
786	70.5	6.6	1060	2	Q96JE7_HUMAN	Q96je7	homo sapien
787	70.5	6.6	1061	2	Q5T5J3_HUMAN	Q5t5j3	homo sapien
788	70.5	6.6	1143	2	Q67C34_TOXGO	Q67c34	toxoplasma
789	70.5	6.6	1148	2	Q4NWB8_9DELT	Q4nwb8	anaeromyxob
790	70.5	6.6	1168	2	Q7SFD3_NEUCR	Q7sfd3	neurospora
791	70.5	6.6	1185	2	Q5ZJ69_CHICK	Q5zj69	gallus gall
792	70.5	6.6	1279	2	Q60E39_ORYSA	Q60e39	oryza sativ
793	70.5	6.6	1291	2	Q4P8Z4_USTMA	Q4p8z4	ustilago ma
794	70.5	6.6	1301	2	Q658Z4_HUMAN	Q658z4	homo sapien
795	70.5	6.6	1369	2	Q7XK18_ORYSA	Q7xk18	oryza sativ
796	70.5	6.6	1626	2	Q60EG9_ORYSA	Q60eg9	oryza sativ
797	70.5	6.6	1743	2	Q4QJD2_LEIMA	Q4qjd2	leishmania
798	70.5	6.6	1744	2	Q75L09_ORYSA	Q75l09	oryza sativ
799	70.5	6.6	1798	2	Q14997_HUMAN	Q14997	homo sapien
800	70.5	6.6	1809	2	Q75LQ3_ORYSA	Q75lq3	oryza sativ
801	70.5	6.6	1992	2	Q94LL4_ORYSA	Q94ll4	oryza sativ
802	70.5	6.6	2002	2	Q8H7Y0_ORYSA	Q8h7y0	oryza sativ
803	70.5	6.6	2027	2	Q5W7A5_ORYSA	Q5w7a5	oryza sativ
804	70.5	6.6	2027	2	Q60EK1_ORYSA	Q60ek1	oryza sativ
805	70.5	6.6	2027	2	Q7X5X7_ORYSA	Q7x5x7	oryza sativ
806	70.5	6.6	2027	2	Q7XJU8_ORYSA	Q7xju8	oryza sativ
807	70.5	6.6	2027	2	Q7XQ50_ORYSA	Q7xq50	oryza sativ
808	70.5	6.6	2429	2	Q5BB54_EMENI	Q5bb54	aspergillus
809	70.5	6.6	2434	2	Q4QIC5_LEIMA	Q4qic5	leishmania
810	70.5	6.6	3255	2	Q80P68_9POTV	Q80p68	lettuce mos
811	70	6.5	174	2	Q6ZVB0_HUMAN	Q6zvb0	homo sapien
812	70	6.5	176	2	Q60DE0_ORYSA	Q60de0	oryza sativ
813	70	6.5	195	2	Q8C685_MOUSE	Q8c685	mus musculu
814	70	6.5	203	2	Q8PT08_METMA	Q8pt08	methanosarc
815	70	6.5	205	2	Q4RBB5_TETNG	Q4rbb5	tetraodon n
816	70	6.5	231	2	Q5YZF7_NOCFA	Q5yzf7	nocardia fa
817	70	6.5	239	2	Q7WA04_BORPA	Q7wa04	bordetella
818	70	6.5	240	2	Q5TSH9_ANOGA	Q5tsh9	anopheles g
819	70	6.5	257	2	Q4W8A9_9CAUL	Q4w8a9	brevundimon
820	70	6.5	270	2	Q7F1T9_ORYSA	Q7f1t9	oryza sativ
821	70	6.5	288	2	Q6AFH6_LEIXX	Q6afh6	leifsonia x
822	70	6.5	299	2	Q4QDH1_LEIMA	Q4qdh1	leishmania
823	70	6.5	313	2	Q8N6H5_HUMAN	Q8n6h5	homo sapien
824	70	6.5	322	2	Q8NF12_HUMAN	Q8nf12	homo sapien
825	70	6.5	331	2	Q6P0G2_BRARE	Q6p0g2	brachydanio
826	70	6.5	349	2	Q4NJN5_9MICC	Q4njn5	arthrobacte
827	70	6.5	349	2	Q60C13_METCA	Q60c13	methylococc
828	70	6.5	374	2	Q9C5L2_ARATH	Q9c5l2	arabidopsis
829	70	6.5	381	1	SEPP1_HUMAN	P49908	homo sapien
830	70	6.5	393	2	Q58DV4_BOVIN	Q58dv4	bos taurus
831	70	6.5	393	2	Q9AK05_STRCO	Q9ak05	streptomyce
832	70	6.5	409	2	Q5PQP0_RAT	Q5pqp0	rattus norv
833	70	6.5	411	1	HOX3_BRAFL	P50901	branchiosto
834	70	6.5	420	2	Q9QVZ9_9MURI	Q9qvz9	mus sp. . b

835	70	6.5	452	2	Q5FR24_GLUOX	Q5fr24	gluconobact	908	69.5	6.5	355	2	Q7NEZ2_GLOVI	Q7nez2	gloeobacter
836	70	6.5	453	2	Q755B1_ASHGO	Q755b1	ashbya goss	909	69.5	6.5	364	2	Q51QJ7_MAGGR	Q51qj7	magnaporthe
837	70	6.5	475	2	Q6WB40_ALCFA	Q6wb40	alcaligenes	910	69.5	6.5	370	2	Q8N1P9_HUMAN	Q8n1p9	homo sapien
838	70	6.5	478	2	Q9DWF5_RCMVM	Q9dwf5	rat cytomeg	911	69.5	6.5	375	2	Q4PBU4_USTMA	Q4pbu4	ustilago ma
839	70	6.5	490	2	Q9M0C6_ARATH	Q9m0c6	arabidopsis	912	69.5	6.5	377	2	Q8JTC0_9PAPI	Q8jtc0	human papil
840	70	6.5	501	2	Q8NCL9_HUMAN	Q8ncl9	homo sapien	913	69.5	6.5	383	2	Q6X908_SALET	Q6x908	salmonella
841	70	6.5	510	2	Q9P6E6_NEUCR	Q9p6e6	neurospora	914	69.5	6.5	383	2	Q7BLG6_SALDU	Q7blg6	salmonella
842	70	6.5	516	2	Q7RVQ6_NEUCR	Q7rvq6	neurospora	915	69.5	6.5	383	2	Q8XQ65_RALSO	Q8xq65	ralstonia s
843	70	6.5	522	2	Q9FPK8_SOYBN	Q9fpk8	glycine max	916	69.5	6.5	383	2	O51802_SALTI	O51802	salmonella
844	70	6.5	537	2	Q8STL6_ENCCU	Q8stl6	encephalito	917	69.5	6.5	387	2	Q8XS28_RALSO	Q8xs28	ralstonia s
845	70	6.5	556	2	Q6CT22_KLULA	Q6ct22	kluyveromyc	918	69.5	6.5	389	2	Q4RQR8_TETNG	Q4rqr8	tetraodon n
846	70	6.5	598	2	Q4RKU3_TETNG	Q4rku3	tetraodon n	919	69.5	6.5	392	2	Q4WRX7_ASPFU	Q4wrx7	aspergillus
847	70	6.5	626	2	Q4PCP5_USTMA	Q4pcp5	ustilago ma	920	69.5	6.5	398	2	Q9W4Q1_DROME	Q9w4q1	drosophila
848	70	6.5	630	2	Q5Y0P4_9ALPH	Q5y0p4	cercopithec	921	69.5	6.5	399	1	BMP8B_MOUSE	P55105	mus musculu
849	70	6.5	640	1	GIDA_ANASP	Q8yr87	anabaena sp	922	69.5	6.5	399	2	Q8BNM2_MOUSE	Q8bnm2	mus musculu
850	70	6.5	673	2	Q8CI03_MOUSE	Q8ci03	mus musculu	923	69.5	6.5	410	2	Q4LES8_CHICK	Q4les8	gallus gall
851	70	6.5	701	2	Q4Q9D8_LEIMA	Q4q9d8	leishmania	924	69.5	6.5	414	2	Q6YYN0_ORYSA	Q6yyn0	oryza sativ
852	70	6.5	704	2	Q9ZQF9_ARATH	Q9zqf9	arabidopsis	925	69.5	6.5	418	2	Q6GLD9_XENTR	Q6gld9	xenopus tro
853	70	6.5	721	2	Q7SBP1_NEUCR	Q7sbp1	neurospora	926	69.5	6.5	427	2	Q7U9L5_SYNPX	Q7u9l5	synechococc
854	70	6.5	729	2	Q7NL00_GLOVI	Q7nl00	gloeobacter	927	69.5	6.5	429	2	Q58DC6_BOVIN	Q58dc6	bos taurus
855	70	6.5	733	2	Q4WQJ3_ASPFU	Q4wqj3	aspergillus	928	69.5	6.5	437	2	Q4Q1Z9_LEIMA	Q4q1z9	leishmania
856	70	6.5	750	2	Q8U9Q3_AGRT5	Q8u9q3	agrobacteri	929	69.5	6.5	441	2	Q8WUA3_HUMAN	Q8wua3	homo sapien
857	70	6.5	770	2	Q7CT18_AGRT5	Q7ct18	agrobacteri	930	69.5	6.5	470	2	Q4LTF0_9BURK	Q4ltf0	burkholderi
858	70	6.5	839	1	ZFP95_HUMAN	Q9y218	homo sapien	931	69.5	6.5	474	2	Q9M2K7_ARATH	Q9m2k7	arabidopsis
859	70	6.5	839	2	Q8N718_HUMAN	Q8n718	homo sapien	932	69.5	6.5	476	2	Q8W4L8_ARATH	Q8w418	arabidopsis
860	70	6.5	850	2	Q4J460_AZOVI	Q4j460	azotobacter	933	69.5	6.5	480	2	Q7UWG8_RHOBA	Q7uwg8	rhodopirell
861	70	6.5	900	2	Q5VX12_HUMAN	Q5vx12	homo sapien	934	69.5	6.5	482	2	Q5IAS7_PETMA	Q5ias7	petromyzon
862	70	6.5	903	2	Q4Q1T5_LEIMA	Q4q1t5	leishmania	935	69.5	6.5	497	2	Q55WA4_CRYNE	Q55wa4	cryptococcu
863	70	6.5	910	2	Q4QDC3_LEIMA	Q4qdc3	leishmania	936	69.5	6.5	497	2	Q5KJZ3_CRYNE	Q5kjz3	cryptococcu
864	70	6.5	913	1	E41LB_HUMAN	Q9h329	homo sapien	937	69.5	6.5	503	2	Q7G4G4_ORYSA	Q7g4g4	oryza sativ
865	70	6.5	914	2	Q6P9P8_MOUSE	Q6p9p8	mus musculu	938	69.5	6.5	504	2	Q6XUU8_DROYA	Q6xuu8	drosophila
866	70	6.5	939	2	O50435_MYCTU	O50435	mycobacteri	939	69.5	6.5	509	2	Q4QIW1_LEIMA	Q4qiw1	leishmania
867	70	6.5	939	2	Q7U0G3_MYCBO	Q7u0g3	mycobacteri	940	69.5	6.5	516	2	O54737_MOUSE	O54737	mus musculu
868	70	6.5	976	1	EPHA1_HUMAN	P21709	homo sapien	941	69.5	6.5	520	2	Q871E3_NEUCR	Q871e3	neurospora
869	70	6.5	977	2	Q8TET1_HUMAN	Q8tet1	homo sapien	942	69.5	6.5	521	2	Q5B339_EMENI	Q5b339	aspergillus
870	70	6.5	1020	2	Q4SE02_TETNG	Q4se02	tetraodon n	943	69.5	6.5	525	1	HRG_HUMAN	P04196	homo sapien
871	70	6.5	1112	2	Q7SBC1_NEUCR	Q7sbc1	neurospora	944	69.5	6.5	528	1	PDZK7_PONPY	Q5rbi7	pongo pygma
872	70	6.5	1150	2	Q872W5_NEUCR	Q872w5	neurospora	945	69.5	6.5	530	1	TBX21_MOUSE	Q9jkd8	mus musculu
873	70	6.5	1172	2	Q4JT60_CORJK	Q4jt60	corynebacte	946	69.5	6.5	533	2	Q9L398_9SPHN	Q9l398	sphingomona
874	70	6.5	1235	2	Q8PF69_XANAC	Q8pf69	xanthomonas	947	69.5	6.5	545	2	Q9BIE7_LEIDO	Q9bie7	leishmania
875	70	6.5	1236	2	Q9NED7_LEIMA	Q9ned7	leishmania	948	69.5	6.5	548	2	Q52ER6_MAGGR	Q52er6	magnaporthe
876	70	6.5	1249	2	Q9I1H0_PSEAE	Q9i1h0	pseudomonas	949	69.5	6.5	557	2	Q61TY0_CAEBR	Q61ty0	caenorhabdi
877	70	6.5	1284	2	Q4VXQ5_HUMAN	Q4vxq5	homo sapien	950	69.5	6.5	597	2	Q60EH4_ORYSA	Q60eh4	oryza sativ
878	70	6.5	1284	2	Q6PI59_HUMAN	Q6pi59	homo sapien	951	69.5	6.5	602	2	Q6ZMU2_HUMAN	Q6zmu2	homo sapien
879	70	6.5	1297	2	Q4VXQ4_HUMAN	Q4vxq4	homo sapien	952	69.5	6.5	603	2	Q4Q3U5_LEIMA	Q4q3u5	leishmania
880	70	6.5	1329	1	K1510_HUMAN	Q9p218	homo sapien	953	69.5	6.5	608	2	Q54PV7_DICDI	Q54pv7	dictyosteli
881	70	6.5	1387	2	Q59HC5_HUMAN	Q59hc5	homo sapien	954	69.5	6.5	624	2	Q62065_MOUSE	Q62065	mus musculu
882	70	6.5	1390	2	O49145_9BRAS	O49145	arabidopsis	955	69.5	6.5	625	2	Q91ZZ6_MOUSE	Q91zz6	mus musculu
883	70	6.5	1528	2	Q4Q6D2_LEIMA	Q4q6d2	leishmania	956	69.5	6.5	630	2	Q5AXR7_EMENI	Q5axr7	aspergillus
884	70	6.5	1558	2	Q4S160_TETNG	Q4s160	tetraodon n	957	69.5	6.5	633	2	Q7S6H3_NEUCR	Q7s6h3	neurospora
885	70	6.5	1683	2	Q4PAA9_USTMA	Q4paa9	ustilago ma	958	69.5	6.5	639	2	Q7NXL6_CHRVO	Q7nxl6	chromobacte
886	70	6.5	1845	1	ZN236_HUMAN	Q9ul36	homo sapien	959	69.5	6.5	646	2	Q8C750_MOUSE	Q8c750	mus musculu
887	70	6.5	1912	2	Q70P95_9DELT	Q70p95	melittangiu	960	69.5	6.5	663	2	Q7TN12_MOUSE	Q7tn12	mus musculu
888	70	6.5	2030	1	DOCK3_HUMAN	Q8izd9	homo sapien	961	69.5	6.5	702	2	Q9JME1_MOUSE	Q9jme1	mus musculu
889	70	6.5	2126	1	WNK1_RAT	Q9jih7	rattus norv	962	69.5	6.5	706	2	Q6C842_YARLI	Q6c842	yarrowia li
890	70	6.5	2153	2	Q4SI85_TETNG	Q4si85	tetraodon n	963	69.5	6.5	717	2	Q72CZ1_DESVH	Q72cz1	desulfovibr
891	70	6.5	3908	2	Q7N4L0_PHOLL	Q7n4l0	photorhabdu	964	69.5	6.5	745	2	Q4S5H3_TETNG	Q4s5h3	tetraodon n
892	70	6.5	4998	2	Q8CG65_MOUSE	Q8cg65	mus musculu	965	69.5	6.5	780	2	Q4WKJ3_ASPFU	Q4wkj3	aspergillus
893	69.5	6.5	39	2	Q9TUP3_PIG	Q9tup3	sus scrofa	966	69.5	6.5	794	2	Q9ZV35_ARATH	Q9zv35	arabidopsis
894	69.5	6.5	39	2	Q9TUP4_SHEEP	Q9tup4	ovis aries	967	69.5	6.5	796	2	Q84W96_ARATH	Q84w96	arabidopsis
895	69.5	6.5	39	2	Q9TUP5_BOVIN	Q9tup5	bos taurus	968	69.5	6.5	809	2	Q6ZQI5_MOUSE	Q6zqi5	mus musculu
896	69.5	6.5	146	2	Q9S2C5_STRCO	Q9s2c5	streptomyce	969	69.5	6.5	848	2	Q4P2C4_USTMA	Q4p2c4	ustilago ma
897	69.5	6.5	185	2	Q6Z3W7_ORYSA	Q6z3w7	oryza sativ	970	69.5	6.5	853	2	Q5T5P1_HUMAN	Q5t5p1	homo sapien
898	69.5	6.5	187	2	Q8C6B6_MOUSE	Q8c6b6	mus musculu	971	69.5	6.5	854	2	Q9QZS8_MOUSE	Q9qzs8	mus musculu
899	69.5	6.5	213	2	Q7WX35_ALCEU	Q7wx35	alcaligenes	972	69.5	6.5	863	2	Q7X6I5_ORYSA	Q7x6i5	oryza sativ
900	69.5	6.5	238	2	Q8NRF2_CORGL	Q8nrf2	corynebacte	973	69.5	6.5	866	2	Q51W43_MAGGR	Q51w43	magnaporthe
901	69.5	6.5	257	2	Q6I5I7_ORYSA	Q6i5i7	oryza sativ	974	69.5	6.5	882	2	Q80TZ9_MOUSE	Q80tz9	mus musculu
902	69.5	6.5	279	2	Q5E9I2_BOVIN	Q5e9i2	bos taurus	975	69.5	6.5	895	2	Q5H070_XANOR	Q5h070	xanthomonas
903	69.5	6.5	293	1	METRN_HUMAN	Q9ujh8	homo sapien	976	69.5	6.5	915	2	Q4QJK2_LEIMA	Q4qjk2	leishmania
904	69.5	6.5	342	2	Q89DI9_BRAJA	Q89di9	bradyrhizob	977	69.5	6.5	928	2	Q4QG25_LEIMA	Q4qg25	leishmania
905	69.5	6.5	346	2	Q4TA93_TETNG	Q4ta93	tetraodon n	978	69.5	6.5	963	2	Q53JI0_ORYSA	Q53ji0	oryza sativ
906	69.5	6.5	350	2	Q57YX9_9TRYP	Q57yx9	trypanosoma	979	69.5	6.5	981	2	Q8CBC0_MOUSE	Q8cbc0	mus musculu
907	69.5	6.5	353	2	Q7W0K5_BORPE	Q7w0k5	bordetella	980	69.5	6.5	981	2	Q8C881_MOUSE	Q8c881	mus musculu

981	69.5	6.5	981	2	Q6NSW2_MOUSE	Q6nsw2	mus musculu
982	69.5	6.5	985	2	Q6P9A4_HUMAN	Q6p9a4	homo sapien
983	69.5	6.5	989	2	Q99ML9_MOUSE	Q99ml9	mus musculu
984	69.5	6.5	994	2	Q6ZNA4_HUMAN	Q6zna4	homo sapien
985	69.5	6.5	995	2	Q9Y2W4_HUMAN	Q9y2w4	homo sapien
986	69.5	6.5	1006	2	Q4J097_AZOVI	Q4j097	azotobacter
987	69.5	6.5	1006	2	Q62901_RAT	Q62901	rattus norv
988	69.5	6.5	1008	2	Q4WI81_ASPFU	Q4wi81	aspergillus
989	69.5	6.5	1012	2	O43393_HUMAN	O43393	homo sapien
990	69.5	6.5	1012	2	O75359_HUMAN	O75359	homo sapien
991	69.5	6.5	1021	2	Q4LQQ6_9BURK	Q4lqq6	burkholderi
992	69.5	6.5	1058	2	Q4WPY5_ASPFU	Q4wpy5	aspergillus
993	69.5	6.5	1093	2	Q5F4A7_CHICK	Q5f4a7	gallus gall
994	69.5	6.5	1096	2	Q6AUQ8_ORYSA	Q6auq8	oryza sativ
995	69.5	6.5	1167	2	Q5H6K1_XANOR	Q5h6k1	xanthomonas
996	69.5	6.5	1168	1	HIPK2_MESAU	Q9wum7	mesocricetu
997	69.5	6.5	1169	2	Q5D0E9_MOUSE	Q5d0e9	mus musculu
998	69.5	6.5	1196	1	HIPK2_MOUSE	Q9qzr5	mus musculu
999	69.5	6.5	1221	2	Q6F2R9_ORYSA	Q6f2r9	oryza sativ
1000	69.5	6.5	1264	2	Q5T5P3_HUMAN	Q5t5p3	homo sapien
1001	69.5	6.5	1296	2	O75046_HUMAN	O75046	homo sapien
1002	69.5	6.5	1298	2	Q5VY47_HUMAN	Q5vy47	homo sapien
1003	69.5	6.5	1339	2	Q9ULK3_HUMAN	Q9ulk3	homo sapien
1004	69.5	6.5	1384	2	Q7FAE8_ORYSA	Q7fae8	oryza sativ
1005	69.5	6.5	1469	2	Q8GDM7_PHOLU	Q8gdm7	photorhabdu
1006	69.5	6.5	1471	2	Q7N9I0_PHOLL	Q7n9i0	photorhabdu
1007	69.5	6.5	1506	2	Q6P6B9_HUMAN	Q6p6b9	homo sapien
1008	69.5	6.5	1547	2	Q7XQB4_ORYSA	Q7xqb4	oryza sativ
1009	69.5	6.5	1566	2	Q9P2R6_HUMAN	Q9p2r6	homo sapien
1010	69.5	6.5	1566	2	Q5VXL9_HUMAN	Q5vxl9	homo sapien
1011	69.5	6.5	1622	2	Q84KC9_HORVU	Q84kc9	hordeum vul
1012	69.5	6.5	1641	2	Q846W5_STRCM	Q846w5	streptomyce
1013	69.5	6.5	1740	2	Q8LN99_ORYSA	Q8ln99	oryza sativ
1014	69.5	6.5	1807	2	Q7XE08_ORYSA	Q7xe08	oryza sativ
1015	69.5	6.5	1850	2	Q8LN70_ORYSA	Q8ln70	oryza sativ
1016	69.5	6.5	1862	2	Q60EM9_ORYSA	Q60em9	oryza sativ
1017	69.5	6.5	1863	2	Q5T5P2_HUMAN	Q5t5p2	homo sapien
1018	69.5	6.5	1863	2	Q6AU96_ORYSA	Q6au96	oryza sativ
1019	69.5	6.5	1909	2	Q7XPN1_ORYSA	Q7xpn1	oryza sativ
1020	69.5	6.5	1910	2	Q7XU19_ORYSA	Q7xu19	oryza sativ
1021	69.5	6.5	1937	2	Q75M23_ORYSA	Q75m23	oryza sativ
1022	69.5	6.5	1946	2	Q7XNG6_ORYSA	Q7xng6	oryza sativ
1023	69.5	6.5	1975	2	Q7XNY4_ORYSA	Q7xny4	oryza sativ
1024	69.5	6.5	1989	2	Q6ATB5_ORYSA	Q6atb5	oryza sativ
1025	69.5	6.5	1992	2	Q65WT1_ORYSA	Q65wt1	oryza sativ
1026	69.5	6.5	1992	2	Q7XWS1_ORYSA	Q7xws1	oryza sativ
1027	69.5	6.5	2015	2	Q7XT04_ORYSA	Q7xt04	oryza sativ
1028	69.5	6.5	2025	2	Q7G4G2_ORYSA	Q7g4g2	oryza sativ
1029	69.5	6.5	2026	2	Q7XE40_ORYSA	Q7xe40	oryza sativ
1030	69.5	6.5	2027	2	Q5VSX0_ORYSA	Q5vsx0	oryza sativ
1031	69.5	6.5	2027	2	Q65X63_ORYSA	Q65x63	oryza sativ
1032	69.5	6.5	2027	2	Q7F9Y4_ORYSA	Q7f9y4	oryza sativ
1033	69.5	6.5	2027	2	Q7X7G0_ORYSA	Q7x7g0	oryza sativ
1034	69.5	6.5	2027	2	Q7XLL0_ORYSA	Q7xll0	oryza sativ
1035	69.5	6.5	2027	2	Q7XLL4_ORYSA	Q7xll4	oryza sativ
1036	69.5	6.5	2027	2	Q7XNC3_ORYSA	Q7xnc3	oryza sativ
1037	69.5	6.5	2027	2	Q7XT93_ORYSA	Q7xt93	oryza sativ
1038	69.5	6.5	2027	2	Q84T69_ORYSA	Q84t69	oryza sativ
1039	69.5	6.5	2027	2	Q8GTA9_ORYSA	Q8gta9	oryza sativ
1040	69.5	6.5	2027	2	Q94LM2_ORYSA	Q94lm2	oryza sativ
1041	69.5	6.5	2027	2	Q75G96_ORYSA	Q75g96	oryza sativ
1042	69.5	6.5	2027	2	Q53NC4_ORYSA	Q53nc4	oryza sativ
1043	69.5	6.5	2028	2	Q7XL20_ORYSA	Q7xl20	oryza sativ
1044	69.5	6.5	2028	2	Q7XQS6_ORYSA	Q7xqs6	oryza sativ
1045	69.5	6.5	2158	2	Q9RR50_VIBCH	Q9rr50	vibrio chol
1046	69.5	6.5	2433	2	Q7Q6M0_ANOGA	Q7q6m0	anopheles g
1047	69	6.4	109	1	CORT_MOUSE	P56469	mus musculu
1048	69	6.4	146	1	VEGFA_SHEEP	P50412	ovis aries
1049	69	6.4	183	2	Q7WLD2_BORBR	Q7wld2	bordetella
1050	69	6.4	183	2	Q7VX35_BORPE	Q7vx35	bordetella
1051	69	6.4	190	2	O77643_SHEEP	O77643	ovis aries
1052	69	6.4	210	2	Q6II77_DROME	Q6ii77	drosophila
1053	69	6.4	220	2	Q4T034_TETNG	Q4t034	tetraodon n
1054	69	6.4	224	1	TCTD_SALTY	P22104	salmonella
1055	69	6.4	224	2	Q57KZ0_SALCH	Q57kz0	salmonella
1056	69	6.4	224	2	Q5PEW9_SALPA	Q5pew9	salmonella
1057	69	6.4	230	2	Q8IV78_HUMAN	Q8iv78	homo sapien
1058	69	6.4	256	2	Q53Q42_ORYSA	Q53q42	oryza sativ
1059	69	6.4	264	2	Q53WD3_THET8	Q53wd3	thermus the
1060	69	6.4	306	2	Q4HYM6_GIBZE	Q4hym6	gibberella
1061	69	6.4	308	2	Q6WN33_HUMAN	Q6wn33	homo sapien
1062	69	6.4	311	2	Q6B7I8_DROVI	Q6b7i8	drosophila
1063	69	6.4	315	2	Q7T7M3_9VIRU	Q7t7m3	tobacco cur
1064	69	6.4	315	2	Q7T7M5_9VIRU	Q7t7m5	tobacco cur
1065	69	6.4	315	2	Q4LBA4_9VIRU	Q4lba4	tobacco lea
1066	69	6.4	315	2	Q4LBA5_9VIRU	Q4lba5	tobacco lea
1067	69	6.4	317	2	Q84H95_STRCZ	Q84h95	streptomyce
1068	69	6.4	325	2	Q5R0I7_IDILO	Q5r0i7	idiomarina
1069	69	6.4	339	2	Q7U9U8_SYNPX	Q7u9u8	synechococc
1070	69	6.4	352	2	Q8XR24_RALSO	Q8xr24	ralstonia s
1071	69	6.4	370	2	Q7S6P1_NEUCR	Q7s6p1	neurospora
1072	69	6.4	379	2	Q9YKK1_9VIRU	Q9ykk1	epizootic h
1073	69	6.4	395	2	Q67RJ2_SYMTH	Q67rj2	symbiobacte
1074	69	6.4	407	2	Q7NEQ6_GLOVI	Q7neq6	gloeobacter
1075	69	6.4	410	2	Q93HA2_STRAW	Q93ha2	streptomyce
1076	69	6.4	412	2	P91666_DROME	P91666	drosophila
1077	69	6.4	419	1	GSC_DROME	P54366	drosophila
1078	69	6.4	424	2	Q8VMP8_PSEPU	Q8vmp8	pseudomonas
1079	69	6.4	429	1	CRDL2_HUMAN	Q6wn34	homo sapien
1080	69	6.4	436	2	Q67UQ7_ORYSA	Q67uq7	oryza sativ
1081	69	6.4	438	2	Q73ZU8_MYCPA	Q73zu8	mycobacteri
1082	69	6.4	445	2	Q9LS39_ARATH	Q9ls39	arabidopsis
1083	69	6.4	459	2	Q4TRK9_9SPHN	Q4trk9	erythrobact
1084	69	6.4	475	2	O22794_ARATH	O22794	arabidopsis
1085	69	6.4	489	2	Q4Q8T9_LEIMA	Q4q8t9	leishmania
1086	69	6.4	493	2	Q4PBE8_USTMA	Q4pbe8	ustilago ma
1087	69	6.4	493	2	Q4NTU5_9DELT	Q4ntu5	anaeromyxob
1088	69	6.4	494	2	Q6PKG4_HUMAN	Q6pkg4	homo sapien
1089	69	6.4	495	2	Q5R4V6_PONPY	Q5r4v6	pongo pygma
1090	69	6.4	508	1	CP27B_HUMAN	O15528	h 25-hydrox
1091	69	6.4	508	2	Q548T3_HUMAN	Q548t3	homo sapien
1092	69	6.4	510	2	Q4WU97_ASPFU	Q4wu97	aspergillus
1093	69	6.4	521	2	Q6INA0_HUMAN	Q6ina0	homo sapien
1094	69	6.4	526	2	Q8PQL8_XANAC	Q8pql8	xanthomonas
1095	69	6.4	558	1	C4BP_RAT	Q63514	rattus norv
1096	69	6.4	565	2	Q8JT91_9INFA	Q8jt91	influenza a
1097	69	6.4	569	2	Q7W4P6_BORPA	Q7w4p6	bordetella
1098	69	6.4	569	2	Q7WG72_BORBR	Q7wg72	bordetella
1099	69	6.4	574	2	O95038_HUMAN	O95038	homo sapien
1100	69	6.4	574	2	Q9CZ49_MOUSE	Q9cz49	mus musculu
1101	69	6.4	583	2	Q9PD62_XYLFA	Q9pd62	xylella fas
1102	69	6.4	583	2	Q8CAW8_MOUSE	Q8caw8	mus musculu
1103	69	6.4	594	2	Q9NWE7_HUMAN	Q9nwe7	homo sapien
1104	69	6.4	601	2	Q5M891_RAT	Q5m891	rattus norv
1105	69	6.4	609	2	Q6P5Y2_HUMAN	Q6p5y2	homo sapien
1106	69	6.4	624	2	Q4NMI9_9MICC	Q4nmi9	arthrobacte
1107	69	6.4	625	2	Q923I5_RAT	Q923i5	rattus norv
1108	69	6.4	633	2	Q4SBN0_TETNG	Q4sbn0	tetraodon n
1109	69	6.4	636	2	Q4Q4S4_LEIMA	Q4q4s4	leishmania
1110	69	6.4	639	2	Q6SWG8_HCMV	Q6swg8	human cytom
1111	69	6.4	639	2	Q6SWM3_HCMV	Q6swm3	human cytom
1112	69	6.4	646	1	ARHG7_RAT	O55043	rattus norv
1113	69	6.4	658	2	Q7SAM2_NEUCR	Q7sam2	neurospora
1114	69	6.4	658	2	Q66HC8_RAT	Q66hc8	rattus norv
1115	69	6.4	671	1	HMOC_DROME	P22810	drosophila
1116	69	6.4	705	2	Q52NK0_RAT	Q52nk0	rattus norv
1117	69	6.4	717	2	Q9VW27_DROME	Q9vw27	drosophila
1118	69	6.4	768	2	Q4Q642_LEIMA	Q4q642	leishmania
1119	69	6.4	770	2	Q6YSG5_ORYSA	Q6ysg5	oryza sativ
1120	69	6.4	780	2	Q6L5C9_ORYSA	Q6l5c9	oryza sativ
1121	69	6.4	782	2	Q5NKL4_CRYNV	Q5nkl4	cryptococcu
1122	69	6.4	810	2	Q5KNA7_CRYNE	Q5kna7	cryptococcu
1123	69	6.4	836	2	Q5NKL7_CRYNV	Q5nkl7	cryptococcu
1124	69	6.4	843	2	Q55YZ1_CRYNE	Q55yz1	cryptococcu
1125	69	6.4	850	2	Q6FY00_CANGA	Q6fy00	candida gla
1126	69	6.4	873	2	Q4PGS2_USTMA	Q4pgs2	ustilago ma

1127	69	6.4	926	2	Q6MFS5_NEUCR	Q6mfs5 neurospora	1200	68.5	6.4	281	2	Q68L53_9DIPT	Q68153 drosophila				
1128	69	6.4	939	2	Q4NZ34_9DELT	Q4nz34 anaeromyxob	1201	68.5	6.4	282	2	Q68L04_9DIPT	Q68104 drosophila				
1129	69	6.4	954	1	GCSP_AGRT5	Q8ufd6 agrobacteri	1202	68.5	6.4	282	2	Q68L07_9DIPT	Q68107 drosophila				
1130	69	6.4	1003	1	MBD6_HUMAN	Q96dn6 homo sapien	1203	68.5	6.4	282	2	Q68L12_9DIPT	Q68112 drosophila				
1131	69	6.4	1003	2	Q6P0P0_HUMAN	Q6p0p0 homo sapien	1204	68.5	6.4	282	2	Q68L15_9DIPT	Q68115 drosophila				
1132	69	6.4	1011	2	Q6VU50_MANSE	Q6vu50 manduca sex	1205	68.5	6.4	282	2	Q68L16_9DIPT	Q68116 drosophila				
1133	69	6.4	1025	2	Q4QGS8_LEIMA	Q4qgs8 leishmania	1206	68.5	6.4	282	2	Q68L73_9DIPT	Q68173 drosophila				
1134	69	6.4	1032	2	Q9SSW6_ORYSA	Q9ssw6 oryza sativ	1207	68.5	6.4	283	2	Q68KY6_9DIPT	Q68ky6 drosophila				
1135	69	6.4	1051	2	Q4SML2_TETNG	Q4sml2 tetraodon n	1208	68.5	6.4	283	2	Q68KZ0_9DIPT	Q68kz0 drosophila				
1136	69	6.4	1116	2	Q07898_HUMAN	Q07898 homo sapien	1209	68.5	6.4	283	2	Q68KZ4_9DIPT	Q68kz4 drosophila				
1137	69	6.4	1151	2	Q07899_HUMAN	Q07899 homo sapien	1210	68.5	6.4	283	2	Q68KZ5_9DIPT	Q68kz5 drosophila				
1138	69	6.4	1154	2	Q4HYE3_GIBZE	Q4hye3 gibberella	1211	68.5	6.4	283	2	Q68L02_9DIPT	Q68102 drosophila				
1139	69	6.4	1156	2	Q86VB7_HUMAN	Q86vb7 homo sapien	1212	68.5	6.4	283	2	Q68L18_9DIPT	Q68118 drosophila				
1140	69	6.4	1156	2	Q07900_HUMAN	Q07900 homo sapien	1213	68.5	6.4	283	2	Q68L19_9DIPT	Q68119 drosophila				
1141	69	6.4	1172	2	Q89LE3_BRAJA	Q89le3 bradyrhizob	1214	68.5	6.4	283	2	Q68L44_9DIPT	Q68144 drosophila				
1142	69	6.4	1289	2	Q4WXZ2_ASPFU	Q4wxz2 aspergillus	1215	68.5	6.4	283	2	Q68L47_9DIPT	Q68147 drosophila				
1143	69	6.4	1395	2	Q88KC1_PSEPK	Q88kc1 pseudomonas	1216	68.5	6.4	283	2	Q68L50_9DIPT	Q68150 drosophila				
1144	69	6.4	1440	1	URFB1_HUMAN	Q6bds2 homo sapien	1217	68.5	6.4	283	2	Q68L58_9DIPT	Q68158 drosophila				
1145	69	6.4	1510	2	Q570Z6_MOUSE	Q570z6 mus musculu	1218	68.5	6.4	283	2	Q68L67_9DIPT	Q68167 drosophila				
1146	69	6.4	1513	2	Q4RNH1_TETNG	Q4rnh1 tetraodon n	1219	68.5	6.4	283	2	Q68L72_9DIPT	Q68172 drosophila				
1147	69	6.4	1610	2	Q22173_CAEEL	Q22173 caenorhabdi	1220	68.5	6.4	283	2	Q5VR94_ORYSA	Q5vr94 oryza sativ				
1148	69	6.4	1673	2	Q4RSP7_TETNG	Q4rsp7 tetraodon n	1221	68.5	6.4	284	2	Q68L48_9DIPT	Q68148 drosophila				
1149	69	6.4	1710	2	Q4PEE4_USTMA	Q4pee4 ustilago ma	1222	68.5	6.4	284	2	Q68KZ9_9DIPT	Q68kz9 drosophila				
1150	69	6.4	1776	1	POLR_OYMV	P20127 ononis yell	1223	68.5	6.4	284	2	Q68L00_9DIPT	Q68100 drosophila				
1151	69	6.4	1778	2	Q8IWR5_HUMAN	Q8iwr5 homo sapien	1224	68.5	6.4	284	2	Q68L01_9DIPT	Q68101 drosophila				
1152	69	6.4	1831	2	Q7X8X0_ORYSA	Q7x8x0 oryza sativ	1225	68.5	6.4	284	2	Q68L09_9DIPT	Q68109 drosophila				
1153	69	6.4	1858	2	Q8IZD2_HUMAN	Q8izd2 homo sapien	1226	68.5	6.4	284	2	Q68L17_9DIPT	Q68117 drosophila				
1154	69	6.4	1858	2	Q8NFF8_HUMAN	Q8nff8 homo sapien	1227	68.5	6.4	284	2	Q68L22_9DIPT	Q68122 drosophila				
1155	69	6.4	1953	2	Q60DU9_ORYSA	Q60du9 oryza sativ	1228	68.5	6.4	284	2	Q68L33_9DIPT	Q68133 drosophila				
1156	69	6.4	1986	2	Q8LMM6_ORYSA	Q8lmm6 oryza sativ	1229	68.5	6.4	284	2	Q68L34_9DIPT	Q68134 drosophila				
1157	69	6.4	1992	2	Q7F9R8_ORYSA	Q7f9r8 oryza sativ	1230	68.5	6.4	284	2	Q68L40_9DIPT	Q68140 drosophila				
1158	69	6.4	1995	2	Q7XDS6_ORYSA	Q7xds6 oryza sativ	1231	68.5	6.4	284	2	Q68L41_9DIPT	Q68141 drosophila				
1159	69	6.4	2004	2	Q5GR23_9VIRU	Q5gr23 daphne viru	1232	68.5	6.4	284	2	Q68L54_9DIPT	Q68154 drosophila				
1160	69	6.4	2010	2	Q7XPQ7_ORYSA	Q7xpq7 oryza sativ	1233	68.5	6.4	284	2	Q68L60_9DIPT	Q68160 drosophila				
1161	69	6.4	2013	2	Q7XXB9_ORYSA	Q7xxb9 oryza sativ	1234	68.5	6.4	284	2	Q68L61_9DIPT	Q68161 drosophila				
1162	69	6.4	2017	2	Q8LMM4_ORYSA	Q8lmm4 oryza sativ	1235	68.5	6.4	285	2	Q68L06_9DIPT	Q68106 drosophila				
1163	69	6.4	2017	2	Q93Y89_ORYSA	Q93y89 oryza sativ	1236	68.5	6.4	285	2	Q68L08_9DIPT	Q68108 drosophila				
1164	69	6.4	2167	1	SHAN1_RAT	Q9wv48 rattus norv	1237	68.5	6.4	285	2	Q68L11_9DIPT	Q68111 drosophila				
1165	69	6.4	2429	2	Q4PAD1_USTMA	Q4pad1 ustilago ma	1238	68.5	6.4	285	2	Q68L14_9DIPT	Q68114 drosophila				
1166	69	6.4	2689	2	Q4QF64_LEIMA	Q4qf64 leishmania	1239	68.5	6.4	285	2	Q68L25_9DIPT	Q68125 drosophila				
1167	69	6.4	2699	2	Q5BLQ2_HUMAN	Q5blq2 homo sapien	1240	68.5	6.4	285	2	Q68L27_9DIPT	Q68127 drosophila				
1168	69	6.4	2869	2	Q28398_ERIEU	Q28398 erinaceus e	1241	68.5	6.4	285	2	Q68L29_9DIPT	Q68129 drosophila				
1169	68.5	6.4	95	2	Q7QZN9_GIALA	Q7qzn9 giardia lam	1242	68.5	6.4	285	2	Q68L31_9DIPT	Q68131 drosophila				
1170	68.5	6.4	128	2	Q6WZL9_MOUSE	Q6wzl9 mus musculu	1243	68.5	6.4	285	2	Q68L32_9DIPT	Q68132 drosophila				
1171	68.5	6.4	141	2	O70123_MOUSE	O70123 mus musculu	1244	68.5	6.4	285	2	Q68L37_9DIPT	Q68137 drosophila				
1172	68.5	6.4	153	2	Q6H5R0_ORYSA	Q6h5r0 oryza sativ	1245	68.5	6.4	285	2	Q68L62_9DIPT	Q68162 drosophila				
1173	68.5	6.4	176	2	Q6XIH5_DROYA	Q6xih5 drosophila	1246	68.5	6.4	285	2	Q68L64_9DIPT	Q68164 drosophila				
1174	68.5	6.4	183	2	Q9RZ51_DEIRA	Q9rz51 deinococcus	1247	68.5	6.4	285	2	Q68L66_9DIPT	Q68166 drosophila				
1175	68.5	6.4	189	2	Q8U770_AGRT5	Q8u770 agrobacteri	1248	68.5	6.4	286	2	Q68KY9_9DIPT	Q68ky9 drosophila				
1176	68.5	6.4	198	2	Q6AC58_LEIXX	Q6ac58 leifsonia x	1249	68.5	6.4	286	2	Q68L05_9DIPT	Q68105 drosophila				
1177	68.5	6.4	200	2	Q6B6N6_9MAMM	Q6b6n6 tachyglossu	1250	68.5	6.4	286	2	Q68L28_9DIPT	Q68128 drosophila				
1178	68.5	6.4	209	2	Q6B6N5_GEONI	Q6b6n5 geochelone	1251	68.5	6.4	286	2	Q68L30_9DIPT	Q68130 drosophila				
1179	68.5	6.4	232	2	Q5YNY0_NOCFA	Q5yny0 nocardia fa	1252	68.5	6.4	286	2	Q68L35_9DIPT	Q68135 drosophila				
1180	68.5	6.4	255	2	Q5CZL7_XENTR	Q5czl7 xenopus tro	1253	68.5	6.4	286	2	Q68L38_9DIPT	Q68138 drosophila				
1181	68.5	6.4	256	2	Q5LUR8_SILPO	Q5lur8 silicibacte	1254	68.5	6.4	286	2	Q68L42_9DIPT	Q68142 drosophila				
1182	68.5	6.4	260	2	Q82MM5_STRAW	Q82mm5 streptomyce	1255	68.5	6.4	286	2	Q68L51_9DIPT	Q68151 drosophila				
1183	68.5	6.4	261	2	Q7XI01_ORYSA	Q7xi01 oryza sativ	1256	68.5	6.4	286	2	Q68L52_9DIPT	Q68152 drosophila				
1184	68.5	6.4	261	2	Q5YR00_NOCFA	Q5yr00 nocardia fa	1257	68.5	6.4	286	2	Q68L56_9DIPT	Q68156 drosophila				
1185	68.5	6.4	272	2	Q743X3_MYCPA	Q743x3 mycobacteri	1258	68.5	6.4	286	2	Q68L57_9DIPT	Q68157 drosophila				
1186	68.5	6.4	277	2	Q68KY7_9DIPT	Q68ky7 drosophila	1259	68.5	6.4	286	2	Q68L75_9DIPT	Q68175 drosophila				
1187	68.5	6.4	278	2	Q68KY5_9DIPT	Q68ky5 drosophila	1260	68.5	6.4	287	2	Q68KZ3_9DIPT	Q68kz3 drosophila				
1188	68.5	6.4	279	2	Q68KY8_9DIPT	Q68ky8 drosophila	1261	68.5	6.4	287	2	Q68KZ7_9DIPT	Q68kz7 drosophila				
1189	68.5	6.4	279	2	Q68KZ8_9DIPT	Q68kz8 drosophila	1262	68.5	6.4	287	2	Q68L36_9DIPT	Q68136 drosophila				
1190	68.5	6.4	279	2	Q68L24_9DIPT	Q68124 drosophila	1263	68.5	6.4	287	2	Q68L59_9DIPT	Q68159 drosophila				
1191	68.5	6.4	279	2	Q68L45_9DIPT	Q68145 drosophila	1264	68.5	6.4	289	2	Q68L13_9DIPT	Q68113 drosophila				
1192	68.5	6.4	279	2	Q68L68_9DIPT	Q68168 drosophila	1265	68.5	6.4	289	2	Q68L26_9DIPT	Q68126 drosophila				
1193	68.5	6.4	279	2	Q68L70_9DIPT	Q68170 drosophila	1266	68.5	6.4	289	2	Q68L78_9DIPT	Q68178 drosophila				
1194	68.5	6.4	280	2	Q68L21_9DIPT	Q68121 drosophila	1267	68.5	6.4	295	2	Q96NH7_HUMAN	Q96nh7 homo sapien				
1195	68.5	6.4	280	2	Q68L55_9DIPT	Q68155 drosophila	1268	68.5	6.4	303	2	Q7PLL0_DROME	Q7pll0 drosophila				
1196	68.5	6.4	280	2	Q8QGD5_HETFR	Q8qgd5 heterodontu	1269	68.5	6.4	307	2	Q62K96_BURMA	Q62k96 burkholderi				
1197	68.5	6.4	281	2	Q68KZ6_9DIPT	Q68kz6 drosophila	1270	68.5	6.4	308	2	Q5YF01_9VIRU	Q5yf01 rock bream				
1198	68.5	6.4	281	2	Q68L03_9DIPT	Q68103 drosophila	1271	68.5	6.4	308	2	Q4KS67_9VIRU	Q4ks67 orange-spot				
1199	68.5	6.4	281	2	Q68L43_9DIPT	Q68143 drosophila	1272	68.5	6.4	311	2	Q82N03_STRAW	Q82n03 streptomyce				

1273	68.5	6.4	319	2	Q8MRR2_DROME	Q8mrr2 drosophila
1274	68.5	6.4	325	2	Q4H709_9DEIO	Q4h709 deinococcus
1275	68.5	6.4	331	2	Q89EW6_BRAJA	Q89ew6 bradyrhizob
1276	68.5	6.4	337	2	Q80ZA2_MOUSE	Q80za2 mus musculu
1277	68.5	6.4	338	2	Q8W0U7_SORBI	Q8w0u7 sorghum bic
1278	68.5	6.4	338	2	Q60CU1_METCA	Q60cu1 methylococc
1279	68.5	6.4	341	2	Q8KUG1_ACTPA	Q8kug1 actinosynne
1280	68.5	6.4	358	2	Q4SAL6_TETNG	Q4sal6 tetraodon n
1281	68.5	6.4	362	2	Q5NAG0_ORYSA	Q5nag0 oryza sativ
1282	68.5	6.4	367	2	Q6WAW5_TOXGO	Q6waw5 toxoplasma
1283	68.5	6.4	367	2	Q9I5I5_PSEAE	Q9i5i5 pseudomonas
1284	68.5	6.4	374	1	HIS7_BACFR	Q64re9 bacteroides
1285	68.5	6.4	374	2	Q5LB00_BACFN	Q51b00 bacteroides
1286	68.5	6.4	383	2	Q4QEZ9_LEIMA	Q4qez9 leishmania
1287	68.5	6.4	384	2	Q8BIK5_MOUSE	Q8bik5 mus musculu
1288	68.5	6.4	393	1	Y762_TREPA	O83743 treponema p
1289	68.5	6.4	402	1	B4GT1_BOVIN	P08037 b beta-1,4-
1290	68.5	6.4	421	1	PO4F1_MOUSE	P17208 mus musculu
1291	68.5	6.4	421	2	Q78NA5_MOUSE	Q78na5 mus musculu
1292	68.5	6.4	422	2	Q8K0F9_MOUSE	Q8k0f9 mus musculu
1293	68.5	6.4	456	2	Q7T3G1_BRARE	Q7t3g1 brachydanio
1294	68.5	6.4	489	2	Q8T9W7_DROSI	Q8t9w7 drosophila
1295	68.5	6.4	502	2	Q8X0F5_NEUCR	Q8x0f5 neurospora
1296	68.5	6.4	505	2	Q7QJU0_ANOGA	Q7qju0 anopheles g
1297	68.5	6.4	510	2	O97425_DROME	O97425 drosophila
1298	68.5	6.4	513	1	PRI2_NEUCR	Q8niz4 neurospora
1299	68.5	6.4	525	2	Q4X226_ASPFU	Q4x226 aspergillus
1300	68.5	6.4	534	2	Q83YD1_STRHY	Q83yd1 streptomyce
1301	68.5	6.4	541	2	Q960X4_DROME	Q960x4 drosophila
1302	68.5	6.4	558	2	Q4QEQ7_LEIMA	Q4qeq7 leishmania
1303	68.5	6.4	559	1	PHAR3_HUMAN	Q96kr7 homo sapien
1304	68.5	6.4	577	2	Q5Y0S8_9ALPH	Q5y0s8 cercopithec
1305	68.5	6.4	581	2	Q7SFB2_NEUCR	Q7sfb2 neurospora
1306	68.5	6.4	588	2	Q5XHY1_RAT	Q5xhy1 rattus norv
1307	68.5	6.4	606	2	Q8R1U9_MOUSE	Q8r1u9 mus musculu
1308	68.5	6.4	617	2	Q4K8E1_PSEF5	Q4k8e1 pseudomonas
1309	68.5	6.4	646	1	SCG1_BOVIN	P23389 bos taurus
1310	68.5	6.4	653	2	Q8ZN79_SALTY	Q8zn79 salmonella
1311	68.5	6.4	654	2	Q8R133_MOUSE	Q8r133 mus musculu
1312	68.5	6.4	659	2	Q4RRM1_TETNG	Q4rrm1 tetraodon n
1313	68.5	6.4	660	2	Q51U26_MAGGR	Q51u26 magnaporthe
1314	68.5	6.4	661	2	Q86K10_DICDI	Q86k10 dictyosteli
1315	68.5	6.4	674	2	Q6PGI1_MOUSE	Q6pgi1 mus musculu
1316	68.5	6.4	675	2	Q8C8L6_MOUSE	Q8c8l6 mus musculu
1317	68.5	6.4	680	2	Q610Y1_CAEBR	Q610y1 caenorhabdi
1318	68.5	6.4	741	2	Q7VV73_BORPE	Q7vv73 bordetella
1319	68.5	6.4	741	2	Q7W4E0_BORPA	Q7w4e0 bordetella
1320	68.5	6.4	741	2	Q7WFU8_BORBR	Q7wfu8 bordetella
1321	68.5	6.4	742	2	Q4P3G2_USTMA	Q4p3g2 ustilago ma
1322	68.5	6.4	748	2	Q523S1_MAGGR	Q523s1 magnaporthe
1323	68.5	6.4	750	1	APBA2_MOUSE	P98084 mus musculu
1324	68.5	6.4	778	2	Q8MMC0_DROME	Q8mmc0 drosophila
1325	68.5	6.4	786	2	Q503P9_BRARE	Q503p9 brachydanio
1326	68.5	6.4	802	1	OPHN1_MOUSE	Q99j31 mus musculu
1327	68.5	6.4	802	2	Q8C4C7_MOUSE	Q8c4c7 mus musculu
1328	68.5	6.4	802	2	Q544K7_MOUSE	Q544k7 m 16 days n
1329	68.5	6.4	867	2	Q7XL47_ORYSA	Q7xl47 oryza sativ
1330	68.5	6.4	910	2	Q7QVK7_GIALA	Q7qvk7 giardia lam
1331	68.5	6.4	914	2	Q4FWS0_LEIMA	Q4fws0 leishmania
1332	68.5	6.4	917	2	Q7S1R3_NEUCR	Q7s1r3 neurospora
1333	68.5	6.4	936	2	Q9XHX5_ORYSA	Q9xhx5 oryza sativ
1334	68.5	6.4	938	2	Q7XVE8_ORYSA	Q7xve8 oryza sativ
1335	68.5	6.4	960	2	Q8CIE4_MOUSE	Q8cie4 mus musculu
1336	68.5	6.4	960	2	Q8BSZ1_MOUSE	Q8bsz1 mus musculu
1337	68.5	6.4	976	1	CLCN1_CANFA	Q9mzt1 canis famil
1338	68.5	6.4	985	2	Q9NHD2_MUSDO	Q9nhd2 musca domes
1339	68.5	6.4	1047	2	Q9S2X5_STRCO	Q9s2x5 streptomyce
1340	68.5	6.4	1061	2	Q5HYF6_HUMAN	Q5hyf6 homo sapien
1341	68.5	6.4	1072	2	Q5AW92_EMENI	Q5aw92 aspergillus
1342	68.5	6.4	1193	2	Q4X042_ASPFU	Q4x042 aspergillus
1343	68.5	6.4	1207	2	Q5W7A0_ORYSA	Q5w7a0 oryza sativ
1344	68.5	6.4	1242	2	Q7XRX0_ORYSA	Q7xrx0 oryza sativ
1345	68.5	6.4	1350	2	Q4WHG2_ASPFU	Q4whg2 aspergillus
1346	68.5	6.4	1350	2	Q5J8K1_MOUSE	Q5j8k1 mus musculu
1347	68.5	6.4	1431	2	Q6ATT1_ORYSA	Q6att1 oryza sativ
1348	68.5	6.4	1509	2	Q4SII6_TETNG	Q4sii6 tetraodon n
1349	68.5	6.4	1514	2	Q6L5D6_ORYSA	Q6l5d6 oryza sativ
1350	68.5	6.4	1603	2	Q53PY0_ORYSA	Q53py0 oryza sativ
1351	68.5	6.4	1618	2	Q4S703_TETNG	Q4s703 tetraodon n
1352	68.5	6.4	1640	2	Q86Z91_GIBMO	Q86z91 gibberella
1353	68.5	6.4	1688	2	Q5W6X8_ORYSA	Q5w6x8 oryza sativ
1354	68.5	6.4	1743	2	Q688I6_ORYSA	Q688i6 oryza sativ
1355	68.5	6.4	1765	2	Q7XEI5_ORYSA	Q7xei5 oryza sativ
1356	68.5	6.4	1801	2	Q75LU1_ORYSA	Q75lu1 oryza sativ
1357	68.5	6.4	1851	2	Q6AVG8_ORYSA	Q6avg8 oryza sativ
1358	68.5	6.4	1858	2	Q5BBI6_EMENI	Q5bbi6 aspergillus
1359	68.5	6.4	1858	2	Q9Y7B3_EMENI	Q9y7b3 emericella
1360	68.5	6.4	1888	2	Q7XWL1_ORYSA	Q7xwl1 oryza sativ
1361	68.5	6.4	1911	2	Q84JT1_ORYSA	Q84jt1 oryza sativ
1362	68.5	6.4	1914	2	Q53J46_ORYSA	Q53j46 oryza sativ
1363	68.5	6.4	1923	2	Q60EI3_ORYSA	Q60ei3 oryza sativ
1364	68.5	6.4	1938	2	Q7FAA9_ORYSA	Q7faa9 oryza sativ
1365	68.5	6.4	1938	2	Q7XS55_ORYSA	Q7xs55 oryza sativ
1366	68.5	6.4	1958	2	Q6MW78_ORYSA	Q6mw78 oryza sativ
1367	68.5	6.4	1992	2	Q6AU86_ORYSA	Q6au86 oryza sativ
1368	68.5	6.4	2021	2	Q75HX8_ORYSA	Q75hx8 oryza sativ
1369	68.5	6.4	2027	1	DOCK3_MOUSE	Q8ciq7 mus musculu
1370	68.5	6.4	2027	2	Q8H7K1_ORYSA	Q8h7k1 oryza sativ
1371	68.5	6.4	2027	2	Q53QC3_ORYSA	Q53qc3 oryza sativ
1372	68.5	6.4	2184	2	Q4P5Y6_USTMA	Q4p5y6 ustilago ma
1373	68.5	6.4	2242	2	Q9P2P9_HUMAN	Q9p2p9 homo sapien
1374	68.5	6.4	3094	2	Q695L1_HUMAN	Q695l1 homo sapien
1375	68.5	6.4	3255	1	POLG_LMV0	P31999 l genome po
1376	68.5	6.4	3440	2	Q4QCV0_LEIMA	Q4qcv0 leishmania
1377	68.5	6.4	8426	2	Q5YPH7_NOCFA	Q5yph7 nocardia fa
1378	68	6.3	82	2	Q6K6Q4_ORYSA	Q6k6q4 oryza sativ
1379	68	6.3	113	2	Q74FD4_GEOSL	Q74fd4 geobacter s
1380	68	6.3	157	2	Q4VIT9_DROBU	Q4vit9 drosophila
1381	68	6.3	159	2	Q6KAF4_ORYSA	Q6kaf4 oryza sativ
1382	68	6.3	160	2	Q8N2B6_HUMAN	Q8n2b6 homo sapien
1383	68	6.3	170	2	Q91CH8_9ALPH	Q91ch8 macropodid
1384	68	6.3	190	1	VEGFA_BOVIN	P15691 bos taurus
1385	68	6.3	212	2	Q4J286_AZOVI	Q4j286 azotobacter
1386	68	6.3	225	2	Q8NSS6_CORGL	Q8nss6 corynebacte
1387	68	6.3	239	2	Q9HRD3_HALSA	Q9hrd3 halobacteri
1388	68	6.3	246	2	Q6K6D2_ORYSA	Q6k6d2 oryza sativ
1389	68	6.3	256	2	Q8VK54_MYCTU	Q8vk54 mycobacteri
1390	68	6.3	263	2	Q5RCS3_PONPY	Q5rcs3 pongo pygma
1391	68	6.3	265	2	Q4WNN9_ASPFU	Q4wnn9 aspergillus
1392	68	6.3	271	2	Q4X0N2_ASPFU	Q4x0n2 aspergillus
1393	68	6.3	272	1	HXA9_HUMAN	P31269 homo sapien
1394	68	6.3	274	2	Q59KL9_CANAL	Q59kl9 candida alb
1395	68	6.3	291	2	Q4LJC5_9BURK	Q4ljc5 burkholderi
1396	68	6.3	295	2	P71625_MYCTU	P71625 mycobacteri
1397	68	6.3	295	2	Q7TXS0_MYCBO	Q7txs0 mycobacteri
1398	68	6.3	299	2	Q82LE1_STRAW	Q82le1 streptomyce
1399	68	6.3	312	1	Y1368_XYLFA	Q9pdl1 xylella fas
1400	68	6.3	315	2	Q7D6H9_MYCTU	Q7d6h9 mycobacteri
1401	68	6.3	323	2	Q4KD45_PSEF5	Q4kd45 pseudomonas
1402	68	6.3	326	2	Q4HUC2_GIBZE	Q4huc2 gibberella
1403	68	6.3	328	2	Q5ZMR6_CHICK	Q5zmr6 gallus gall
1404	68	6.3	330	2	Q8GGS1_STRAZ	Q8ggs1 streptomyce
1405	68	6.3	330	2	Q5SJE2_THET8	Q5sje2 thermus the
1406	68	6.3	330	2	Q72JR1_THET2	Q72jr1 thermus the
1407	68	6.3	347	2	Q70DX3_9ACTO	Q70dx3 streptomyce
1408	68	6.3	359	1	BXDC2_DROME	Q9vze6 drosophila
1409	68	6.3	359	2	Q67863_HPBV0	Q67863 hepatitis b
1410	68	6.3	391	2	Q9K3T4_STRCO	Q9k3t4 streptomyce
1411	68	6.3	392	1	ODD_DROME	P23803 drosophila
1412	68	6.3	401	2	Q5I616_DROAE	Q5i616 drosophila
1413	68	6.3	408	2	Q6AYS7_RAT	Q6ays7 rattus norv
1414	68	6.3	412	2	Q83WE0_MICGR	Q83we0 micromonosp
1415	68	6.3	415	2	Q53RM0_ORYSA	Q53rm0 oryza sativ
1416	68	6.3	421	2	Q6NR09_DROME	Q6nr09 drosophila
1417	68	6.3	426	2	Q51560_PSEAE	Q51560 pseudomonas
1418	68	6.3	426	2	Q9HYD1_PSEAE	Q9hyd1 pseudomonas

1419	68	6.3	451	2	Q4J1T0_AZOVI	Q4j1t0 azotobacter
1420	68	6.3	463	2	Q74G23_GEOSL	Q74g23 geobacter s
1421	68	6.3	470	2	Q8PHB1_XANAC	Q8phb1 xanthomonas
1422	68	6.3	482	2	O81077_ARATH	O81077 arabidopsis
1423	68	6.3	491	2	Q7U5F0_SYNPX	Q7u5f0 synechococc
1424	68	6.3	494	2	Q8CFX7_MOUSE	Q8cfx7 mus musculu
1425	68	6.3	498	2	Q5FWI1_MOUSE	Q5fwi1 mus musculu
1426	68	6.3	500	2	Q5Z4D7_ORYSA	Q5z4d7 oryza sativ
1427	68	6.3	533	2	Q6CP39_KLULA	Q6cp39 kluyveromyc
1428	68	6.3	534	2	Q99LH7_MOUSE	Q99lh7 mus musculu
1429	68	6.3	535	2	Q7Y011_ORYSA	Q7y011 oryza sativ
1430	68	6.3	540	2	Q7Y000_ORYSA	Q7y000 oryza sativ
1431	68	6.3	541	1	GFI1_DROME	Q9n658 drosophila
1432	68	6.3	541	2	Q4QPR0_DROME	Q4qpr0 drosophila
1433	68	6.3	542	2	Q4VIT8_DROBU	Q4vit8 drosophila
1434	68	6.3	545	2	Q7QYI2_GIALA	Q7qyi2 giardia lam
1435	68	6.3	546	2	Q4Q757_LEIMA	Q4q757 leishmania
1436	68	6.3	567	2	Q4J631_AZOVI	Q4j631 azotobacter
1437	68	6.3	576	2	Q6AA38_PROAC	Q6aa38 propionibac
1438	68	6.3	583	2	Q87DF3_XYLFT	Q87df3 xylella fas
1439	68	6.3	590	2	Q4QBS3_LEIMA	Q4qbs3 leishmania
1440	68	6.3	605	2	Q5JBS9_TOXGO	Q5jbs9 toxoplasma
1441	68	6.3	631	2	Q5VV66_HUMAN	Q5vv66 homo sapien
1442	68	6.3	636	2	Q4NTB7_9DELT	Q4ntb7 anaeromyxob
1443	68	6.3	639	2	Q6SWS9_HCMV	Q6sws9 human cytom
1444	68	6.3	643	2	Q4QIF8_LEIMA	Q4qif8 leishmania
1445	68	6.3	659	2	Q9BUJ3_HUMAN	Q9buj3 homo sapien
1446	68	6.3	668	2	Q4SUB1_TETNG	Q4sub1 tetraodon n
1447	68	6.3	702	2	Q62L46_BURMA	Q62l46 burkholderi
1448	68	6.3	702	2	Q63T90_BURPS	Q63t90 burkholderi
1449	68	6.3	729	1	CLPB_PROFR	Q7wsy8 propionibac
1450	68	6.3	747	1	PDE4D_MOUSE	Q01063 mus musculu
1451	68	6.3	774	2	Q59FW4_HUMAN	Q59fw4 homo sapien
1452	68	6.3	788	2	Q6BLL8_DEBHA	Q6bll8 debaryomyce
1453	68	6.3	796	2	Q4NR10_9DELT	Q4nr10 anaeromyxob
1454	68	6.3	809	2	Q5T232_HUMAN	Q5t232 homo sapien
1455	68	6.3	811	2	Q4T352_TETNG	Q4t352 tetraodon n
1456	68	6.3	819	2	Q8TEE5_HUMAN	Q8tee5 homo sapien
1457	68	6.3	837	2	Q8RWY7_ARATH	Q8rwy7 arabidopsis
1458	68	6.3	838	2	Q5NKN0_CRYNV	Q5nkn0 cryptococcu
1459	68	6.3	855	2	Q8NF24_HUMAN	Q8nf24 homo sapien
1460	68	6.3	857	2	Q9SUV0_ARATH	Q9suv0 arabidopsis
1461	68	6.3	857	2	Q4NNF2_9DELT	Q4nnf2 anaeromyxob
1462	68	6.3	859	2	Q5SSL4_MOUSE	Q5ssl4 mus musculu
1463	68	6.3	863	2	Q91A90_9GAMA	Q91a90 ovine herpe
1464	68	6.3	863	2	Q91A92_9GAMA	Q91a92 ovine herpe
1465	68	6.3	887	2	Q5BDH0_EMENI	Q5bdh0 aspergillus
1466	68	6.3	896	2	Q6L5H9_ORYSA	Q6l5h9 oryza sativ
1467	68	6.3	904	2	Q4IPL2_GIBZE	Q4ipl2 gibberella
1468	68	6.3	906	1	RIR1_HCMVA	P16782 human cytom
1469	68	6.3	906	2	Q6RXH3_HCMV	Q6rxh3 human cytom
1470	68	6.3	906	2	Q6SW87_HCMV	Q6sw87 human cytom
1471	68	6.3	954	1	GCSP_RHIME	Q92q11 rhizobium m
1472	68	6.3	967	2	Q7QFJ6_ANOGA	Q7qfj6 anopheles g
1473	68	6.3	1038	2	Q63X21_BURPS	Q63x21 burkholderi
1474	68	6.3	1091	2	Q4H737_9DEIO	Q4h737 deinococcus
1475	68	6.3	1141	2	Q5T233_HUMAN	Q5t233 homo sapien
1476	68	6.3	1175	2	P70200_MOUSE	P70200 mus musculu
1477	68	6.3	1175	2	O35126_MOUSE	O35126 mus musculu
1478	68	6.3	1183	1	ATN1_RAT	P54258 rattus norv
1479	68	6.3	1185	1	ATN1_HUMAN	P54259 homo sapien
1480	68	6.3	1186	1	ATN1_PANTR	Q5is70 pan troglod
1481	68	6.3	1191	2	Q86V38_HUMAN	Q86v38 homo sapien
1482	68	6.3	1194	2	Q9VE59_DROME	Q9ve59 drosophila
1483	68	6.3	1205	2	Q9LAT9_ANAPH	Q9lat9 anaplasma p
1484	68	6.3	1205	2	Q9RPM8_ANAPH	Q9rpm8 anaplasma p
1485	68	6.3	1207	2	Q9C095_HUMAN	Q9c095 homo sapien
1486	68	6.3	1304	2	Q60UJ8_CAEBR	Q60uj8 caenorhabdi
1487	68	6.3	1384	2	Q4T2F3_TETNG	Q4t2f3 tetraodon n
1488	68	6.3	1404	2	Q800Z9_BRARE	Q800z9 brachydanio
1489	68	6.3	1513	2	Q5LPX2_SILPO	Q5lpx2 silicibacte
1490	68	6.3	1542	2	Q6P3W1_HUMAN	Q6p3w1 homo sapien
1491	68	6.3	1644	2	Q4QCX0_LEIMA	Q4qcx0 leishmania
1492	68	6.3	1664	2	Q9BZE5_HUMAN	Q9bze5 homo sapien
1493	68	6.3	1664	2	Q6P3U5_HUMAN	Q6p3u5 homo sapien
1494	68	6.3	1664	2	Q5VV67_HUMAN	Q5vv67 homo sapien
1495	68	6.3	1666	2	Q76N31_HUMAN	Q76n31 homo sapien
1496	68	6.3	1671	2	Q6Z7R3_ORYSA	Q6z7r3 oryza sativ
1497	68	6.3	1696	2	Q4Q766_LEIMA	Q4q766 leishmania
1498	68	6.3	1988	2	Q60EL1_ORYSA	Q60el1 oryza sativ
1499	68	6.3	2001	2	Q7XS25_ORYSA	Q7xs25 oryza sativ
1500	68	6.3	2004	2	Q75M60_ORYSA	Q75m60 oryza sativ

ALIGNMENTS

RESULT 1
IL17C_HUMAN
ID IL17C_HUMAN STANDARD; PRT; 197 AA.
AC Q9P0M4; Q9HC75;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin-17C precursor (IL-17C) (Cytokine CX2).
GN Name=IL17C; ORFNames=UNQ561/PRO1122;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20105548; PubMed=10639155; DOI=10.1073/pnas.97.2.773;
RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
RA Gurney A.L., Wood W.I.;
RT "Cloning and characterization of IL-17B and IL-17C, two new members of
RT the IL-17 cytokine family.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Zhang W., He L., Wan T., Yuan Z., Cao X.;
RT "Novel human cytokine CX2 with homology to IL-17.";
RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Stimulates the release of tumor necrosis factor alpha
CC       and IL-1beta from the monocytic cell line THP-1.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the IL-17 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF152099; AAF28105.1; -; mRNA.
DR   EMBL; AF142410; AAG27921.1; -; mRNA.
DR   EMBL; AY358471; AAQ88835.1; -; mRNA.
DR   EMBL; BC069152; AAH69152.1; -; mRNA.
DR   HSSP; Q96PD4; 1JPY.
DR   Ensembl; ENSG00000124391; Homo sapiens.
DR   HGNC; HGNC:5983; IL17C.
DR   MIM; 604628; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0005125; F:cytokine activity; TAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
KW   Cytokine; Signal.
FT   SIGNAL       1     18       Potential.
FT   CHAIN       19    197       Interleukin-17C.
FT   DISULFID   129    189       By similarity.
FT   DISULFID   134    191       By similarity.
FT   CONFLICT    50     50       H -> R (in Ref. 2).
SQ   SEQUENCE   197 AA;  21765 MW;  BAE0152E18DE7D08 CRC64;

  Query Match             100.0%;  Score 1073;  DB 1;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-89;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60

Qy         61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120

Qy        121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180

Qy        181 EFIHVPVGCTCVLPRSV 197
              |||||||||||||||||
Db        181 EFIHVPVGCTCVLPRSV 197


RESULT 2
Q8K4C5_MOUSE
ID   Q8K4C5_MOUSE PRELIMINARY;      PRT;   194 AA.
AC   Q8K4C5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IL-17C.
GN   Name=Il17c;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22072219; PubMed=12077275;
RA   Hurst S.D., Muchamuel T., Gorman D.M., Gilbert J.M., Clifford T.,
RA   Kwan S., Menon S., Seymour B., Jackson C., Kung T.T., Brieland J.K.,
RA   Zurawski S.M., Chapman R.W., Zurawski G., Coffman R.L.;
RT   "New IL-17 family members promote Th1 or Th2 responses in the lung: in
RT   vivo function of the novel cytokine IL-25.";
RL   J. Immunol. 169:443-453(2002).
DR   EMBL; AF458061; AAM77565.1; -; mRNA.
DR   HSSP; Q96PD4; 1JPY.
DR   Ensembl; ENSMUSG00000046108; Mus musculus.
DR   MGI; MGI:2446486; Il17c.
DR   GO; GO:0005125; F:cytokine activity; IDA.
DR   GO; GO:0030223; P:neutrophil differentiation; IDA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   194 AA;  21591 MW;  95797A630574BD1E CRC64;

  Query Match             73.4%;  Score 788;  DB 2;  Length 194;
  Best Local Similarity   77.9%;  Pred. No. 1.1e-63;
  Matches  148;  Conservative   13;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          7 LLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVAL 66
              || | || | : | ||   | | || |  |||||||  |||||||| | |:| |||||||
Db          3 LLLLGWLPTGMTHQDPPSWGKPRSHRTLRCYSAEELSHGQAPPHLLTRSARWEQALPVAL 62

Qy         67 VSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAF 126
              |:||||  || :|| | | ||||||||||||||||||:|||||||||:|||||:|||||||
Db         63 VASLEATGHRRQHEGPLAGTQCPVLRPEEVLEADTHERSISPWRYRIDTDENRYPQKLAV 122

Qy        127 AECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVP 186
              |||||||||:|:||||||||||:||||||||||:||||||:  ||||:|||||||| ||
Db        123 AECLCRGCINAKTGRETAALNSVQLLQSLLVLRRQPCSRDGTADPTPGSFAFHTEFIRVP 182

Qy        187 VGCTCVLPRS 196
              ||||||||||
Db        183 VGCTCVLPRS 192


RESULT 3
IL17D_HUMAN
ID   IL17D_HUMAN    STANDARD;      PRT;   202 AA.
AC   Q8TAD2;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Interleukin-17D precursor (IL-17D) (Interleukin-27) (IL-27).
GN   Name=IL17D; Synonyms=IL27; ORFNames=UNQ3096/PRO21175;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Hadj-Slimane R., Bobe P.;
RT   "Interleukin 27 (IL27): a newly identified cytokine.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE, FUNCTION, AND TISSUE SPECIFICITY.
RA   Starnes T., Broxmeyer H.E., Robertson M.J., Hromas R.;
RT   "IL-17D, a novel member of the IL-17 family, stimulates cytokine
RT   production and inhibits hemopoiesis.";
RL   J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 169:642-646(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Gilbert J.M., Gorman D.M.;
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RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Induces expression of IL-6, IL-8, and GM-CSF from
CC       endothelial cells.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed preferentially in adipose, skeletal
CC       muscle and CNS.
CC   -!- SIMILARITY: Belongs to the IL-17 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AY078238; AAL86911.1; -; mRNA.
DR   EMBL; AF479775; AAM12734.1; -; mRNA.
DR   EMBL; AF458062; AAM77566.1; -; mRNA.
DR   EMBL; AY359113; AAQ89471.1; -; mRNA.
DR   EMBL; BC036243; AAH36243.1; -; mRNA.
DR   HSSP; Q96PD4; 1JPY.
DR   Ensembl; ENSG00000172458; Homo sapiens.
DR   HGNC; HGNC:5984; IL17D.
DR   MIM; 607587; -.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL       1     15       Potential.
FT   CHAIN       16    202       Interleukin-17D.
FT   CARBOHYD     68     68       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    181    181       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     78     78       A -> G (in Ref. 4).
SQ   SEQUENCE   202 AA;  21893 MW;  D171C5FB2DD039C3 CRC64;
```

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  Query Match           18.5%;  Score 199;  DB 1;  Length 202;
  Best Local Similarity   30.6%;  Pred. No. 5.6e-10;
  Matches   57;  Conservative   14;  Mismatches   49;  Indels   66;  Gaps    7;

Qy         51 LLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLE------------ 98
              |||    |    | |           ||  ||:    |   ||||:||
Db          7 LLALPPSWAAGAPRA----------GR--RPARPRGC-ADRPEELLEQLYGRLAAGVLS 52

Qy         99 -------------------------AD------THQRSISPWRYRVDTDEDRYPQKLAFA 127
                                         ||      |: ||:||| ||:  |  |||: |  |
Db         53 AFHHTLQLGPREQARNASCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEA 112

Qy        128 ECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTE-FIHVP 186
              ||||||:    | |      |  :    :|||| |    |  :        :|| :: :|
Db        113 YCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSV--------YTEAYVTIP 164

Qy        187 VGCTCV 192
              ||||||
Db        165 VGCTCV 170
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RESULT 4
Q5VUZ7_HUMAN
ID   Q5VUZ7_HUMAN PRELIMINARY;      PRT;   202 AA.
AC   Q5VUZ7;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Interleukin 17D.
GN   Name=IL17D; ORFNames=RP11-261P13.1-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Johnson C.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Holt K.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL512652; CAH71796.1; -; Genomic_DNA.
DR   EMBL; AL161772; CAH70875.1; -; Genomic_DNA.
DR   EMBL; AL161772; CAH71796.1; JOINED; Genomic_DNA.
DR   EMBL; AL512652; CAH70875.1; JOINED; Genomic_DNA.
DR   Ensembl; ENSG00000172458; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006954; P:inflammatory response; IEA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   202 AA;  21893 MW;  D171C5FB2DD039C3 CRC64;
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  Query Match           18.5%;  Score 199;  DB 2;  Length 202;
  Best Local Similarity   30.6%;  Pred. No. 5.6e-10;
  Matches   57;  Conservative   14;  Mismatches   49;  Indels   66;  Gaps    7;

Qy         51 LLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLE------------ 98
              |||    |    | |           ||  ||:    |   ||||:||
Db          7 LLALPPSWAAGAPRA----------GR--RPARPRGC-ADRPEELLEQLYGRLAAGVLS 52

Qy         99 -------------------------AD------THQRSISPWRYRVDTDEDRYPQKLAFA 127
                                         ||      |: ||:||| ||:  |  |||: |  |
Db         53 AFHHTLQLGPREQARNASCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEA 112

Qy        128 ECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTE-FIHVP 186
              ||||||:    | |      |  :    :|||| |    |  :        :|| :: :|
Db        113 YCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSV--------YTEAYVTIP 164

Qy        187 VGCTCV 192
              ||||||
```

```
Db        165 VGCTCV 170


RESULT 5
Q5BJ95_RAT
ID   Q5BJ95_RAT  PRELIMINARY;      PRT;   153 AA.
AC   Q5BJ95;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Interleukin 17F (Predicted).
GN   Name=Il17f_predicted;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RG   NIH MGC Project;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC091568; AAH91568.1; -; mRNA.
DR   InterPro; IPR010345; IL17.
DR   InterPro; IPR012293; RNAP_RPB6_omega.
DR   InterPro; IPR011991; Wing_hlx_DNA_bd.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   153 AA;  16874 MW;  77DCF89E566067CB CRC64;

  Query Match            18.4%;  Score 197.5;  DB 2;  Length 153;
  Best Local Similarity  34.9%;  Pred. No. 5.5e-10;
  Matches   53;  Conservative   20;  Mismatches   46;  Indels   33;  Gaps    6;

Qy         62 LPVALVSSLEAASHRGRHERPSATTQ---CPVLRPEEV-------------LEADTHQR 104
              |  |::||   |: |      ||  :   || |     |              :  |   |
Db         10 LGFAIISS--GAARRNPKVGLSALQKAGNCPPLEDNSVRVDIRIFNQNQGISVPRDFQNR 67

Qy        105 SISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRP-- 162
              | ||| | :  | ||:| ::| |:|   |||:|: |:|  ::||| : | :|||| |
Db         68 SSSPWDYNITRDPDRFPSEIAEAQCRHSGCINAQ-GQEDGSMNSVPIQQEILVLRREPQG 126

Qy        163 CSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
              ||            :|  | : : ||||| |
Db        127 CSN----------SFRLEKMLIKVGCTCVTP 147


RESULT 6
Q8VHH8_MOUSE
ID   Q8VHH8_MOUSE PRELIMINARY;      PRT;   169 AA.
AC   Q8VHH8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IL25.
GN   Name=Il17e;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6;
RX   MEDLINE=21629216; PubMed=11754819; DOI=10.1016/S1074-7613(01)00243-6;
RA   Fort M.M., Cheung J., Yen D., Li J., Zurawski S.M., Lo S., Menon S.,
RA   Clifford T., Hunte B., Lesley R., Muchamuel T., Hurst S.D.,
RA   Zurawski G., Leach M.W., Gorman D.M., Rennick D.M.;
RT   "IL-25 induces IL-4, IL-5, and IL-13 and Th2-associated pathologies in
RT   vivo.";
RL   Immunity 15:985-995(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6;
RA   Hurst S.D., Muchamuel T., Gorman D.M., Gilbert J.M., Clifford T.,
RA   Kwan S., Menon S., Seymour B., Jackson C., Kung T., Brieland J.,
RA   Zurawski S.M., Chapman R., Zurawski G., Coffman R.L.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF458060; AAL57623.1; -; mRNA.
DR   HSSP; Q96PD4; 1JPY.
DR   Ensembl; ENSMUSG00000040770; Mus musculus.
DR   MGI; MGI:2155888; Il17e.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005125; F:cytokine activity; IDA.
DR   GO; GO:0030222; P:eosinophil differentiation; IDA.
DR   GO; GO:0006954; P:inflammatory response; IDA.
DR   GO; GO:0009624; P:response to nematodes; IDA.
DR   GO; GO:0009621; P:response to pathogenic fungi; IDA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   169 AA;  19210 MW;  CFAD2CEDE452C94D CRC64;

  Query Match            18.0%;  Score 193;  DB 2;  Length 169;
  Best Local Similarity  31.0%;  Pred. No. 1.6e-09;
  Matches   58;  Conservative   17;  Mismatches   86;  Indels   26;  Gaps    6;

Qy         10 LTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVSS 69
              : :|   :  |  |||        | |  ::|    | ||        ||       | ||
Db          5 VAFLAMIVGTHTVSLRIQEGCSHLPSCCPSKE----QEPPE---EWLKWSS----ASVSP 53

Qy         70 LEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAEC 129
              |  ||    |   |:   |:           : |:|||| | :| | :| || |  | |
Db         54 PEPLSHTHHAESCRASKDGPL----------NSRAISPWSYELDRDLNRVPQDLYHARC 102

Qy        130 LCRGCIDARTGRETAAL-NSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVG 188
              ||  |:  :||      | ||| |  :  |  ||||  :     |   :        | :
Db        103 LCPHCVSLQTGSHMDPLGNSVPLYHNQTVFYRRPCHGEEG---THRRYCLERRLYRVSLA 159

Qy        189 CTCVLPR 195
              | || ||
Db        160 CVCVRPR 166


RESULT 7
Q8VHC9_MOUSE
ID   Q8VHC9_MOUSE PRELIMINARY;      PRT;   153 AA.
AC   Q8VHC9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Interleukin 17E (Fragment).
GN   Name=Il17e;
OS   Mus musculus (Mouse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21571724; PubMed=11714825;
RA   Pan G., French D., Mao W., Maruoka M., Risser P., Lee J., Foster J.,
RA   Aggarwal S., Nicholes K., Guillet S., Schow P., Gurney A.L.;
RT   "Forced expression of murine IL-17E induces growth retardation,
RT   jaundice, a Th2-biased response, and multiorgan inflammation in
RT   mice.";
RL   J. Immunol. 167:6559-6567(2001).
DR   EMBL; AY034088; AAK59816.1; -; mRNA.
DR   HSSP; Q96PD4; 1JPY.
DR   MGI; MGI:2155888; Il17e.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005125; F:cytokine activity; IDA.
DR   GO; GO:0030222; P:eosinophil differentiation; IDA.
DR   GO; GO:0006954; P:inflammatory response; IDA.
DR   GO; GO:0009624; P:response to nematodes; IDA.
DR   GO; GO:0009621; P:response to pathogenic fungi; IDA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
FT   CHAIN        <1    153       interleukin 17E.
FT   NON_TER       1      1
SQ   SEQUENCE   153 AA;  17456 MW;  A0EE897842E6EB39 CRC64;

  Query Match             17.3%;  Score 186;  DB 2;  Length 153;
  Best Local Similarity   32.2%;  Pred. No. 6.2e-09;
  Matches   56;  Conservative   14;  Mismatches   78;  Indels   26;  Gaps    6;

Qy         23 SLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERP 82
              |||         | |  ::|    | ||        ||       | ||  |   ||    |
Db          2 SLRIQEGCSHLPSCCPSKE----QEPPE---EWLKWSS----ASVSPPEPLSHTHHAESC 50

Qy         83 SATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRE 142
               |:   |:           : |:|||| | :| | :| || |  | |||  |:  :||
Db         51 RASKDGPL-----------NSRAISPWSYELDRDLNRVPQDLYHARCLCPHCVSLQTGSH 99

Qy        143 TAAL-NSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPR 195
              | ||| |  :  |  ||||  :     |   :        | : | || ||
Db        100 MDPLGNSVPLYHNQTVFYRRPCHGEEG---THRHYCLERRLYRVSLACVCVRPR 150


RESULT 8
Q8K4C3_MOUSE
ID   Q8K4C3_MOUSE PRELIMINARY;      PRT;   153 AA.
AC   Q8K4C3;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IL-17F.
GN   Name=Il17f;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gilbert J.M., Gorman D.M.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF458064; AAM77568.1; -; mRNA.
DR   HSSP; Q96PD4; 1JPY.
DR   Ensembl; ENSMUSG00000041872; Mus musculus.
DR   MGI; MGI:2676631; Il17f.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006954; P:inflammatory response; IEA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   153 AA;  17020 MW;  894494F904ECCAAD CRC64;

  Query Match             17.1%;  Score 184;  DB 2;  Length 153;
  Best Local Similarity   32.4%;  Pred. No. 9.4e-09;
  Matches   48;  Conservative   20;  Mismatches   40;  Indels   40;  Gaps    5;

Qy         63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEV-------------LEADTHQRSISP 108
              | | | :|: | :             || |    |               :  :   || ||
Db         24 PKAGVPALQKAGN-----------CPPLEDNTVRVDIRIFNQNQGISVPREFQNRSSSP 71

Qy        109 WRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRP--CSRD 166
              | | :  |  |:| ::| |:|   |||:|: |:| : :||| : | :|||||  |  ||
Db         72 WDYNITRDPHRFPSEIAEAQCRHSGCINAQ-GQEDSTMNSVAIQQEILVLRREPQGCSN- 129

Qy        167 GSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                      :|  | : : |||||| |
Db        130 ----------SFRLEKMLLKVGCTCVKP 147


RESULT 9
Q7TNI7_MOUSE
ID   Q7TNI7_MOUSE PRELIMINARY;      PRT;   161 AA.
AC   Q7TNI7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Interleukin 17F, transcript variant.
GN   Name=Il17f; Synonyms=mIL-17Ftv;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kawaguchi M., Kokubu F., Suzuki S., Watanabe S., Ieki K.,
RA   Matsukura S., Kurokawa M., Adachi M.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Oda N., Huang S.-K.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB116259; BAC81535.1; -; mRNA.
DR   EMBL; AY380822; AAQ88439.1; -; mRNA.
DR   HSSP; Q96PD4; 1JPY.
DR   MGI; MGI:2676631; Il17f.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006954; P:inflammatory response; IEA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   161 AA;  17941 MW;  649D57E491301CAA CRC64;

  Query Match             17.1%;  Score 184;  DB 2;  Length 161;
  Best Local Similarity   32.4%;  Pred. No. 1e-08;
  Matches   48;  Conservative   20;  Mismatches   40;  Indels   40;  Gaps    5;

Qy         63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEV-------------LEADTHQRSISP 108
              | | | :|: | :             || |    |               :  :   || ||
Db         32 PKAGVPALQKAGN-----------CPPLEDNTVRVDIRIFNQNQGISVPREFQNRSSSP 79

Qy        109 WRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRP--CSRD 166
              | | :  |  |:| ::| |:|   |||:|: |:| : :||| : | :|||||  |  ||
Db         80 WDYNITRDPHRFPSEIAEAQCRHSGCINAQ-GQEDSTMNSVAIQQEILVLRREPQGCSN- 137

Qy        167 GSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
                      :|  | : : |||||| |
Db        138 ----------SFRLEKMLLKVGCTCVKP 155


RESULT 10
Q8K4C4_MOUSE
ID   Q8K4C4_MOUSE PRELIMINARY;      PRT;   205 AA.
AC   Q8K4C4;
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DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IL-17D.
GN   Name=Il17d;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gilbert J.M., Gorman D.M.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF458063; AAM77567.1; -; mRNA.
DR   HSSP; Q96PD4; 1JPY.
DR   Ensembl; ENSMUSG00000050222; Mus musculus.
DR   MGI; MGI:2446510; Il17d.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006954; P:inflammatory response; IEA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   205 AA;  22390 MW;  6705746EF013318D CRC64;

  Query Match             17.1%;  Score 183;  DB 2;  Length 205;
  Best Local Similarity   31.2%;  Pred. No. 1.6e-08;
  Matches   54;  Conservative   16;  Mismatches   49;  Indels   54;  Gaps    7;

Qy          64 VALVSSLEAASHR-GRHERPSATTQCPVLRPEEVLE---------------------- 98
               :||      | : | ||  ||:    |   ||||:||
Db          15 LALAPGRAAGALRTGR--RPARPRDC-ADRPEELLEQLYGRLAAGVLSAFHHTLQLGPRE 71

Qy          99 -------------AD------THQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDART 139
                           ||      |: ||:||| ||:  |  |:|: |  | ||||||:
Db          72 QARNASCPAGGRAADRRFRPPTNLRSVSPWAYRISYDPARFPRYLPEAYCLCRGCLTGLY 131

Qy         140 GRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
               | |     |  :    :||||      |  :     :| |  :| :|||||||
Db         132 GEEDFRFRSTPVFSPAVVLRRTAACAGGRSV-----YAEH--YITIPVGCTCV 177


RESULT 11
Q5TKT1_BRARE
ID   Q5TKT1_BRARE PRELIMINARY;      PRT;   212 AA.
AC   Q5TKT1;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Interleukin 17_4.
GN   Name=IL-17_4;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Irengbam G.D., Ram S., Sakai M.;
RT   "Cloning and analysis of IL-17 genes in zebrafish.";
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB195259; BAD72789.1; -; Genomic_DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006954; P:inflammatory response; IEA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   212 AA;  23624 MW;  EFED941CB795D53D CRC64;

  Query Match             17.0%;  Score 182;  DB 2;  Length 212;
  Best Local Similarity   27.8%;  Pred. No. 2.1e-08;
  Matches   52;  Conservative   26;  Mismatches   89;  Indels   20;  Gaps    6;

Qy           8 LFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALV 67
               | | ||  |      |  ||   |   |   | :|     |  :| :  :|: | | ::
Db           9 LVLVWLWCC--GSAPGERGQKVSRRAPRTRSCLDL-----PEEILEQ--MFGR-LSVGVL 58

Qy          68 SSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFA 127
               |:          || : :      :      : |:||| ||:  |  |||: |  |
Db          59 SAFHHTLQLATPERQNLSCGSASRLARDRPRTPVNLLSLSPWAYRISHDPARYPRYLPEA 118

Qy         128 ECLCRGCIDARTGRETAALNSVRLLQSLLVLRRR--PCSRDGSGLPTPGAFAFHTEFIHV 185
               |||:||:    | |:   |  :   ::|||   ||         |  ::   :: :
Db         119 YCLCKGCLSGLNGEESDRFRSTPVYMPTVILRRTVGPC--------VGGRHSYTESYVSI 170

Qy         186 PVGCTCV 192
               |||||||
Db         171 AVGCTCV 177


RESULT 12
Q6L5M6_CIOIN
ID   Q6L5M6_CIOIN PRELIMINARY;      PRT;   171 AA.
AC   Q6L5M6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Interleukin 17-1.
GN   Name=IL-17-1;
OS   Ciona intestinalis.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Cionidae; Ciona.
OX   NCBI_TaxID=7719;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ram S., Sakai M.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB181456; BAD22760.1; -; Genomic_DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006954; P:inflammatory response; IEA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   171 AA;  19211 MW;  8667A1D278D2115D CRC64;

  Query Match             16.7%;  Score 179;  DB 2;  Length 171;
  Best Local Similarity   38.6%;  Pred. No. 3e-08;
  Matches   49;  Conservative   14;  Mismatches   44;  Indels   20;  Gaps    5;

Qy          75 HRGRHERPSATTQCPVLRPEEVLEADTH----QRSISPWRYRVDTDEDRYPQKLAFAECL 130
               |  ||:|  :|  ||||  | :|   ||    :||:||:    | |  | |  |  | ||
Db          59 HGIRHKRSQST--CPVLSDEYLL---THTRQEERSLSPYVIEDDIDRLRIPMVLPRARCL 113

Qy         131 CRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCT 190
               | ||||  : ||  :  || | ||  | :|   : :|          |    : ||||
Db         114 CDGCIDMSSRRENFSPASVPLKQSFTVRKRN--TENG---------PLETVTQTITVGCT 162

Qy         191 CVLPRSV 197
               ||:|| :
Db         163 CVVPRRI 169


RESULT 13
Q5TKT2_BRARE
ID   Q5TKT2_BRARE PRELIMINARY;      PRT;   167 AA.
AC   Q5TKT2;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Interleukin 17_3.
GN   Name=IL-17_3;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
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RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Irengbam G.D., Ram S., Sakai M.;
RT   "Cloning and analysis of IL-17 genes in zebrafish.";
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB195258; BAD72788.1; -; Genomic_DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006954; P:inflammatory response; IEA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   167 AA;  19140 MW;  3668F46393263AF6 CRC64;

  Query Match             16.5%;  Score 177.5;  DB 2;  Length 167;
  Best Local Similarity   35.9%;  Pred. No. 4.1e-08;
  Matches   37;  Conservative   16;  Mismatches   35;  Indels   15;  Gaps    3;

Qy        100 DTHQRSISPWR-------YRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLL 152
              |   ||:||||       :|   : | || |   |:||| |||     |    : ||| :
Db         72 DLKHRSLSPWRTSISLVFFRTVENPDMYPSKYEEAQCLCDGCI--INGELNRSYNSVPVF 129

Qy        153 QSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPR 195
              :: : |:: ||  |       |  ::|  | : ||| ||| :|:
Db        130 KTHVFLKKHPCPSD------PDKYSFTFEHVQVPVACTCAVPK 166


RESULT 14
Q6DIY0_XENTR
ID   Q6DIY0_XENTR PRELIMINARY;      PRT;   203 AA.
AC   Q6DIY0;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Interleukin 17B.
GN   Name=il17b-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole body;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC075405; AAH75405.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005125; F:cytokine activity; IEA.
DR   GO; GO:0006954; P:inflammatory response; IEA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
SQ   SEQUENCE   203 AA;  22744 MW;  5FC4FEE26A0DE62B CRC64;

  Query Match             16.5%;  Score 177.5;  DB 2;  Length 203;
  Best Local Similarity   27.2%;  Pred. No. 5.1e-08;
  Matches   56;  Conservative   41;  Mismatches   78;  Indels   31;  Gaps    8;

Qy          8 LFLTWLHTCLAHH-------DPS---LRGH---PHSHGTPHCYSAEELPLGQAPPHLLAR 54
              |||    : |  |       :||   :||    ::|||      |::   |:| |  :
Db          7 LFLLIATSLLVAHALSSDTPNPSKGRKKGHLKGKNTHGT-----AQDRAKGKASPDPVLG 61

Qy         55 GAKWGQALPVALV----SSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWR 110
              |  :  :  :||     ||   :: |:   :  :| |     :    :::||:|||
Db         62 GNSFAPSQLYSLVEDYEQSLMEMVNQLRNNSDVSANRCEV----SLRLWLSNRRSLSPWA 117

Qy        111 YRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGL 170
              | :: ||:| |  :  | ||| ||::  | :|  :: |:  : | : :||| |    | :
Db        118 YSINHDENRIPIDIPEARCLCTGCVNPFTMKEDFSMTSIP-IYSKIPVRRRLCEGSSSPI 176

Qy        171 PTPGAFAFHTEFI----HVPVGCTCV 192
                  | |::    :: |||||:
Db        177 RARRRKKCHKEYMAVMENIAVGCTCI 202


RESULT 15
IL17F_HUMAN
ID   IL17F_HUMAN    STANDARD;      PRT;   153 AA.
AC   Q96PD4; Q7Z6P4; Q96PI8; Q9NUE6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Interleukin-17F precursor (IL-17F) (Interleukin-24) (IL-24) (Cytokine
DE   ML-1).
GN   Name=IL17F; Synonyms=IL24;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21475830; PubMed=11591732;
RA   Starnes T., Robertson M.J., Sledge G., Kelich S., Nakshatri H.,
RA   Broxmeyer H.E., Hromas R.;
RT   "IL-17F, a novel cytokine selectively expressed in activated T cells
RT   and monocytes, regulates angiogenesis and endothelial cell cytokine
RT   production.";
RL   J. Immunol. 167:4137-4140(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 2-153.
RX   MEDLINE=21475866; PubMed=11591768;
RA   Kawaguchi M., Onuchic L.F., Li X.-D., Essayan D.M., Schroeder J.,
RA   Xiao H.-Q., Liu M.C., Krishnaswamy G., Germino G., Huang S.-K.;
RT   "Identification of a novel cytokine, ML-1, and its expression in
RT   subjects with asthma.";
RL   J. Immunol. 167:4430-4435(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
RA   Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
RA   Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA   Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
RA   Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
RA   Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
RA   Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA   Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA   Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
RA   Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
RA   Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
RA   Culley K.M., Dhami P., Davies J., Dunn M., Earthrowl M.E.,
RA   Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA   Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
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RA   Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,
RA   Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
RA   Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,
RA   Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA   Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA   Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA   Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA   Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA   Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
RA   McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA   Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA   Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA   Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
RA   Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
RA   Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA   Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA   Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA   Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA   Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA   Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
RT   "The DNA sequence and analysis of human chromosome 6.";
RL   Nature 425:805-811(2003).
RN   [4]
RP   PROTEIN SEQUENCE OF 21-35.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS), AND CHARACTERIZATION.
RX   MEDLINE=21458422; PubMed=11574464; DOI=10.1093/emboj/20.19.5332;
RA   Hymowitz S.G., Filvaroff E.H., Yin J.P., Lee J., Cai L., Risser P.,
RA   Maruoka M., Mao W., Foster J., Kelley R.F., Pan G., Gurney A.L.,
RA   de Vos A.M., Starovasnik M.A.;
RT   "IL-17s adopt a cystine knot fold: structure and activity of a novel
RT   cytokine, IL-17F, and implications for receptor binding.";
RL   EMBO J. 20:5332-5341(2001).
CC   -!- FUNCTION: Stimulates the production of other cytokines such as IL-
CC       6, IL-8 and granulocyte colony-stimulating factor, and can
CC       regulate cartilage matrix turnover. Stimulates PBMC and T-cell
CC       proliferation. Inhibits angiogenesis.
CC   -!- SUBUNIT: Homodimer; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed in activated, but not resting, CD4+
CC       T cells and activated monocytes.
CC   -!- SIMILARITY: Belongs to the IL-17 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF384857; AAK83350.1; ALT_INIT; mRNA.
DR   EMBL; AF332389; AAL14427.1; ALT_INIT; mRNA.
DR   EMBL; AL034343; CAD92646.1; -; Genomic_DNA.
DR   EMBL; AL034343; CAD92647.1; -; Genomic_DNA.
DR   PDB; 1JPY; X-ray; A/B/X/Y=21-153.
DR   Ensembl; ENSG00000112116; Homo sapiens.
DR   HGNC; HGNC:16404; IL17F.
DR   MIM; 606496; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005125; F:cytokine activity; IDA.
DR   GO; GO:0019955; F:cytokine binding; IDA.
DR   GO; GO:0042803; F:protein homodimerization activity; IDA.
DR   GO; GO:0051216; P:cartilage development; IDA.
DR   GO; GO:0016525; P:negative regulation of angiogenesis; IDA.
DR   GO; GO:0006029; P:proteoglycan metabolism; IDA.
DR   GO; GO:0045423; P:regulation of granulocyte macrophage colony. . .; IDA.
DR   GO; GO:0045076; P:regulation of interleukin-2 biosynthesis; IDA.
DR   GO; GO:0045408; P:regulation of interleukin-6 biosynthesis; IDA.
DR   GO; GO:0045414; P:regulation of interleukin-8 biosynthesis; IDA.
DR   GO; GO:0017015; P:regulation of transforming growth factor be. . .; IDA.
DR   GO; GO:0042109; P:tumor necrosis factor-beta biosynthesis; IDA.
DR   InterPro; IPR010345; IL17.
DR   Pfam; PF06083; IL17; 1.
KW   3D-structure; Cytokine; Direct protein sequencing; Glycoprotein;
KW   Signal.
FT   SIGNAL       1    20
FT   CHAIN       21   153       Interleukin-17F.
FT   CARBOHYD    73    73       N-linked (GlcNAc. . .).
FT   DISULFID    37    37       Interchain (with C-127).
FT   DISULFID    92   142
FT   DISULFID    97   144
FT   DISULFID   127   127       Interchain (with C-37).
FT   STRAND      29    29
FT   TURN        35    36
FT   STRAND      45    47
FT   STRAND      52    52
FT   TURN        53    55
FT   TURN        62    66
FT   STRAND      68    68
FT   STRAND      72    78
FT   TURN        80    81
FT   STRAND      82    83
FT   STRAND      86    92
FT   STRAND      97    98
FT   TURN       100   101
FT   STRAND     104   105
FT   TURN       106   107
FT   STRAND     109   123
FT   TURN       126   127
FT   STRAND     130   145
SQ   SEQUENCE   153 AA;  17009 MW;  BB489BED883D57CE CRC64;

  Query Match            16.1%;  Score 173;  DB 1;  Length 153;
  Best Local Similarity  39.0%;  Pred. No. 9.4e-08;
  Matches   39;  Conservative   16;  Mismatches   31;  Indels   14;  Gaps    3;

Qy         97 LEADTHQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLL 156
              :  :    || ||| | |  | :||| ::  |:|   |||:|: |:|  ::||| : |  |
Db         60 MSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQ-GKEDISMNSVPIQQETL 118

Qy        157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLP 194
              |:||:   ||           :|  | : | |||||| |
Db        119 VVRRKHQGCS----------VSFQLEKVLVTVGCTCVTP 147


Search completed: April 27, 2006, 17:23:44
Job time : 284 secs
```

OM protein - protein search, using sw model
Run on: April 27, 2006, 17:19:35 ; Search time 187 Seconds
(without alignments)
462.875 Million cell updates/sec
Title: US-09-854-280-3
Perfect score: 1073
Sequence: 1 MTLLPGLLFLTWLHTCLAHH.....FHTEFIHVPVGCTCVLPRSV 197
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description

RESULT 1
ID AAY44460 standard; protein; 197 AA.
DE Human Interleukin 17C, PRO1122 polypeptide.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 2
ID AAY53892 standard; protein; 197 AA.
DE Amino acid sequence of human interleukin-21.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1073; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 3
ID AAY92238 standard; protein; 197 AA.
DE Human interleukin-17 (IL-17) homologue.
PN WO200020593-A1.
PD 13-APR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 100.0%; Score 1073; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 4
ID AAB18911 standard; protein; 197 AA.
DE A novel polypeptide designated PRO1122.
PN WO200056889-A2.
PD 28-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 5
ID AAB07684 standard; protein; 197 AA.
DE A human interleukin-171 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 100.0%; Score 1073; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 6
ID AAB07602 standard; protein; 197 AA.
DE A human interleukin (IL) 171 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 100.0%; Score 1073; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 7
ID AAU29247 standard; protein; 197 AA.
DE Human PRO polypeptide sequence #224.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 8
ID AAG66121 standard; protein; 197 AA.
DE Human interleukin (IL)-21 amino acid sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Query Match 100.0%; Score 1073; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 9
ID AAU04951 standard; protein; 197 AA.
DE Human Interleukin 17C ligand, IL-17C.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 10
ID AAE23792 standard; protein; 197 AA.
DE Human LP-48 protein.
PN WO200233083-A2.
PD 25-APR-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 100.0%; Score 1073; DB 5; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 11
ID ABU58623 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 12
ID ABU88171 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 13
ID ABU84486 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 14
ID ABR66360 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 15
ID ABR65750 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;

RESULT 16
ID ABU99690 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 17
ID ABU82929 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 18
ID ABU90050 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 19
ID ABR68299 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 20
ID ABU96352 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 21
ID ABU92783 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 22
ID ABU69105 standard; protein; 197 AA.
DE Human PRO polypeptide #3.
PN US2003032061-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 23
ID ABO08860 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 24
ID ABO02912 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 25
ID ABR75066 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 26
ID ABR94828 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 27
ID ABU85801 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 28
ID ABU98961 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 29
ID ABU98176 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 30
ID ABU91882 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 31
ID ABU89575 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 32
ID ABU86416 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 33
ID ABU67629 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 34
ID ABU80657 standard; protein; 197 AA.
DE Human PRO protein #224.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 35
ID ABR99575 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 36

ID ABR98965 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 37
ID ABO16488 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 38
ID ABR92388 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 39
ID ABO19421 standard; protein; 197 AA.
DE Human secreted / transmembrane polypeptide PRO1122.
PN US2003027249-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 40
ID ABO19029 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 41
ID ABR78450 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 42
ID ABU85186 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 43
ID ABO00325 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 44
ID ABO11657 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 45
ID ABO02302 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 46
ID ABU88876 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 47
ID ABU83571 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 48
ID ABO06372 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 49
ID ABR59408 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 50
ID ABO09470 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 51
ID ABO19334 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 52
ID ABO11352 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 53
ID ABR66970 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 54
ID ABO16183 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 55
ID ABO13889 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 56
ID ABU65792 standard; protein; 197 AA.
DE Human secreted/transmembrane protein, SEQ ID 448.
PN US2003036156-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 57
ID ABO07640 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 58
ID ABO03827 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 59
ID ABR67275 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 60
ID ABO15878 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 61
ID ABU56159 standard; protein; 197 AA.
DE Human secreted/transmembrane protein, PRO1122.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 62
ID ABU65487 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 63
ID ABU95432 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 64
ID ABU71335 standard; protein; 197 AA.
DE Human PRO1122 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 65
ID ABO07945 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 66
ID ABR70186 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 67
ID ABR69519 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 68
ID ABU69082 standard; protein; 197 AA.
DE Human PRO polypeptide #3.
PN US2003008348-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 69
ID ABO01660 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 70
ID ABU81462 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 71
ID ABR60259 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 72
ID ABR67994 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 73
ID ABR65382 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 74
ID ABR68604 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 75
ID ABR72016 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 76
ID ABU85496 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003022295-A1.
PD 30-JAN-2003.

Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 77
ID ABU89186 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 78
ID ABU83266 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 79
ID ABU95122 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 80
ID ABU90670 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 81
ID ABU84181 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 82
ID ABU93832 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 83
ID ABR65077 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 84
ID ABR68909 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 85
ID ABO06725 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 86
ID ABR99270 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 87
ID ABU57154 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 88
ID ABU86106 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 89
ID ABU82393 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 90
ID ABU87404 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 91
ID ABU83876 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 92
ID ABO08250 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 93
ID ABU89698 standard; protein; 197 AA.
DE Human interleukin 17 homologue h-IL17-C/PRO1122.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 94
ID ABU81961 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 95
ID ABU66125 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 96
ID ABR59954 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 97
ID ABU94142 standard; protein; 197 AA.

DE Novel human secreted and transmembrane protein PRO1122.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 98
ID ABO00015 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 99
ID ABR66665 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 100
ID ABR91083 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 101
ID ABU94510 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 102
ID ABU79392 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 103
ID ABU86721 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 104
ID ABU87026 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 105
ID ABU94815 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 106
ID ABO04742 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 107
ID ABR70491 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 108
ID ABU98656 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 109
ID ABR66055 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 110
ID ABR64772 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 111
ID ABU79697 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 112
ID ABU93088 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 113
ID ABU96047 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 114
ID ABU91267 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 115
ID ABU90360 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 116
ID ABO09775 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 117
ID ABO11047 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;

Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 118
ID ABR71101 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 119
ID ABU87709 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 120
ID ABU91577 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 121
ID ABU84791 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 122
ID ABR69881 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 123
ID ABU80258 standard; protein; 197 AA.
DE Human PRO protein #224.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 124
ID ABU72593 standard; protein; 197 AA.
DE Human IL-17 family member, PRO1122, h-IL17C.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 125
ID ABU93527 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 126
ID ABO10080 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 127
ID ABO09165 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 128
ID ABU10733 standard; protein; 197 AA.
DE Human secreted/transmembrane protein #224.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 129
ID ABU95742 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 130
ID ABU96951 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 131
ID ABR70796 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 132
ID ABU81546 standard; protein; 197 AA.
DE Human secreted polypeptide PRO122.
PN US2002192751-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 133
ID ABO05147 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 134
ID ABO08555 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 135
ID ABO05762 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 136
ID ABR74151 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 137
ID ABR95743 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;

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  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 138
ID   ABR81040 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003049741-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 139
ID   ABR81345 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003049743-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 140
ID   ABM01041 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003049769-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 141
ID   ABR88643 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003068743-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 142
ID   ABM77464 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003054479-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 143
ID   ABO28948 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003068685-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 144
ID   ABO31693 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003068725-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 145
ID   ADA76536 standard; protein; 197 AA.
DE   Novel human secreted and transmembrane protein PRO1122.
PN   US2003036114-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 146
ID   ABM08110 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003068752-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 147
ID   ABO40590 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003068682-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 148
ID   ABO36015 standard; protein; 197 AA.
DE   Human PRO polypeptide #224.
PN   US2003068701-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 149
ID   ABO44154 standard; protein; 197 AA.
DE   Human PRO polypeptide #224.
PN   US2003068755-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 150
ID   ADA78200 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003073180-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 151
ID   ABM24949 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003104539-A1.
PD   05-JUN-2003.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 152
ID   ABO03217 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003036131-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 153
ID   ABR90473 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003040075-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 154
ID   ABM17387 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003054459-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 155
ID   ABR95133 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003044930-A1.
PD   06-MAR-2003.
  Query Match             100.0%;  Score 1073;  DB 6;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 156
ID   ABR95438 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003040071-A1.
PD   27-FEB-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 157
ID ABO21676 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 158
ID ABR97940 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 159
ID ABR87728 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 160
ID ABM77769 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 161
ID ABM27999 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 162
ID ADA43227 standard; protein; 197 AA.
DE Human interleukin 17 related mammalian cytokine polypeptide #2.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 163
ID ABM06280 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 164
ID ABM03786 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 165
ID ABM35237 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 166
ID ABM26474 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 167
ID ABO48256 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 168
ID ABR92998 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 169
ID ABO24759 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 170
ID ABM11770 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 171
ID ABM02871 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 172
ID ABM16167 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 173
ID ABO27728 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 174
ID ABM29219 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;

RESULT 175
ID ABM07195 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 176
ID ABM21289 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 177
ID ABM09635 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 178
ID ABO41505 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 179
ID ABO36320 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 180
ID ABO43849 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 181
ID ABM76549 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 182
ID ABM76245 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 183
ID ABM25864 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 184
ID ABM26169 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 185
ID ABO03522 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 186
ID ABO02607 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 187
ID ABR90778 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 188
ID ABR73846 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 189
ID ABO17098 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 190
ID ABR94523 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 191
ID ABR76030 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 192
ID ABR71406 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 193
ID ABR93303 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 194
ID ABR93608 standard; protein; 197 AA.

DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 195
ID ABR88033 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 196
ID ABO28033 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 197
ID ABO30168 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 198
ID ABO33377 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 199
ID ABM05065 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 200
ID ABM09025 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 201
ID ABO36625 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 202
ID ABO35710 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 203
ID ABO39675 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 204
ID ABM10550 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 205
ID ABM12075 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 206
ID ABO52221 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 207
ID ABO52526 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 208
ID ABO23844 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 209
ID ABR97330 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 210
ID ABR87118 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 211
ID ABM11160 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 212
ID ABM28304 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054476-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 213
ID ABO32303 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 214
ID ABM15430 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 215
ID ABM06585 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 216
ID ABM04396 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 217
ID ABM22509 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 218
ID ABM07805 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 219
ID ABO40895 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 220
ID ABM35542 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 221
ID ABM33305 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 222
ID ABO52831 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 223
ID ABO50391 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 224
ID ABU99385 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 225
ID ABO04437 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 226
ID ABO06067 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 227
ID ABM18607 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 228
ID ABR97635 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 229
ID ABR80735 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 230
ID ABM01346 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 231
ID ABR88948 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.

PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 232
ID ABM13600 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 233
ID ABM20984 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 234
ID ABO42115 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 235
ID ABO42725 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 236
ID ABM10245 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 237
ID ABO38760 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 238
ID ABM33000 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 239
ID ABM22814 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 240
ID ABM75025 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 241
ID ADA79992 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 242
ID ABR96415 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 243
ID ABM02566 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 244
ID ABR86508 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 245
ID ABR86813 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 246
ID ABM16777 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 247
ID ABM29829 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 248
ID ABO29253 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 249
ID ABM24034 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 250
ID ABM23424 standard; protein; 197 AA.

DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 251
ID ABM22204 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 252
ID ABO37845 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 253
ID ABM28609 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 254
ID ABM28914 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 255
ID ABM66558 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 256
ID ABM75940 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 257
ID ABM34220 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 258
ID ABM34525 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 259
ID ABO20456 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 260
ID ABO21371 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 261
ID ABO22286 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 262
ID ABR96720 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 263
ID ABR85898 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 264
ID ABR99880 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 265
ID ABM00431 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 266
ID ABM00736 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 267
ID ABO29863 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 268
ID ABM23729 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 269
ID ABM29524 standard; protein; 197 AA.

DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 270
ID ABO38455 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 271
ID ABO45755 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 272
ID ABM20679 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 273
ID ADA81719 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 274
ID ABO16793 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 275
ID ABO18419 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 276
ID ABO22846 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 277
ID ABO23151 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 278
ID ABR92693 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 279
ID ABR81650 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 280
ID ABM78074 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 281
ID ABR89863 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 282
ID ABM26779 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 283
ID ABM13905 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 284
ID ABO28643 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 285
ID ABO30473 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 286
ID ABM07500 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 287
ID ABM04091 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 288

ID ABO37235 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 289
ID ABO41810 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 290
ID ABO35405 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 291
ID ABM25254 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 292
ID ABO47646 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 293
ID ABO47951 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 294
ID ABO48561 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 295
ID ABO51611 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 296
ID ABO51916 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 297
ID ABO50696 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 298
ID ABR79820 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 299
ID ABM17082 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 300
ID ABO18114 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 301
ID ABO21066 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 302
ID ABR97025 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 303
ID ABM12380 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 304
ID ABM16472 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 305
ID ABM24339 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 306
ID ABM14820 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;

RESULT 307
ID ABM04701 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 308
ID ABM06890 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 309
ID ABM09330 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 310
ID ABO39370 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 311
ID ABM75635 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 312
ID ABM25559 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 313
ID ABM20069 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 314
ID ABO46975 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 315
ID ABO47280 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 316
ID ADA83517 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 317
ID ABR71711 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 318
ID ABR72321 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 319
ID ABR98660 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 320
ID ABO07030 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 321
ID ABR84983 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 322
ID ABR73541 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 323
ID ABR76635 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 324
ID ABR73236 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 325
ID ABM18302 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 326
ID ABO20761 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.

PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 327
ID ABO25504 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 328
ID ABO25809 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 329
ID ABR94218 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 330
ID ABR80125 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 331
ID ABM11465 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 332
ID ABO33072 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 333
ID ABO30778 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 334
ID ABO31083 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 335
ID ABM27389 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 336
ID ABM30134 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 337
ID ABM05670 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 338
ID ABM15735 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 339
ID ABM08720 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 340
ID ABO42420 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 341
ID ABO38150 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 342
ID ABO46060 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 343
ID ABM66863 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 344
ID ADB20560 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;

RESULT 345
ID ABM19764 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 346
ID ABO49476 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 347
ID ABO49781 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 348
ID ADA78812 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 349
ID ABR88338 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 350
ID ABM27084 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 351
ID ABM03481 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 352
ID ABO39980 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 353
ID ABO50086 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 354
ID ABO51001 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 355
ID ABO05457 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 356
ID ABR74761 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 357
ID ABO25129 standard; protein; 197 AA.
DE Human secreted/transmembrane protein PRO1122.
PN US2003044842-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 358
ID ABR77240 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 359
ID ABM17997 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 360
ID ABR96048 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 361
ID ABO21981 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 362
ID ABO20151 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 363
ID ABO24454 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;

RESULT 364
ID ABR86203 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 365
ID ABM10855 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 366
ID ABM76854 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 367
ID ABR89558 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 368
ID ABM12685 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 369
ID ABM05975 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 370
ID ABO35100 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 371
ID ABM03176 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 372
ID ABM19154 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 373
ID ABM19459 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 374
ID ABO46670 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 375
ID ABO49171 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 376
ID ABR69214 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 377
ID ABR89253 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 378
ID ABR72626 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 379
ID ABR74456 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 380
ID ABO18724 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 381
ID ABR80430 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 382
ID ABM01651 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;

Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 383
ID ABM02261 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 384
ID ABR87423 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 385
ID ABM12990 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 386
ID ABM30744 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 387
ID ADA49768 standard; protein; 197 AA.
DE Human interleukin-17/interleukin-17 receptor related PRO1122.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 388
ID ABM24644 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 389
ID ABO29558 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 390
ID ABO31388 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 391
ID ABM14515 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 392
ID ABM09940 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 393
ID ABO39065 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 394
ID ABM34830 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 395
ID ABO51306 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 396
ID ABO04132 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 397
ID ABO10602 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 398
ID ABR77845 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 399
ID ABR79055 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 400
ID ABO24149 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 401
ID ABR93913 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

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  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 402
ID   ABM01956 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003059883-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 403
ID   ABM78379 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003049764-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 404
ID   ABR90168 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003073177-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 405
ID   ABM27694 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003064442-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 406
ID   ABM13295 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003064450-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 407
ID   ADA26961 standard; protein; 197 AA.
DE   Human PRO polypeptide #2.
PN   US2002182673-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 408
ID   ABO31998 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003068731-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 409
ID   ABM14210 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003068683-A1.
PD   10-APR-2003.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 410
ID   ABM08415 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003068754-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 411
ID   ABO40285 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003068681-A1.
PD   10-APR-2003.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 412
ID   ABM74720 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003096351-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 413
ID   ABM33915 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003096358-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 414
ID   ABM20374 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003104556-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 415
ID   ABO48866 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003049756-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 416
ID   ABR72931 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003036122-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 417
ID   ABO15573 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003036121-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 418
ID   ABR85288 standard; protein; 197 AA.
DE   Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN   US2003040065-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 419
ID   ABO15268 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003044919-A1.
PD   06-MAR-2003.
  Query Match             100.0%;  Score 1073;  DB 7;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
RESULT 420
ID   ABO17403 standard; protein; 197 AA.
DE   Human secreted/transmembrane protein (PRO) #224.
PN   US2003040077-A1.
PD   27-FEB-2003.
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Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 421
ID ABM17692 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 422
ID ABR85593 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 423
ID ABM77159 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 424
ID ABO28338 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 425
ID ABM23119 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 426
ID ABM30439 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 427
ID ABM21899 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 428
ID ABM21594 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 429
ID ABM15125 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 430
ID ABO41200 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 431
ID ABO36930 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 432
ID ABO37540 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 433
ID ABM75330 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 434
ID ABM33610 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 435
ID ABO46365 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 436
ID ADA82883 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 437
ID ABM31964 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 438
ID ABM31354 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 439
ID ADB32010 standard; protein; 197 AA.

DE Human interleukin 171, IL-171.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 440
ID ADB86191 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 441
ID ABM32269 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 442
ID ABM32574 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 443
ID ABM31659 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 444
ID ABM31049 standard; protein; 197 AA.
DE Human secreted polypeptide PRO1122, SEQ ID NO:448.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 445
ID ADB66895 standard; protein; 197 AA.
DE Human PRO polypeptide #2.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 446
ID AAE39099 standard; protein; 197 AA.
DE Human PRO1122 protein.
PN US2003049733-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 447
ID AAE39036 standard; protein; 197 AA.
DE Human PRO1122 protein.
PN US2003049734-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 448
ID ADC29767 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003092063-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 449
ID ADD05921 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 450
ID ADC78793 standard; protein; 197 AA.
DE Human PRO protein #11.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 451
ID ABW02054 standard; protein; 197 AA.
DE Human IL-17C ligand (PRO1122) protein.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 452
ID ADG02916 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 453
ID ADG01623 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 454
ID ADF95798 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 455
ID ADG12613 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 456
ID ADG87379 standard; protein; 197 AA.
DE Human PRO1122 protein from clone DNA62377-1381-1.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 457
ID ADH09273 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003207395-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 458
ID ADL16675 standard; protein; 197 AA.
DE Human PRO1122 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 459
ID ADL33052 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 460
ID ADM30588 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 461
ID ADE83317 standard; protein; 197 AA.
DE Human IL-17 family member #3.
PN US2003124092-A1.
PD 03-JUL-2003.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 462
ID ADE74585 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 463
ID ADE75197 standard; protein; 197 AA.
DE Human secreted/transmembrane protein (PRO) #224.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 464
ID ADF09210 standard; protein; 197 AA.
DE Human secreted and transmembrane protein PRO1122.
PN US2003134327-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 465
ID ADF96410 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 466
ID ADG04681 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 467
ID ADG00841 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 468
ID ADG83097 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 469
ID ADH26378 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 470
ID ADH33347 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 471
ID ADJ61746 standard; protein; 197 AA.
DE Human interleukin-21 (IL-21) protein #2.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 472
ID ADJ55086 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 473
ID ADL16636 standard; protein; 197 AA.
DE Human PRO1122 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 474
ID ADL71296 standard; protein; 197 AA.
DE Human IL-17C (PRO1122) protein.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 475
ID ADJ64857 standard; protein; 197 AA.
DE Human PRO polypeptide #224.
PN US2004038337-A1.
PD 26-FEB-2004.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 476
ID ADM31753 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 477
ID ADM36800 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 478
ID ADM40605 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 479
ID ADN38213 standard; protein; 197 AA.
DE Novel human secreted and transmembrane protein PRO1122.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 480
ID ADP12602 standard; protein; 197 AA.
DE Protein encoded by mRNA of the invention #212.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 481
ID ADR13813 standard; protein; 197 AA.
DE Human interleukin-171 (IL-171) polypeptide.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 100.0%; Score 1073; DB 8; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 482
ID ADW12442 standard; protein; 197 AA.
DE Human PRO1122 protein.
PN US2004265966-A1.
PD 30-DEC-2004.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (PANJ/) PAN J.
PA (STEW/) STEWART T A.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 100.0%; Score 1073; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 483
ID ADW64915 standard; protein; 197 AA.
DE Human IL-17 like protein related family member, hIL-17c.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 100.0%; Score 1073; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 484
ID ADZ14892 standard; protein; 197 AA.
DE Human IL-17C protein, SEQ ID NO: 8.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 100.0%; Score 1073; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 485
ID AEB55668 standard; protein; 197 AA.
DE Human IL-17C cytokine receptor subunit.
PN WO2005065711-A2.
PD 21-JUL-2005.
PA (SCHE) SCHERING CORP.
Query Match 100.0%; Score 1073; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.9e-108;
RESULT 486
ID AAY44485 standard; protein; 206 AA.
DE Human Interleukin 17C with C-terminal Gly(His)8 tag, IL-17C.his.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 2e-108;
RESULT 487
ID AAY44462 standard; protein; 425 AA.
DE Human Interleukin 17C-IgG1 Fc fusion protein, hIL-17C.fc.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1073; DB 3; Length 425;
Best Local Similarity 100.0%; Pred. No. 5e-108;
RESULT 488
ID AAE08676 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein.
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 99.1%; Score 1063; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.8e-107;
RESULT 489
ID AAE08680 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Leu47Ile).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.9%; Score 1061; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 4.6e-107;
RESULT 490
ID AAE08682 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Leu47Met).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.9%; Score 1061; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 4.6e-107;
RESULT 491
ID AAE08681 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Leu47Val).
PN WO200159120-A2.

PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.8%; Score 1060; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 5.9e-107;
RESULT 492
ID AAE08685 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Glu110Asp).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.8%; Score 1060; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 5.9e-107;
RESULT 493
ID AAE08684 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Leu47Phe).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.7%; Score 1059; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 7.5e-107;
RESULT 494
ID AAE08687 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Tyr141Phe).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.7%; Score 1059; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 7.5e-107;
RESULT 495
ID AAE08683 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Leu47Ala).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.6%; Score 1058; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 9.7e-107;
RESULT 496
ID AAE08686 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Tyr141Trp).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.6%; Score 1058; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 9.7e-107;
RESULT 497
ID AAE08679 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Leu47Nle).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.6%; Score 1058; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 9.7e-107;
RESULT 498
ID AAE08690 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Pro151Ala).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.3%; Score 1055; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 2.1e-106;
RESULT 499
ID AAE08703 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys221Ala).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.2%; Score 1054; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
RESULT 500
ID AAE08688 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Tyr141Thr).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.2%; Score 1054; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
RESULT 501
ID AAE08691 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Pro151Gly).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.2%; Score 1054; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
RESULT 502
ID AAE08697 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys164Ala).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.2%; Score 1054; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
RESULT 503
ID AAE08693 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys159Ala).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.2%; Score 1054; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
RESULT 504
ID AAE08695 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys161Ala).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.2%; Score 1054; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
RESULT 505
ID AAE08701 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys219Ala).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.2%; Score 1054; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
RESULT 506
ID AAE08689 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Tyr141Ser).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.2%; Score 1054; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
RESULT 507
ID AAE08699 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys193Ala).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.2%; Score 1054; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
RESULT 508
ID AAE08700 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys219Ser).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.1%; Score 1053; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 3.4e-106;
RESULT 509
ID AAE08696 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys164Ser).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.

Query Match 98.1%; Score 1053; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 3.4e-106;
RESULT 510
ID AAE08694 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys161Ser).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.1%; Score 1053; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 3.4e-106;
RESULT 511
ID AAE08702 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys221Ser).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.1%; Score 1053; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 3.4e-106;
RESULT 512
ID AAE08698 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys193Ser).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.1%; Score 1053; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 3.4e-106;
RESULT 513
ID AAE08692 standard; protein; 227 AA.
DE Human interleukin (IL)-17 like protein mutant (Cys159Ser).
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 98.1%; Score 1053; DB 4; Length 227;
Best Local Similarity 99.5%; Pred. No. 3.4e-106;
RESULT 514
ID AAE08677 standard; protein; 223 AA.
DE Human mature interleukin (IL)-17 like protein.
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 96.4%; Score 1034; DB 4; Length 223;
Best Local Similarity 99.0%; Pred. No. 4e-104;
RESULT 515
ID AAE23794 standard; protein; 187 AA.
DE Mature human LP-48 protein fused to the flag epitope tag.
PN WO200233083-A2.
PD 25-APR-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 90.8%; Score 974; DB 5; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
RESULT 516
ID ADA49808 standard; protein; 184 AA.
DE Human interleukin-17C (IL-17C).
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 85.9%; Score 922; DB 7; Length 184;
Best Local Similarity 96.6%; Pred. No. 5.2e-92;
RESULT 517
ID AAY53890 standard; protein; 87 AA.
DE Partial amino acid sequence of human interleukin-21.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 42.8%; Score 459; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.2e-42;
RESULT 518
ID AAG66119 standard; protein; 87 AA.
DE Human interleukin (IL)-21 partial amino acid sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.

Query Match 42.8%; Score 459; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.2e-42;
RESULT 519
ID ADJ61719 standard; protein; 87 AA.
DE Human interleukin-21 (IL-21) protein #1.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 42.8%; Score 459; DB 8; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.2e-42;
RESULT 520
ID AAB07683 standard; protein; 123 AA.
DE A human interleukin-171 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 41.6%; Score 446; DB 3; Length 123;
Best Local Similarity 100.0%; Pred. No. 3e-40;
RESULT 521
ID AAB07601 standard; protein; 123 AA.
DE A human interleukin (IL) 171 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 41.6%; Score 446; DB 3; Length 123;
Best Local Similarity 100.0%; Pred. No. 3e-40;
RESULT 522
ID ADB32008 standard; protein; 123 AA.
DE Human partial interleukin 171, IL-171.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 41.6%; Score 446; DB 7; Length 123;
Best Local Similarity 100.0%; Pred. No. 3e-40;
RESULT 523
ID ADR13811 standard; protein; 123 AA.
DE Human interleukin-171 (IL-171) partial polypeptide.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 41.6%; Score 446; DB 8; Length 123;
Best Local Similarity 100.0%; Pred. No. 3e-40;
RESULT 524
ID ADF16493 standard; protein; 794 AA.
DE Human albumin therapeutic fusion protein SeqID1590.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Query Match 19.2%; Score 205.5; DB 7; Length 794;
Best Local Similarity 31.5%; Pred. No. 6.2e-13;
RESULT 525
ID ADH21792 standard; protein; 794 AA.
DE Human albumin/interleukin-22 fragment fusion protein, SEQ ID NO:589.
PN WO2003059934-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 19.2%; Score 205.5; DB 7; Length 794;
Best Local Similarity 31.5%; Pred. No. 6.2e-13;
RESULT 526
ID AAY70653 standard; protein; 202 AA.
DE Human transforming growth factor beta-9, Ztgfbeta-9 protein.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.5%; Score 199; DB 3; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 527
ID AAB07689 standard; protein; 202 AA.
DE A human interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.

PA (SCHE) SCHERING CORP.
Query Match 18.5%; Score 199; DB 3; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 528
ID AAB07595 standard; protein; 202 AA.
DE A human interleukin (IL) 173 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 18.5%; Score 199; DB 3; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 529
ID AAE36017 standard; protein; 202 AA.
DE Human interleukin-17D (IL-17D) protein #1.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.5%; Score 199; DB 6; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 530
ID ADB31996 standard; protein; 202 AA.
DE Human interleukin 173, IL-173.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 18.5%; Score 199; DB 7; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 531
ID ADF16654 standard; protein; 202 AA.
DE Human albumin fusion protein-related protein SeqID1756.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Query Match 18.5%; Score 199; DB 7; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 532
ID ADF16656 standard; protein; 202 AA.
DE Human albumin fusion protein-related protein SeqID1758.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Query Match 18.5%; Score 199; DB 7; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 533
ID ADH21867 standard; protein; 202 AA.
DE Human interleukin-22 fragment, SEQ ID NO:664.
PN WO2003059934-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 18.5%; Score 199; DB 7; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 534
ID ADH21869 standard; protein; 202 AA.
DE Human interleukin-22 fragment, SEQ ID NO:666.
PN WO2003059934-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 18.5%; Score 199; DB 7; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 535
ID ADR13798 standard; protein; 202 AA.
DE Human interleukin-173 (IL-173) polypeptide.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 18.5%; Score 199; DB 8; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 536
ID ADQ91999 standard; protein; 202 AA.
DE Human transforming growth factor beta-9 (Ztgfbeta-9) protein.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.5%; Score 199; DB 8; Length 202;
Best Local Similarity 30.6%; Pred. No. 5.4e-13;
RESULT 537
ID AAY70662 standard; protein; 209 AA.
DE Human transforming growth factor beta-9, Ztgfbeta-9 variant protein.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.5%; Score 199; DB 3; Length 209;
Best Local Similarity 30.6%; Pred. No. 5.6e-13;
RESULT 538
ID AAE36021 standard; protein; 209 AA.
DE Human interleukin-17D (IL-17D) protein #5.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.5%; Score 199; DB 6; Length 209;
Best Local Similarity 30.6%; Pred. No. 5.6e-13;
RESULT 539
ID ADE34353 standard; protein; 209 AA.
DE Transforming growth factor beta-9 #SEQ ID 34.
PN WO2003048394-A1.
PD 12-JUN-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 18.5%; Score 199; DB 7; Length 209;
Best Local Similarity 30.6%; Pred. No. 5.6e-13;
RESULT 540
ID ADQ92014 standard; protein; 209 AA.
DE Human transforming growth factor beta-9 (Ztgfbeta-9) variant protein.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.5%; Score 199; DB 8; Length 209;
Best Local Similarity 30.6%; Pred. No. 5.6e-13;
RESULT 541
ID AAU04953 standard; protein; 202 AA.
DE Human Interleukin 17D ligand, IL-17D.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 4; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 542
ID AAU83635 standard; protein; 202 AA.
DE Human PRO protein, Seq ID No 88.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 5; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 543
ID ADY31828 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN WO200193983-A1.
PD 13-DEC-2001.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 5; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 544
ID ABU80782 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 6; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 545
ID ABO33748 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.

PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 6; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 546
ID ABU89700 standard; protein; 202 AA.
DE Human interleukin 17 homologue h-IL17-D/PRO21175.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 6; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 547
ID ABU82091 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 6; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 548
ID ABU72595 standard; protein; 202 AA.
DE Human IL-17 family member, PRO21175, h-IL17D.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 6; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 549
ID ABJ72271 standard; protein; 202 AA.
DE Human PRO21175 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 6; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 550
ID ADA43231 standard; protein; 202 AA.
DE Human interleukin 17 related mammalian cytokine polypeptide #4.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 6; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 551
ID ABJ72399 standard; protein; 202 AA.
DE Human PRO21175 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 6; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 552
ID ABO34294 standard; protein; 202 AA.
DE Human secreted/transmembrane polypeptide PRO 21175.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 6; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 553
ID ADA49772 standard; protein; 202 AA.
DE Human interleukin-17/interleukin-17 receptor related PRO21175.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 554
ID ADA26965 standard; protein; 202 AA.
DE Human PRO polypeptide #4.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 555
ID ABJ72101 standard; protein; 202 AA.
DE Human membrane bound receptor/protein PRO21175 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 556
ID ADB83578 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 557
ID ADB80684 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 558
ID ADB73225 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 559
ID ADB78307 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 560
ID ADB84955 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 561
ID ADB78061 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 562
ID ADB87127 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 563
ID ADB84709 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003092890-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 564
ID ADB83824 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 565
ID ADB72979 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 566
ID ADB66899 standard; protein; 202 AA.
DE Human PRO polypeptide #4.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 567
ID ADC36817 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 568
ID ADC21807 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 569
ID ADC49838 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 570
ID ADC49037 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 571
ID ADC49554 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 572
ID ADC47415 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 573
ID ADC47160 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 574
ID ADC78035 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 575
ID ADD06270 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 576
ID ADC77789 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 577
ID ADD50752 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 578
ID ADD50998 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 579
ID ADD50479 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 580
ID ADD50233 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 581
ID ADD51244 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;

Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 582
ID ABW02056 standard; protein; 202 AA.
DE Human IL-17D ligand (PRO21175) protein.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 583
ID ADG87383 standard; protein; 202 AA.
DE Human PRO21175 protein cDNA from clone DNA173894-2947.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 584
ID ADL16679 standard; protein; 202 AA.
DE Human PRO21175 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 7; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 585
ID ADC48791 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 586
ID ADE20962 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 587
ID ADE05806 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 588
ID ADD75035 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 589
ID ADD75781 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 590
ID ADD85013 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 591
ID ADD86839 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 592
ID ADE20716 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 593
ID ADE39013 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 594
ID ADE05560 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 595
ID ADD73545 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 596
ID ADD78385 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 597
ID ADE21208 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 598
ID ADD77323 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 599
ID ADE20470 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 600

ID ADD75535 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 601
ID ADD74051 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 602
ID ADD74297 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 603
ID ADD76027 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 604
ID ADD85519 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 605
ID ADE05068 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 606
ID ADD75281 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 607
ID ADD76825 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 608
ID ADD86593 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 609
ID ADD78061 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 610
ID ADD77569 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 611
ID ADD77815 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 612
ID ADD85273 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 613
ID ADD73805 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 614
ID ADD74543 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 615
ID ADD77071 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 616
ID ADD85765 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 617
ID ADE05314 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 618
ID ADD74789 standard; protein; 202 AA.
DE Human PRO polypeptide #44.

PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 619
ID ADG05601 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 620
ID ADG27155 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 621
ID ADG11218 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 622
ID ADG11997 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 623
ID ADF94554 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 624
ID ADG06650 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 625
ID ADH38994 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 626
ID ADG34084 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 627
ID ADI33554 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 628
ID ADH69648 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 629
ID ADI29809 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 630
ID ADL16640 standard; protein; 202 AA.
DE Human PRO21175 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 631
ID ADL71300 standard; protein; 202 AA.
DE Human IL-17D (PRO21175) protein.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 632
ID ADM27206 standard; protein; 202 AA.
DE Novel human secreted and transmembrane protein PRO21175.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 633
ID ADK66564 standard; protein; 202 AA.
DE Human PRO polypeptide #44.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 18.4%; Score 197; DB 8; Length 202;
Best Local Similarity 29.6%; Pred. No. 8.9e-13;
RESULT 634
ID AAY70655 standard; protein; 186 AA.
DE Mature human transforming growth factor beta-9, Ztgfbeta-9 protein-2.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.2%; Score 195.5; DB 3; Length 186;
Best Local Similarity 33.1%; Pred. No. 1.2e-12;
RESULT 635
ID AAE36019 standard; protein; 186 AA.
DE Human interleukin-17D (IL-17D) protein #3.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.2%; Score 195.5; DB 6; Length 186;
Best Local Similarity 33.1%; Pred. No. 1.2e-12;
RESULT 636
ID ADQ92001 standard; protein; 186 AA.
DE Human mature transforming growth factor beta-9 (Ztgfbeta-9) protein #2.
PN US2004132136-A1.
PD 08-JUL-2004.

PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.2%; Score 195.5; DB 8; Length 186;
Best Local Similarity 33.1%; Pred. No. 1.2e-12;
RESULT 637
ID AAY70663 standard; protein; 187 AA.
DE Mature human Ztgfbeta-9 variant protein.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.2%; Score 195.5; DB 3; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.2e-12;
RESULT 638
ID AAY70654 standard; protein; 187 AA.
DE Mature human transforming growth factor beta-9, Ztgfbeta-9 protein-1.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.2%; Score 195.5; DB 3; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.2e-12;
RESULT 639
ID AAE36018 standard; protein; 187 AA.
DE Human interleukin-17D (IL-17D) protein #2.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.2%; Score 195.5; DB 6; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.2e-12;
RESULT 640
ID AAE36022 standard; protein; 187 AA.
DE Human interleukin-17D (IL-17D) protein #6.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.2%; Score 195.5; DB 6; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.2e-12;
RESULT 641
ID ADQ92000 standard; protein; 187 AA.
DE Human mature transforming growth factor beta-9 (Ztgfbeta-9) protein #1.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.2%; Score 195.5; DB 8; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.2e-12;
RESULT 642
ID ADQ92015 standard; protein; 187 AA.
DE Human mature Ztgfbeta-9 variant protein.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 18.2%; Score 195.5; DB 8; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.2e-12;
RESULT 643
ID ADF16491 standard; protein; 794 AA.
DE Human albumin therapeutic fusion protein SeqID1588.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Query Match 18.1%; Score 194; DB 7; Length 794;
Best Local Similarity 29.7%; Pred. No. 1.1e-11;
RESULT 644
ID ADH21790 standard; protein; 794 AA.
DE Human albumin/interleukin-22 fragment fusion protein, SEQ ID NO:587.
PN WO2003059934-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 18.1%; Score 194; DB 7; Length 794;
Best Local Similarity 29.7%; Pred. No. 1.1e-11;
RESULT 645
ID AAB07694 standard; protein; 169 AA.
DE A murine interleukin-174 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 18.0%; Score 193; DB 3; Length 169;
Best Local Similarity 31.0%; Pred. No. 1.9e-12;
RESULT 646
ID AAB07600 standard; protein; 169 AA.
DE A murine interleukin (IL) 174 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 18.0%; Score 193; DB 3; Length 169;
Best Local Similarity 31.0%; Pred. No. 1.9e-12;
RESULT 647
ID AAE18121 standard; protein; 169 AA.
DE Mouse Interleukin-17 like (IL-17L) protein.
PN WO200208285-A2.
PD 31-JAN-2002.
PA (AMGE-) AMGEN INC.
Query Match 18.0%; Score 193; DB 5; Length 169;
Best Local Similarity 31.0%; Pred. No. 1.9e-12;
RESULT 648
ID AAM52692 standard; protein; 169 AA.
DE Murine interleukin 174 (IL-174).
PN WO200179288-A2.
PD 25-OCT-2001.
PA (SCHE) SCHERING CORP.
Query Match 18.0%; Score 193; DB 5; Length 169;
Best Local Similarity 31.0%; Pred. No. 1.9e-12;
RESULT 649
ID ADB32006 standard; protein; 169 AA.
DE Mouse interleukin 174, IL-174.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 18.0%; Score 193; DB 7; Length 169;
Best Local Similarity 31.0%; Pred. No. 1.9e-12;
RESULT 650
ID ADE83313 standard; protein; 169 AA.
DE Mouse IL-17 like polypeptide.
PN US2003124092-A1.
PD 03-JUL-2003.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 18.0%; Score 193; DB 8; Length 169;
Best Local Similarity 31.0%; Pred. No. 1.9e-12;
RESULT 651
ID ADR13808 standard; protein; 169 AA.
DE Murine interleukin-174 (IL-174) polypeptide.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 18.0%; Score 193; DB 8; Length 169;
Best Local Similarity 31.0%; Pred. No. 1.9e-12;
RESULT 652
ID ADW64911 standard; protein; 169 AA.
DE Mouse IL-17 like protein.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 18.0%; Score 193; DB 9; Length 169;
Best Local Similarity 31.0%; Pred. No. 1.9e-12;
RESULT 653
ID ADZ14888 standard; protein; 169 AA.
DE Mouse IL-17 like protein, SEQ ID NO: 4.

PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 18.0%; Score 193; DB 9; Length 169;
Best Local Similarity 31.0%; Pred. No. 1.9e-12;
RESULT 654
ID AAY70656 standard; protein; 185 AA.
DE Mature human transforming growth factor beta-9, Ztgfbeta-9 protein-3.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.9%; Score 192.5; DB 3; Length 185;
Best Local Similarity 31.7%; Pred. No. 2.5e-12;
RESULT 655
ID AAE36020 standard; protein; 185 AA.
DE Human interleukin-17D (IL-17D) protein #4.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.9%; Score 192.5; DB 6; Length 185;
Best Local Similarity 31.7%; Pred. No. 2.5e-12;
RESULT 656
ID ADQ92002 standard; protein; 185 AA.
DE Human mature transforming growth factor beta-9 (Ztgfbeta-9) protein #2.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.9%; Score 192.5; DB 8; Length 185;
Best Local Similarity 31.7%; Pred. No. 2.5e-12;
RESULT 657
ID AAB07690 standard; protein; 151 AA.
DE A rat interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 17.9%; Score 192; DB 3; Length 151;
Best Local Similarity 34.3%; Pred. No. 2.1e-12;
RESULT 658
ID AAB07594 standard; protein; 151 AA.
DE A human interleukin (IL) 173 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 17.9%; Score 192; DB 3; Length 151;
Best Local Similarity 34.3%; Pred. No. 2.1e-12;
RESULT 659
ID ADB31994 standard; protein; 151 AA.
DE Human partial interleukin 173, IL-173.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 17.9%; Score 192; DB 7; Length 151;
Best Local Similarity 34.3%; Pred. No. 2.1e-12;
RESULT 660
ID ADR13796 standard; protein; 151 AA.
DE Human interleukin-173 (IL-173) partial polypeptide.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 17.9%; Score 192; DB 8; Length 151;
Best Local Similarity 34.3%; Pred. No. 2.1e-12;
RESULT 661
ID ADE83319 standard; protein; 159 AA.
DE Non secreted mouse IL-17 like polypeptide.
PN US2003124092-A1.
PD 03-JUL-2003.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 17.9%; Score 192; DB 8; Length 159;
Best Local Similarity 32.2%; Pred. No. 2.3e-12;
RESULT 662
ID ADW64917 standard; protein; 159 AA.
DE Non-secreted form of mouse IL-17 like protein.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 17.9%; Score 192; DB 9; Length 159;
Best Local Similarity 32.2%; Pred. No. 2.3e-12;
RESULT 663
ID ADZ14894 standard; protein; 159 AA.
DE Non-secreted form of mouse IL-17 like protein, SEQ ID NO: 10 #1.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 17.9%; Score 192; DB 9; Length 159;
Best Local Similarity 32.2%; Pred. No. 2.3e-12;
RESULT 664
ID AAY53891 standard; protein; 160 AA.
DE Partial amino acid sequence of human interleukin-22.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 17.9%; Score 192; DB 3; Length 160;
Best Local Similarity 35.1%; Pred. No. 2.3e-12;
RESULT 665
ID AAG66120 standard; protein; 160 AA.
DE Human interleukin (IL)-22 amino acid sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Query Match 17.9%; Score 192; DB 4; Length 160;
Best Local Similarity 35.1%; Pred. No. 2.3e-12;
RESULT 666
ID AAE18122 standard; protein; 160 AA.
DE Mouse non-secreted form of Interleukin-17 like (IL-17L) protein.
PN WO200208285-A2.
PD 31-JAN-2002.
PA (AMGE-) AMGEN INC.
Query Match 17.9%; Score 192; DB 5; Length 160;
Best Local Similarity 32.2%; Pred. No. 2.3e-12;
RESULT 667
ID ADJ61721 standard; protein; 160 AA.
DE Human interleukin-22 (IL-22) protein #1.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 17.9%; Score 192; DB 8; Length 160;
Best Local Similarity 35.1%; Pred. No. 2.3e-12;
RESULT 668
ID ADW64932 standard; protein; 160 AA.
DE Non-secreted form of mouse IL-17 like protein, alternative version.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.

PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 17.9%; Score 192; DB 9; Length 160;
Best Local Similarity 32.2%; Pred. No. 2.3e-12;
RESULT 669
ID ADZ14912 standard; protein; 160 AA.
DE Non-secreted form of mouse IL-17 like protein, SEQ ID NO: 10 #2.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 17.9%; Score 192; DB 9; Length 160;
Best Local Similarity 32.2%; Pred. No. 2.3e-12;
RESULT 670
ID AAY53893 standard; protein; 173 AA.
DE Partial amino acid sequence of human interleukin-22.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 17.8%; Score 191; DB 3; Length 173;
Best Local Similarity 34.3%; Pred. No. 3.3e-12;
RESULT 671
ID AAG66122 standard; protein; 173 AA.
DE Human interleukin (IL)-22 amino acid sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Query Match 17.8%; Score 191; DB 4; Length 173;
Best Local Similarity 34.3%; Pred. No. 3.3e-12;
RESULT 672
ID ADJ61749 standard; protein; 173 AA.
DE Human interleukin-22 (IL-22) protein #2.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 17.8%; Score 191; DB 8; Length 173;
Best Local Similarity 34.3%; Pred. No. 3.3e-12;
RESULT 673
ID AAY70657 standard; protein; 205 AA.
DE Murine transforming growth factor beta-9, Ztgf beta-9 protein.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.1%; Score 183; DB 3; Length 205;
Best Local Similarity 31.2%; Pred. No. 3.1e-11;
RESULT 674
ID AAB07691 standard; protein; 205 AA.
DE A murine interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 17.1%; Score 183; DB 3; Length 205;
Best Local Similarity 31.2%; Pred. No. 3.1e-11;
RESULT 675
ID AAB07597 standard; protein; 205 AA.
DE A murine interleukin (IL) 173 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 17.1%; Score 183; DB 3; Length 205;
Best Local Similarity 31.2%; Pred. No. 3.1e-11;
RESULT 676
ID AAE05341 standard; protein; 205 AA.
DE Mouse ZCYTO7 protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 17.1%; Score 183; DB 4; Length 205;
Best Local Similarity 31.2%; Pred. No. 3.1e-11;
RESULT 677
ID AAE36023 standard; protein; 205 AA.
DE Mouse interleukin-17D (IL-17D) protein #1.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.1%; Score 183; DB 6; Length 205;
Best Local Similarity 31.2%; Pred. No. 3.1e-11;
RESULT 678
ID ADB32000 standard; protein; 205 AA.
DE Mouse interleukin 173, IL-173.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 17.1%; Score 183; DB 7; Length 205;
Best Local Similarity 31.2%; Pred. No. 3.1e-11;
RESULT 679
ID ADR13802 standard; protein; 205 AA.
DE Murine interleukin-173 (IL-173) polypeptide.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 17.1%; Score 183; DB 8; Length 205;
Best Local Similarity 31.2%; Pred. No. 3.1e-11;
RESULT 680
ID ADQ92006 standard; protein; 205 AA.
DE Mouse transforming growth factor beta-9 (Ztgfbeta-9) protein.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.1%; Score 183; DB 8; Length 205;
Best Local Similarity 31.2%; Pred. No. 3.1e-11;
RESULT 681
ID AAY70658 standard; protein; 183 AA.
DE Mature murine transforming growth factor beta-9, Ztgfbeta-9 protein.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.0%; Score 182.5; DB 3; Length 183;
Best Local Similarity 31.3%; Pred. No. 3e-11;
RESULT 682
ID AAE36024 standard; protein; 183 AA.
DE Mouse interleukin-17D (IL-17D) protein #2.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.0%; Score 182.5; DB 6; Length 183;
Best Local Similarity 31.3%; Pred. No. 3e-11;
RESULT 683
ID ADQ92009 standard; protein; 183 AA.
DE Mouse mature transforming growth factor beta-9 (Ztgfbeta-9) protein.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.0%; Score 182.5; DB 8; Length 183;
Best Local Similarity 31.3%; Pred. No. 3e-11;
RESULT 684
ID ADZ14911 standard; protein; 177 AA.
DE Human IL-17 like protein #3.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 16.4%; Score 176.5; DB 9; Length 177;
Best Local Similarity 30.9%; Pred. No. 1.3e-10;
RESULT 685
ID ADZ14909 standard; protein; 192 AA.

DE Human IL-17 like protein #1.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 16.4%; Score 176.5; DB 9; Length 192;
Best Local Similarity 30.9%; Pred. No. 1.4e-10;
RESULT 686
ID ABG32033 standard; protein; 109 AA.
DE Human ML-1 protein.
PN WO200264739-A2.
PD 22-AUG-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 16.1%; Score 173; DB 5; Length 109;
Best Local Similarity 39.0%; Pred. No. 1.7e-10;
RESULT 687
ID ADW97214 standard; protein; 133 AA.
DE Human interleukin-17F mature protein.
PN WO2005010044-A2.
PD 03-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 9; Length 133;
Best Local Similarity 39.0%; Pred. No. 2.2e-10;
RESULT 688
ID AEA28891 standard; protein; 133 AA.
DE Human CTLA-8 (IL-17F) mature protein (amino acids 31-163).
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Query Match 16.1%; Score 173; DB 9; Length 133;
Best Local Similarity 39.0%; Pred. No. 2.2e-10;
RESULT 689
ID AEA28889 standard; protein; 135 AA.
DE Human CTLA-8 (IL-17F) protein fragment, B18_F1 (amino acids 29-163).
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Query Match 16.1%; Score 173; DB 9; Length 135;
Best Local Similarity 39.0%; Pred. No. 2.2e-10;
RESULT 690
ID AAW28514 standard; protein; 153 AA.
DE Product of clone B18.
PN WO9707198-A2.
PD 27-FEB-1997.
PA (GEMY) GENETICS INST INC.
Query Match 16.1%; Score 173; DB 2; Length 153;
Best Local Similarity 39.0%; Pred. No. 2.6e-10;
RESULT 691
ID AEA28890 standard; protein; 153 AA.
DE Human CTLA-8 (IL-17F) protein fragment (amino acids 11-163).
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Query Match 16.1%; Score 173; DB 9; Length 153;
Best Local Similarity 39.0%; Pred. No. 2.6e-10;
RESULT 692
ID AAW13651 standard; protein; 163 AA.
DE Human CTLA-8.
PN WO9704097-A2.
PD 06-FEB-1997.
PA (GEMY) GENETICS INST INC.
Query Match 16.1%; Score 173; DB 2; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 693
ID AAB03835 standard; protein; 163 AA.
DE Human cytotoxic T lymphocyte antigen-8 (CTLA-8) amino acid sequence.
PN US6074849-A.
PD 13-JUN-2000.
PA (GEMY) GENETICS INST INC.
Query Match 16.1%; Score 173; DB 3; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 694
ID AAY81986 standard; protein; 163 AA.
DE Human CTLA-8 protein sequence.
PN US6043344-A.
PD 28-MAR-2000.
PA (GEMY) GENETICS INST INC.
Query Match 16.1%; Score 173; DB 3; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 695
ID AAB87605 standard; protein; 163 AA.
DE Human PRO20110.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 4; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 696
ID AAU04954 standard; protein; 163 AA.
DE Human Interleukin 17F ligand, IL-17F.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 4; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 697
ID ABG95930 standard; protein; 163 AA.
DE Human secreted/transmembrane protein PRO20110.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 5; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 698
ID ABU90955 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 699
ID ABO34014 standard; protein; 163 AA.
DE Human secreted/transmembrane protein PRO20110.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 700
ID ABU72031 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 701
ID ABU71585 standard; protein; 163 AA.
DE Human secreted polypeptide PRO20110.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 702
ID ABU72366 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;

Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 703
ID ABU91039 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 704
ID ABO27360 standard; protein; 163 AA.
DE Human secreted/transmembrane polypeptide PRO20110.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 705
ID ABU92555 standard; protein; 163 AA.
DE Human secreted/transmembrane protein PRO20110.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 706
ID ABU89701 standard; protein; 163 AA.
DE Human interleukin 17 homologue h-IL17-F/20110.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 707
ID ABU81225 standard; protein; 163 AA.
DE Human secreted polypeptide PRO20110.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 708
ID ABO53339 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 709
ID ABU98342 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 710
ID ABU89347 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 711
ID ABU82554 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 712
ID ABU72596 standard; protein; 163 AA.
DE Human IL-17 family member, PRO20110, h-IL17F.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 713
ID ABU96518 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 714
ID ABU72188 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 715
ID ADB17217 standard; protein; 163 AA.
DE Human transmembrane PRO polypeptide (SeqID 160).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 716
ID ADA43233 standard; protein; 163 AA.
DE Human interleukin 17 related mammalian cytokine polypeptide #5.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 717
ID ABO44318 standard; protein; 163 AA.
DE Human secreted/transmembrane polypeptide PRO 20110.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 718
ID ADA20022 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 719
ID ADB17405 standard; protein; 163 AA.
DE Human transmembrane PRO polypeptide (SeqID 160).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 720
ID ADA20194 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 721

ID ABO34246 standard; protein; 163 AA.
DE Human secreted/transmembrane polypeptide PRO 20110.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 722
ID ADA00491 standard; protein; 163 AA.
DE Human secreted/transmembrane polypeptide PRO 20110.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 6; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 723
ID ADA49774 standard; protein; 163 AA.
DE Human interleukin-17/interleukin-17 receptor related PRO20110.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 724
ID ADA26967 standard; protein; 163 AA.
DE Human PRO polypeptide #5.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 725
ID ADB85733 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 726
ID ADB68412 standard; protein; 163 AA.
DE Human PRO20110 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 727
ID ADB68219 standard; protein; 163 AA.
DE Human PRO20110 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 728
ID ADB91036 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 729
ID ADB66901 standard; protein; 163 AA.
DE Human PRO polypeptide #5.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 730
ID ADC07116 standard; protein; 163 AA.
DE Human PRO20110 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 731
ID ADC17295 standard; protein; 163 AA.
DE Mammalian PRO polypeptide (SeqID 160).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 732
ID ADC14993 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 733
ID ADC52488 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 734
ID ADC78833 standard; protein; 163 AA.
DE Human PRO protein #31.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 735
ID ADD36164 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 736
ID ABW02057 standard; protein; 163 AA.
DE Human IL-17F ligand (PRO20110) protein.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 737
ID ADG01165 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 738
ID ADG08718 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 739
ID ADF95339 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.

PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 740
ID ADH24192 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 741
ID ADG87385 standard; protein; 163 AA.
DE Human PRO20110 protein from clone DNA166819.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 742
ID ADH34218 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 743
ID ADH30051 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 744
ID ADH24022 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 745
ID ADG85426 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 746
ID ADH24702 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 747
ID ADH37558 standard; protein; 163 AA.
DE Human secreted and transmembrane protein PRO20110.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 748
ID ADH02147 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 749
ID ADH37728 standard; protein; 163 AA.
DE Human secreted and transmembrane protein PRO20110.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 750
ID ADG85766 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 751
ID ADH24362 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 752
ID ADH38656 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 753
ID ADG83777 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 754
ID ADH29585 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 755
ID ADH27701 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 756
ID ADH37898 standard; protein; 163 AA.
DE Human secreted and transmembrane protein PRO20110.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 757
ID ADH38075 standard; protein; 163 AA.
DE Human secreted and transmembrane protein PRO20110.
PN US2003181649-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 758
ID ADH57495 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 759
ID ADH53637 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 760
ID ADH53807 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 761
ID ADH52143 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 762
ID ADH49998 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 763
ID ADI25508 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 764
ID ADH90301 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 765
ID ADI25678 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 766
ID ADH97852 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 767
ID ADI03700 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 768
ID ADI12057 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 769
ID ADH90131 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 770
ID ADH98532 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 771
ID ADI11207 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 772
ID ADI11717 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 773
ID ADH98362 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 774
ID ADH98702 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 775
ID ADH98192 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;

Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 776
ID ADI05180 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 777
ID ADI03530 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 778
ID ADI04925 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 779
ID ADH78379 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 780
ID ADI19723 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 781
ID ADH90471 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 782
ID ADI03190 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 783
ID ADH78039 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 784
ID ADH98022 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 785
ID ADI01407 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 786
ID ADI02102 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 787
ID ADI03360 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 788
ID ADI11547 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 789
ID ADI02449 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 790
ID ADI11887 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 791
ID ADI05524 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 792
ID ADH79596 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 793
ID ADI19553 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 794

ID ADI05354 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 795
ID ADH79766 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 796
ID ADI01592 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 797
ID ADI01762 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 798
ID ADI01932 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 799
ID ADH79936 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 800
ID ADI04754 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 801
ID ADI02890 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 802
ID ADH78209 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 803
ID ADI25848 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 804
ID ADI26018 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 805
ID ADK65530 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 806
ID ADL16681 standard; protein; 163 AA.
DE Human PRO20110 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 807
ID ADH98872 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 808
ID ADH80113 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 809
ID ADL93843 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 810
ID ADC52298 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 811
ID ADH06730 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 812
ID ADH06560 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.

PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 813
ID ADG68981 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 814
ID ADH27871 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 815
ID ADH25212 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 816
ID ADH33844 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 817
ID ADH02487 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 818
ID ADH08094 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 819
ID ADG69491 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 820
ID ADH39311 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 821
ID ADG84052 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 822
ID ADG85596 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 823
ID ADH06390 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 824
ID ADH30220 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 825
ID ADH24532 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 826
ID ADG69661 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 827
ID ADH07924 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 828
ID ADG85936 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 829
ID ADH39482 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 830
ID ADH33674 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181637-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 831
ID ADH34014 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 832
ID ADH01224 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 833
ID ADG69831 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 834
ID ADH02317 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 835
ID ADG69321 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 836
ID ADG86106 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 837
ID ADH25042 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 838
ID ADH39659 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 839
ID ADH02657 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 840
ID ADG69151 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 841
ID ADH07754 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 842
ID ADG86276 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 843
ID ADH24872 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 844
ID ADH25920 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 845
ID ADH38486 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 846
ID ADH57325 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 847
ID ADH52312 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 848
ID ADH49678 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;

Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 849
ID ADH90641 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 850
ID ADI11377 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 851
ID ADH99042 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 852
ID ADI02272 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 853
ID ADH90811 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 854
ID ADJ98686 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 855
ID ADJ98856 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 856
ID ADH79015 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 857
ID ADJ99249 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 858
ID ADJ99419 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 859
ID ADJ99037 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 860
ID ADH79184 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 861
ID ADK01045 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 862
ID ADL16642 standard; protein; 163 AA.
DE Human PRO20110 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 863
ID ADK14566 standard; protein; 163 AA.
DE Novel human secreted and transmembrane protein PRO20110.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 864
ID ADL71302 standard; protein; 163 AA.
DE Human PRO20110 protein.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 865
ID ADM81015 standard; protein; 163 AA.
DE Human PRO polypeptide #80.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 866
ID ADP55884 standard; protein; 163 AA.
DE Human PRO protein sequence SEQ ID NO:1860.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 8; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 867

ID ADW97141 standard; protein; 163 AA.
DE Human interleukin-17F protein.
PN WO2005010044-A2.
PD 03-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 9; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 868
ID ADY19139 standard; protein; 163 AA.
DE PRO polypeptide SEQ ID NO 4945.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 173; DB 9; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 869
ID ADY77855 standard; protein; 163 AA.
DE Neoplastic disease detection protein PRO20110.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 16.1%; Score 173; DB 9; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 870
ID AEA28879 standard; protein; 163 AA.
DE Human CTLA-8 (IL-17F) protein, SEQ ID NO: 2.
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Query Match 16.1%; Score 173; DB 9; Length 163;
Best Local Similarity 39.0%; Pred. No. 2.8e-10;
RESULT 871
ID ADZ14910 standard; protein; 125 AA.
DE Human IL-17 like protein #2.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 15.7%; Score 168.5; DB 9; Length 125;
Best Local Similarity 36.0%; Pred. No. 6.2e-10;
RESULT 872
ID AAE10951 standard; protein; 179 AA.
DE Mouse Zcyto7 protein.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 15.7%; Score 168.5; DB 4; Length 179;
Best Local Similarity 27.0%; Pred. No. 9.8e-10;
RESULT 873
ID ABB99362 standard; protein; 179 AA.
DE Amino acid sequence of murine interleukin 17B (IL-17B).
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 15.7%; Score 168.5; DB 6; Length 179;
Best Local Similarity 27.0%; Pred. No. 9.8e-10;
RESULT 874
ID ABG71975 standard; protein; 179 AA.
DE Mouse full length Zcyto7 protein.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 15.7%; Score 168.5; DB 6; Length 179;
Best Local Similarity 27.0%; Pred. No. 9.8e-10;
RESULT 875
ID AAY28236 standard; protein; 180 AA.
DE Mouse interleukin-17D.
PN WO9935267-A1.
PD 15-JUL-1999.
PA (IMMV) IMMUNEX CORP.
Query Match 15.7%; Score 168.5; DB 2; Length 180;
Best Local Similarity 27.0%; Pred. No. 9.9e-10;
RESULT 876
ID AAW85617 standard; protein; 180 AA.
DE Murine Zcyto7.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 15.7%; Score 168.5; DB 2; Length 180;
Best Local Similarity 27.0%; Pred. No. 9.9e-10;
RESULT 877
ID AAY22198 standard; protein; 180 AA.
DE Murine EDIRF I protein sequence.
PN WO9932632-A1.
PD 01-JUL-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 15.7%; Score 168.5; DB 2; Length 180;
Best Local Similarity 27.0%; Pred. No. 9.9e-10;
RESULT 878
ID AAB07687 standard; protein; 180 AA.
DE A murine interleukin-172 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 15.7%; Score 168.5; DB 3; Length 180;
Best Local Similarity 27.0%; Pred. No. 9.9e-10;
RESULT 879
ID AAB07593 standard; protein; 180 AA.
DE A murine interleukin (IL) 172 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 15.7%; Score 168.5; DB 3; Length 180;
Best Local Similarity 27.0%; Pred. No. 9.9e-10;
RESULT 880
ID ADB31992 standard; protein; 180 AA.
DE Mouse interleukin 172, IL-172.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 15.7%; Score 168.5; DB 7; Length 180;
Best Local Similarity 27.0%; Pred. No. 9.9e-10;
RESULT 881
ID ADR13794 standard; protein; 180 AA.
DE Murine interleukin-172 (IL-172) polypeptide.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 15.7%; Score 168.5; DB 8; Length 180;
Best Local Similarity 27.0%; Pred. No. 9.9e-10;
RESULT 882
ID ADC38644 standard; protein; 163 AA.
DE Human secreted protein #1.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Query Match 15.7%; Score 168; DB 7; Length 163;
Best Local Similarity 39.0%; Pred. No. 9.9e-10;
RESULT 883
ID AAB07692 standard; protein; 161 AA.
DE A human interleukin-174 polypeptide.
PN WO200042187-A1.

PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 15.4%; Score 165.5; DB 3; Length 161;
Best Local Similarity 29.7%; Pred. No. 1.8e-09;
RESULT 884
ID AAB07598 standard; protein; 161 AA.
DE A human interleukin (IL) 174 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 15.4%; Score 165.5; DB 3; Length 161;
Best Local Similarity 29.7%; Pred. No. 1.8e-09;
RESULT 885
ID AAE18120 standard; protein; 161 AA.
DE Human Interleukin-17 like (IL-17L) protein.
PN WO200208285-A2.
PD 31-JAN-2002.
PA (AMGE-) AMGEN INC.
Query Match 15.4%; Score 165.5; DB 5; Length 161;
Best Local Similarity 29.7%; Pred. No. 1.8e-09;
RESULT 886
ID AAM52691 standard; protein; 161 AA.
DE Human interleukin 174 (IL-174).
PN WO200179288-A2.
PD 25-OCT-2001.
PA (SCHE) SCHERING CORP.
Query Match 15.4%; Score 165.5; DB 5; Length 161;
Best Local Similarity 29.7%; Pred. No. 1.8e-09;
RESULT 887
ID AAM47464 standard; protein; 161 AA.
DE Human IL-17 receptor like protein ligand, IL-17E.
PN WO200168705-A2.
PD 20-SEP-2001.
PA (AMGE-) AMGEN INC.
Query Match 15.4%; Score 165.5; DB 5; Length 161;
Best Local Similarity 29.7%; Pred. No. 1.8e-09;
RESULT 888
ID ADB32002 standard; protein; 161 AA.
DE Human interleukin 174, IL-174.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 15.4%; Score 165.5; DB 7; Length 161;
Best Local Similarity 29.7%; Pred. No. 1.8e-09;
RESULT 889
ID ADE83311 standard; protein; 161 AA.
DE Human IL-17 like polypeptide.
PN US2003124092-A1.
PD 03-JUL-2003.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 15.4%; Score 165.5; DB 8; Length 161;
Best Local Similarity 29.7%; Pred. No. 1.8e-09;
RESULT 890
ID ADR13804 standard; protein; 161 AA.
DE Human interleukin-174 (IL-174) polypeptide.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 15.4%; Score 165.5; DB 8; Length 161;
Best Local Similarity 29.7%; Pred. No. 1.8e-09;
RESULT 891
ID ADW64909 standard; protein; 161 AA.
DE Human IL-17 like protein.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 15.4%; Score 165.5; DB 9; Length 161;
Best Local Similarity 29.7%; Pred. No. 1.8e-09;
RESULT 892
ID ADZ14886 standard; protein; 161 AA.
DE Human IL-17 like protein, SEQ ID NO: 2.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 15.4%; Score 165.5; DB 9; Length 161;
Best Local Similarity 29.7%; Pred. No. 1.8e-09;
RESULT 893
ID AAB47299 standard; protein; 177 AA.
DE PRO10272 polypeptide.
PN WO200140465-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 4; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 894
ID AAB87603 standard; protein; 177 AA.
DE Human PRO10272.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 4; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 895
ID AAU04952 standard; protein; 177 AA.
DE Human Interleukin 17E ligand, IL-17E.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 4; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 896
ID ABG95928 standard; protein; 177 AA.
DE Human secreted/transmembrane protein PRO10272.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 5; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 897
ID ABU90953 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 898
ID ABO34012 standard; protein; 177 AA.
DE Human secreted/transmembrane protein PRO10272.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 899
ID ABU72029 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;

Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 900
ID ABU71583 standard; protein; 177 AA.
DE Human secreted polypeptide PRO10272.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 901
ID ABU72364 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 902
ID ABU91037 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 903
ID ABO27358 standard; protein; 177 AA.
DE Human secreted/transmembrane polypeptide PRO10272.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 904
ID ABU92553 standard; protein; 177 AA.
DE Human secreted/transmembrane protein PRO10272.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 905
ID ABU89699 standard; protein; 177 AA.
DE Human interleukin 17 homologue h-IL17-E/PRO10272.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 906
ID ABU81223 standard; protein; 177 AA.
DE Human secreted polypeptide PRO10272.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 907
ID ABO53337 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 908
ID ABU98340 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 909
ID ABU89345 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 910
ID ABU82552 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 911
ID ABU72594 standard; protein; 177 AA.
DE Human IL-17 family member, PRO10272, h-IL17E.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 912
ID ABU96516 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 913
ID ABU72186 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 914
ID ADA26944 standard; protein; 177 AA.
DE Human PRO polypeptide #9.
PN US2003087380-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 915
ID ADB17213 standard; protein; 177 AA.
DE Human transmembrane PRO polypeptide (SeqID 156).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 916
ID ADA43229 standard; protein; 177 AA.
DE Human interleukin 17 related mammalian cytokine polypeptide #3.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 917
ID ABO44316 standard; protein; 177 AA.
DE Human secreted/transmembrane polypeptide PRO 10272.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 918

ID ADA20018 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 919
ID ADB17401 standard; protein; 177 AA.
DE Human transmembrane PRO polypeptide (SeqID 156).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 920
ID ADA20190 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 921
ID ABO34244 standard; protein; 177 AA.
DE Human secreted/transmembrane polypeptide PRO 10272.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 922
ID ADA00487 standard; protein; 177 AA.
DE Human secreted/transmembrane polypeptide PRO 10272.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 6; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 923
ID ADA49770 standard; protein; 177 AA.
DE Human interleukin-17/interleukin-17 receptor related PRO10272.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 924
ID ABU63084 standard; protein; 177 AA.
DE Novel human protein PRO10272.
PN US2003054484-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 925
ID ADA26963 standard; protein; 177 AA.
DE Human PRO polypeptide #3.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 926
ID ADB85729 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 927
ID ADB68408 standard; protein; 177 AA.
DE Human PRO10272 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 928
ID ADB68215 standard; protein; 177 AA.
DE Human PRO10272 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 929
ID ADB91032 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 930
ID ADB66897 standard; protein; 177 AA.
DE Human PRO polypeptide #3.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 931
ID ADC07112 standard; protein; 177 AA.
DE Human PRO10272 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 932
ID ADC17291 standard; protein; 177 AA.
DE Mammalian PRO polypeptide (SeqID 156).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 933
ID ADC14989 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 934
ID ADC52484 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 935
ID ADD36160 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 936
ID ADE86211 standard; protein; 177 AA.
DE Human PRO10272 protein.

PN US2003153015-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 937
ID ABW02055 standard; protein; 177 AA.
DE Human IL-17E ligand (PRO10272) protein.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 938
ID ADG01161 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 939
ID ADG08714 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 940
ID ADF95335 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 941
ID ADH24188 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 942
ID ADG87381 standard; protein; 177 AA.
DE Human PRO10272 protein from clone DNA147531-2821.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 943
ID ADH34214 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 944
ID ADH30047 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 945
ID ADH24018 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 946
ID ADG85422 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 947
ID ADH24698 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 948
ID ADH37554 standard; protein; 177 AA.
DE Human secreted and transmembrane protein PRO10272.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 949
ID ADH02143 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 950
ID ADG87369 standard; protein; 177 AA.
DE Human PRO10272 protein from clone DNA147531-2821.
PN US2003077738-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 951
ID ADH37724 standard; protein; 177 AA.
DE Human secreted and transmembrane protein PRO10272.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 952
ID ADG85762 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 953
ID ADH24358 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 954
ID ADH38652 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181643-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 955
ID ADG88791 standard; protein; 177 AA.
DE Human PRO10272 protein.
PN US2003077737-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 956
ID ADG83773 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 957
ID ADH29581 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 958
ID ADH27697 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 959
ID ADH37894 standard; protein; 177 AA.
DE Human secreted and transmembrane protein PRO10272.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 960
ID ADH38071 standard; protein; 177 AA.
DE Human secreted and transmembrane protein PRO10272.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 961
ID ADH57491 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 962
ID ADH53633 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 963
ID ADH53803 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 964
ID ADH52139 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 965
ID ADH49994 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 966
ID ADI25504 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 967
ID ADH90297 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 968
ID ADI25674 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 969
ID ADH97848 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 970
ID ADI03696 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 971
ID ADI12053 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 972
ID ADH90127 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;

Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 973
ID ADH98528 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 974
ID ADI11203 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 975
ID ADI11713 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 976
ID ADH98358 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 977
ID ADH98698 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 978
ID ADH98188 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 979
ID ADI05176 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 980
ID ADI03526 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 981
ID ADI04921 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 982
ID ADH78375 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 983
ID ADI19719 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 984
ID ADH90467 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 985
ID ADI03186 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 986
ID ADH78035 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 987
ID ADH98018 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 988
ID ADI01403 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 989
ID ADI02098 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 990
ID ADI03356 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 991

ID ADI11543 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 992
ID ADI02445 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 993
ID ADI11883 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 994
ID ADI05520 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 995
ID ADH79592 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 996
ID ADI19549 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 997
ID ADI05350 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 998
ID ADH79762 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 999
ID ADI01588 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1000
ID ADI01758 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1001
ID ADI01928 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1002
ID ADH79932 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1003
ID ADI04750 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1004
ID ADI02886 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1005
ID ADH78205 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1006
ID ADI25844 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1007
ID ADI26014 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1008
ID ADK65526 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1009
ID ADL16677 standard; protein; 177 AA.
DE Human PRO10272 polypeptide.

PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1010
ID ADH98868 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1011
ID ADH80109 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1012
ID ADL93839 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 7; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1013
ID ADC52294 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1014
ID ADH06726 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1015
ID ADH06556 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1016
ID ADG68977 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1017
ID ADH27867 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1018
ID ADH25208 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1019
ID ADH33840 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1020
ID ADH02483 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1021
ID ADH08090 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1022
ID ADG69487 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1023
ID ADH39307 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1024
ID ADG84048 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1025
ID ADG47091 standard; protein; 177 AA.
DE Human PRO10272 protein from clone DNA1475531-2821.
PN US2003100063-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1026
ID ADG85592 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1027
ID ADH06386 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180854-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1028
ID ADH30216 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1029
ID ADH24528 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1030
ID ADG69657 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1031
ID ADH07920 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1032
ID ADG85932 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1033
ID ADH39478 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1034
ID ADH33670 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1035
ID ADH34010 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1036
ID ADH01220 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1037
ID ADG69827 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1038
ID ADH02313 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1039
ID ADG69317 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1040
ID ADG86102 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1041
ID ADH25038 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1042
ID ADH39655 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1043
ID ADH02653 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1044
ID ADG69147 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1045
ID ADH07750 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;

Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1046
ID ADG86272 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1047
ID ADH24868 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1048
ID ADH25916 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1049
ID ADH38482 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1050
ID ADH57321 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1051
ID ADH52308 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1052
ID ADH49674 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1053
ID ADH90637 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1054
ID ADI11373 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1055
ID ADH99038 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1056
ID ADI02268 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1057
ID ADH90807 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1058
ID ADJ98682 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1059
ID ADJ98852 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1060
ID ADH79011 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1061
ID ADJ99245 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1062
ID ADJ99415 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1063
ID ADJ99033 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1064

ID ADH79180 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1065
ID ADK01041 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1066
ID ADL16638 standard; protein; 177 AA.
DE Human PRO10272 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1067
ID ADK14562 standard; protein; 177 AA.
DE Novel human secreted and transmembrane protein PRO10272.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1068
ID ADL71298 standard; protein; 177 AA.
DE Human IL-17E (PRO10272) protein.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1069
ID ADM81011 standard; protein; 177 AA.
DE Human PRO polypeptide #78.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 15.4%; Score 165.5; DB 8; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1070
ID ADY77851 standard; protein; 177 AA.
DE Neoplastic disease detection protein PRO10272.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 15.4%; Score 165.5; DB 9; Length 177;
Best Local Similarity 29.7%; Pred. No. 2.1e-09;
RESULT 1071
ID ADA49805 standard; protein; 133 AA.
DE Human interleukin-17F (IL-17F).
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 15.3%; Score 164; DB 7; Length 133;
Best Local Similarity 36.7%; Pred. No. 2.1e-09;
RESULT 1072
ID AAB19720 standard; protein; 178 AA.
DE Human Clone 2191999 encoded protein.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 15.3%; Score 164; DB 3; Length 178;
Best Local Similarity 27.7%; Pred. No. 3e-09;
RESULT 1073
ID ADD18250 standard; protein; 178 AA.
DE Human molecule (MOL) protein MOL9.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.3%; Score 164; DB 7; Length 178;
Best Local Similarity 27.7%; Pred. No. 3e-09;
RESULT 1074
ID AAW85646 standard; protein; 158 AA.
DE Murine Zcyto7 mature protein variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 15.2%; Score 163.5; DB 2; Length 158;
Best Local Similarity 29.3%; Pred. No. 2.9e-09;
RESULT 1075
ID AAE10968 standard; protein; 158 AA.
DE Human Zcyto7 protein #18.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 15.2%; Score 163.5; DB 4; Length 158;
Best Local Similarity 29.3%; Pred. No. 2.9e-09;
RESULT 1076
ID ABB99379 standard; protein; 158 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 15.2%; Score 163.5; DB 6; Length 158;
Best Local Similarity 29.3%; Pred. No. 2.9e-09;
RESULT 1077
ID ABG71992 standard; protein; 158 AA.
DE Human Zcyto7 variant #17.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 15.2%; Score 163.5; DB 6; Length 158;
Best Local Similarity 29.3%; Pred. No. 2.9e-09;
RESULT 1078
ID AAW85645 standard; protein; 160 AA.
DE Murine Zcyto7 mature protein variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 15.2%; Score 163.5; DB 2; Length 160;
Best Local Similarity 29.3%; Pred. No. 3e-09;
RESULT 1079
ID AAE10967 standard; protein; 160 AA.
DE Human Zcyto7 protein #17.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 15.2%; Score 163.5; DB 4; Length 160;
Best Local Similarity 29.3%; Pred. No. 3e-09;
RESULT 1080
ID ABB99378 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 15.2%; Score 163.5; DB 6; Length 160;
Best Local Similarity 29.3%; Pred. No. 3e-09;

RESULT 1081
ID ABG71991 standard; protein; 160 AA.
DE Human Zcyto7 variant #16.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 15.2%; Score 163.5; DB 6; Length 160;
Best Local Similarity 29.3%; Pred. No. 3e-09;
RESULT 1082
ID AAG65244 standard; protein; 191 AA.
DE Human cell factor-CX1 protein related protein #3.
PN CN1299823-A.
PD 20-JUN-2001.
PA (SHAN-) SHANGHAI HUACHEN BIOLOGICAL TECHNOLOGY I.
Query Match 15.1%; Score 161.5; DB 4; Length 191;
Best Local Similarity 28.9%; Pred. No. 6.2e-09;
RESULT 1083
ID AAG65245 standard; protein; 395 AA.
DE Human cell factor-CX1 protein related protein #4.
PN CN1299823-A.
PD 20-JUN-2001.
PA (SHAN-) SHANGHAI HUACHEN BIOLOGICAL TECHNOLOGY I.
Query Match 15.1%; Score 161.5; DB 4; Length 395;
Best Local Similarity 28.9%; Pred. No. 1.6e-08;
RESULT 1084
ID AAY44461 standard; protein; 408 AA.
DE Human Interleukin 17B-IgG1 Fc fusion protein, hIL-17B.fc.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Query Match 15.1%; Score 161.5; DB 3; Length 408;
Best Local Similarity 28.9%; Pred. No. 1.7e-08;
RESULT 1085
ID ADA26995 standard; protein; 155 AA.
DE Human interleukin-17 (hIL-17).
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 15.0%; Score 161; DB 7; Length 155;
Best Local Similarity 41.8%; Pred. No. 5.4e-09;
RESULT 1086
ID AAR76571 standard; protein; 151 AA.
DE Herpesvirus ORF13 product.
PN WO9518826-A2.
PD 13-JUL-1995.
PA (SCHE) SCHERING CORP.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
Query Match 15.0%; Score 160.5; DB 2; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1087
ID AAW02387 standard; protein; 151 AA.
DE HVS13 (viral homologue of interleukin-17).
PN WO9629408-A1.
PD 26-SEP-1996.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 2; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1088
ID AAW13653 standard; protein; 151 AA.
DE Herpesvirus Saimir ORF13.
PN WO9704097-A2.
PD 06-FEB-1997.
PA (GEMY) GENETICS INST INC.
Query Match 15.0%; Score 160.5; DB 2; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1089
ID AAW92413 standard; protein; 151 AA.
DE Herpesvirus Saimiri ORF13 protein.
PN US5869286-A.
PD 09-FEB-1999.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 2; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1090
ID AAB03837 standard; protein; 151 AA.
DE Herpesvirus Saimiri ORF13 (herpes CTLA-8) protein sequence.
PN US6074849-A.
PD 13-JUN-2000.
PA (GEMY) GENETICS INST INC.
Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1091
ID AAY97134 standard; protein; 151 AA.
DE Herpesvirus saimiri protein HSV13.
PN US6100235-A.
PD 08-AUG-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1092
ID AAY97185 standard; protein; 151 AA.
DE Herpesvirus saimiri protein HSV13.
PN US6096305-A.
PD 01-AUG-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1093
ID AAB03811 standard; protein; 151 AA.
DE Fragment of HVS13 (IL-17 homologue).
PN US6072033-A.
PD 06-JUN-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1094
ID AAY99940 standard; protein; 151 AA.
DE Herpesvirus saimiri HVS13 protein.
PN US6072037-A.
PD 06-JUN-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1095
ID AAY81988 standard; protein; 151 AA.
DE Herpes virus CTLA-8 protein sequence.
PN US6043344-A.
PD 28-MAR-2000.
PA (GEMY) GENETICS INST INC.
Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1096
ID AAB62065 standard; protein; 151 AA.
DE HSV ORF13 polypeptide.
PN US6197525-B1.
PD 06-MAR-2001.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 4; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1097
ID AAY72753 standard; protein; 151 AA.
DE Herpesvirus saimiri (HVS 13) protein.
PN US6191104-B1.
PD 20-FEB-2001.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 4; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1098
ID AAG77950 standard; protein; 151 AA.
DE Herpesvirus saimiri open reading frame ORF13 predicted protein.
PN US6274711-B1.
PD 14-AUG-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (SCHE) SCHERING CORP.
Query Match 15.0%; Score 160.5; DB 5; Length 151;

Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1099
ID ADC17319 standard; protein; 151 AA.
DE Herpesvirus Saimiri ORF13 (KCLF2) protein.
PN US6562333-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 15.0%; Score 160.5; DB 7; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1100
ID ADJ61724 standard; protein; 151 AA.
DE Viral interleukin-17 (IL-17) protein.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.0%; Score 160.5; DB 8; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1101
ID ADJ88263 standard; protein; 151 AA.
DE Herpesvirus saimiri ORF13 (HVS13) protein.
PN US6680057-B1.
PD 20-JAN-2004.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 8; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1102
ID ADR13824 standard; protein; 151 AA.
DE Viral interleukin-170 (IL-170) polypeptide.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 15.0%; Score 160.5; DB 8; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1103
ID ADQ91250 standard; protein; 151 AA.
DE Herpesvirus saimiri ORF 13 protein.
PN US2004120898-A1.
PD 24-JUN-2004.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 8; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1104
ID ADR01306 standard; protein; 151 AA.
DE HVS13.
PN US2004120899-A1.
PD 24-JUN-2004.
PA (IMMV) IMMUNEX CORP.
Query Match 15.0%; Score 160.5; DB 8; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1105
ID AEA28883 standard; protein; 151 AA.
DE Herpesvirus saimiri CTLA-8 (IL-17) protein, SEQ ID NO: 6.
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Query Match 15.0%; Score 160.5; DB 9; Length 151;
Best Local Similarity 28.6%; Pred. No. 5.9e-09;
RESULT 1106
ID AAW85625 standard; protein; 160 AA.
DE Human Zcyto7 mature protein allelic variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 15.0%; Score 160.5; DB 2; Length 160;
Best Local Similarity 29.3%; Pred. No. 6.3e-09;
RESULT 1107
ID AAE10959 standard; protein; 160 AA.
DE Human Zcyto7 protein #9.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 15.0%; Score 160.5; DB 4; Length 160;
Best Local Similarity 29.3%; Pred. No. 6.3e-09;
RESULT 1108
ID ABB99370 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 15.0%; Score 160.5; DB 6; Length 160;
Best Local Similarity 29.3%; Pred. No. 6.3e-09;
RESULT 1109
ID ABG71983 standard; protein; 160 AA.
DE Human Zcyto7 variant #8.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 15.0%; Score 160.5; DB 6; Length 160;
Best Local Similarity 29.3%; Pred. No. 6.3e-09;
RESULT 1110
ID ADW97215 standard; protein; 132 AA.
DE Human interleukin-17 mature protein.
PN WO2005010044-A2.
PD 03-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 14.7%; Score 158; DB 9; Length 132;
Best Local Similarity 39.8%; Pred. No. 9.3e-09;
RESULT 1111
ID AAR76573 standard; protein; 155 AA.
DE Human CTLA-8.
PN WO9518826-A2.
PD 13-JUL-1995.
PA (SCHE) SCHERING CORP.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
Query Match 14.7%; Score 158; DB 2; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1112
ID ABG94289 standard; protein; 155 AA.
DE Human interleukin 17 protein.
PN WO200256905-A2.
PD 25-JUL-2002.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 14.7%; Score 158; DB 5; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1113
ID AAG77952 standard; protein; 155 AA.
DE Human cytokine-like protein CTLA-8.
PN US6274711-B1.
PD 14-AUG-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (SCHE) SCHERING CORP.
Query Match 14.7%; Score 158; DB 5; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1114
ID ABG80601 standard; protein; 155 AA.
DE Human Interleukin 17.
PN WO200256907-A2.
PD 25-JUL-2002.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (NOVS) NOVARTIS PHARMA AG.
PA (MAUR/) MAURER P.
PA (LECH/) LECHNER F.
PA (ORTM/) ORTMANN R.
PA (LUEO/) LUEOEND R.
PA (STAU/) STAUFENBIEL M.
PA (FREY/) FREY P.
Query Match 14.7%; Score 158; DB 5; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1115
ID ABU62351 standard; protein; 155 AA.
DE Human cytotoxic T-lymphocyte antigen CTLA-8 #2.
PN US2003040603-A1.
PD 27-FEB-2003.
PA (GOLS/) GOLSTEIN P.

PA (ROUV/) ROUVIER E.
PA (FOSS/) FOSSIEZ F.
PA (LEBE/) LEBECQUE S J E.
PA (DJOS/) DJOSSOU O.
PA (BANC/) BANCHEREAU J.
Query Match 14.7%; Score 158; DB 6; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1116
ID ADA49804 standard; protein; 155 AA.
DE Human interleukin-17.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 14.7%; Score 158; DB 7; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1117
ID ADC17323 standard; protein; 155 AA.
DE Human cytotoxic T lymphocyte-associated antigen (CTLA-8) protein.
PN US6562333-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 14.7%; Score 158; DB 7; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1118
ID ADC78783 standard; protein; 155 AA.
DE Human PRO protein #6.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.7%; Score 158; DB 7; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1119
ID ADD25544 standard; protein; 155 AA.
DE Binding domain-immunoglobulin fusion protein-associated protein #49.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENECRAFT INC.
Query Match 14.7%; Score 158; DB 7; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1120
ID ADE83314 standard; protein; 155 AA.
DE Human IL-17 family member #1.
PN US2003124092-A1.
PD 03-JUL-2003.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 14.7%; Score 158; DB 8; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1121
ID ADJ61722 standard; protein; 155 AA.
DE Human interleukin-17 (IL-17) protein.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.7%; Score 158; DB 8; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1122
ID ADL24267 standard; protein; 155 AA.
DE Human IL-17 protein.
PN WO2004019866-A2.
PD 11-MAR-2004.
PA (IMMV) IMMUNEX CORP.
Query Match 14.7%; Score 158; DB 8; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1123
ID ADP12489 standard; protein; 155 AA.
DE Protein encoded by mRNA of the invention #99.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 14.7%; Score 158; DB 8; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1124
ID ADR13823 standard; protein; 155 AA.
DE Human interleukin-170 (IL-170) polypeptide.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 14.7%; Score 158; DB 8; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1125
ID ADP55160 standard; protein; 155 AA.
DE Human PRO protein sequence SEQ ID NO:1136.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 14.7%; Score 158; DB 8; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1126
ID ADW64912 standard; protein; 155 AA.
DE Human IL-17 like protein related family member, hIL-17.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 14.7%; Score 158; DB 9; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1127
ID ADW97140 standard; protein; 155 AA.
DE Human interleukin-17 protein.
PN WO2005010044-A2.
PD 03-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 14.7%; Score 158; DB 9; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1128
ID ADZ14889 standard; protein; 155 AA.
DE Human IL-17 protein, SEQ ID NO: 5.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 14.7%; Score 158; DB 9; Length 155;
Best Local Similarity 39.8%; Pred. No. 1.1e-08;
RESULT 1129
ID AAY97259 standard; protein; 345 AA.
DE Human IgG1 Fc-HSV13 fusion protein.
PN US6100235-A.
PD 08-AUG-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 14.5%; Score 156; DB 3; Length 345;
Best Local Similarity 36.7%; Pred. No. 5.4e-08;
RESULT 1130
ID AAY97256 standard; protein; 345 AA.
DE Human IgG1 Fc-HSV13 fusion protein.
PN US6096305-A.
PD 01-AUG-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 14.5%; Score 156; DB 3; Length 345;
Best Local Similarity 36.7%; Pred. No. 5.4e-08;
RESULT 1131
ID AAW85627 standard; protein; 160 AA.
DE Human Zcyto7 mature protein allelic variant.
PN WO9849310-A1.

PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.5%; Score 155.5; DB 2; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.2e-08;
RESULT 1132
ID AAE10961 standard; protein; 160 AA.
DE Human Zcyto7 protein #11.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.5%; Score 155.5; DB 4; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.2e-08;
RESULT 1133
ID ABB99372 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.5%; Score 155.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.2e-08;
RESULT 1134
ID ABG71985 standard; protein; 160 AA.
DE Human Zcyto7 variant #10.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.5%; Score 155.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.2e-08;
RESULT 1135
ID AAW85641 standard; protein; 151 AA.
DE Human Zcyto7 mature protein variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 151;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1136
ID AAE10966 standard; protein; 151 AA.
DE Human Zcyto7 protein #16.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 151;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1137
ID ABB99377 standard; protein; 151 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 151;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1138
ID ABG71990 standard; protein; 151 AA.
DE Human Zcyto7 variant #15.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 151;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1139
ID AAW85642 standard; protein; 153 AA.
DE Human Zcyto7 mature protein variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 153;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1140
ID AAE10969 standard; protein; 153 AA.
DE Human Zcyto7 protein #19.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 153;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1141
ID ABB99380 standard; protein; 153 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 153;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1142
ID ABG71993 standard; protein; 153 AA.
DE Human Zcyto7 variant #18.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 153;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1143
ID AAW85640 standard; protein; 154 AA.
DE Human Zcyto7 mature protein variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 154;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1144
ID AAE10965 standard; protein; 154 AA.
DE Human Zcyto7 protein #15.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 154;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1145
ID ABB99376 standard; protein; 154 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 154;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1146
ID ABG71989 standard; protein; 154 AA.
DE Human Zcyto7 variant #14.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 154;
Best Local Similarity 28.7%; Pred. No. 2.7e-08;
RESULT 1147
ID AAW85644 standard; protein; 157 AA.
DE Human Zcyto7 mature protein variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 157;
Best Local Similarity 28.7%; Pred. No. 2.8e-08;
RESULT 1148
ID AAE10971 standard; protein; 157 AA.
DE Human Zcyto7 protein #21.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.

Query Match 14.4%; Score 154.5; DB 4; Length 157;
Best Local Similarity 28.7%; Pred. No. 2.8e-08;
RESULT 1149
ID ABB99382 standard; protein; 157 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 157;
Best Local Similarity 28.7%; Pred. No. 2.8e-08;
RESULT 1150
ID ABG71995 standard; protein; 157 AA.
DE Human Zcyto7 variant #20.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 157;
Best Local Similarity 28.7%; Pred. No. 2.8e-08;
RESULT 1151
ID AAW85639 standard; protein; 158 AA.
DE Human Zcyto7 mature protein variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 158;
Best Local Similarity 28.7%; Pred. No. 2.8e-08;
RESULT 1152
ID AAE10964 standard; protein; 158 AA.
DE Human Zcyto7 protein #14.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 158;
Best Local Similarity 28.7%; Pred. No. 2.8e-08;
RESULT 1153
ID ABB99375 standard; protein; 158 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 158;
Best Local Similarity 28.7%; Pred. No. 2.8e-08;
RESULT 1154
ID ABG71988 standard; protein; 158 AA.
DE Human Zcyto7 variant #13.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 158;
Best Local Similarity 28.7%; Pred. No. 2.8e-08;
RESULT 1155
ID AAW85619 standard; protein; 160 AA.
DE Human Zcyto7 mature protein allelic variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1156
ID AAW85618 standard; protein; 160 AA.
DE Human Zcyto7 mature protein allelic variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1157
ID AAW85621 standard; protein; 160 AA.
DE Human Zcyto7 mature protein allelic variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1158
ID AAW85620 standard; protein; 160 AA.
DE Human Zcyto7 mature protein allelic variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1159
ID AAW85623 standard; protein; 160 AA.
DE Human Zcyto7 mature protein allelic variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1160
ID AAW85629 standard; protein; 160 AA.
DE Human Zcyto7 mature protein allelic variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1161
ID AAW85624 standard; protein; 160 AA.
DE Human Zcyto7 mature protein allelic variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1162
ID AAW85628 standard; protein; 160 AA.
DE Human Zcyto7 mature protein allelic variant.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1163
ID AAE10952 standard; protein; 160 AA.
DE Human Zcyto7 protein #2.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1164
ID AAE10963 standard; protein; 160 AA.
DE Human Zcyto7 protein #13.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1165
ID AAE10962 standard; protein; 160 AA.
DE Human Zcyto7 protein #12.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1166
ID AAE10953 standard; protein; 160 AA.
DE Human Zcyto7 protein #3.
PN WO200164240-A2.

PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1167
ID AAE10958 standard; protein; 160 AA.
DE Human Zcyto7 protein #8.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1168
ID AAE10954 standard; protein; 160 AA.
DE Human Zcyto7 protein #4.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1169
ID AAE10957 standard; protein; 160 AA.
DE Human Zcyto7 protein #7.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1170
ID AAE10955 standard; protein; 160 AA.
DE Human Zcyto7 protein #5.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1171
ID AAG65243 standard; protein; 160 AA.
DE Human cell factor-CX1 protein related protein #2.
PN CN1299823-A.
PD 20-JUN-2001.
PA (SHAN-) SHANGHAI HUACHEN BIOLOGICAL TECHNOLOGY I.
Query Match 14.4%; Score 154.5; DB 4; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1172
ID ABB99373 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1173
ID ABB99369 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1174
ID ABB99366 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1175
ID ABB99365 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1176
ID ABB99363 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1177
ID ABB99364 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1178
ID ABB99368 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1179
ID ABB99374 standard; protein; 160 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B) polypeptide.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1180
ID ABG71976 standard; protein; 160 AA.
DE Human Zcyto7 variant #1.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1181
ID ABG71978 standard; protein; 160 AA.
DE Human Zcyto7 variant #3.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1182
ID ABG71987 standard; protein; 160 AA.
DE Human Zcyto7 variant #12.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1183
ID ABG71977 standard; protein; 160 AA.
DE Human Zcyto7 variant #2.

PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1184
ID ABG71982 standard; protein; 160 AA.
DE Human Zcyto7 variant #7.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1185
ID ABG71981 standard; protein; 160 AA.
DE Human Zcyto7 variant #6.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1186
ID ABG71979 standard; protein; 160 AA.
DE Human Zcyto7 variant #4.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1187
ID ABG71986 standard; protein; 160 AA.
DE Human Zcyto7 variant #11.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 160;
Best Local Similarity 28.7%; Pred. No. 2.9e-08;
RESULT 1188
ID AAY44484 standard; protein; 175 AA.
DE Human Interleukin 17B with C-terminal Gly(His)8 tag, IL-17B.his.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 3; Length 175;
Best Local Similarity 28.7%; Pred. No. 3.2e-08;
RESULT 1189
ID AAY28235 standard; protein; 180 AA.
DE Human interleukin-17D.
PN WO9935267-A1.
PD 15-JUL-1999.
PA (IMMV) IMMUNEX CORP.
Query Match 14.4%; Score 154.5; DB 2; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1190
ID AAW85615 standard; protein; 180 AA.
DE Human Zcyto7.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1191
ID AAY22197 standard; protein; 180 AA.
DE Human EDIRF I protein sequence.
PN WO9932632-A1.
PD 01-JUL-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 14.4%; Score 154.5; DB 2; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1192
ID AAY41762 standard; protein; 180 AA.
DE Human PRO1031 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 2; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1193
ID AAW97350 standard; protein; 180 AA.
DE Interleukin-20.
PN WO9903982-A1.
PD 28-JAN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.4%; Score 154.5; DB 2; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1194
ID AAB33443 standard; protein; 180 AA.
DE Human PRO1031 protein UNQ516 SEQ ID NO:150.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 3; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1195
ID AAY44459 standard; protein; 180 AA.
DE Human Interleukin 17B, PRO1031 polypeptide.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 3; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1196
ID AAB44318 standard; protein; 180 AA.
DE Human PRO1031 (UNQ516) protein sequence SEQ ID NO:470.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 3; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1197
ID AAB18671 standard; protein; 180 AA.
DE Amino acid sequence of a human PRO1031 polypeptide.
PN WO200053752-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 3; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1198
ID AAB18755 standard; protein; 180 AA.
DE A human interleukin 20 polypeptide.
PN WO200055204-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.4%; Score 154.5; DB 3; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1199
ID AAY93973 standard; protein; 180 AA.
DE Amino acid sequence of a human interleukin-20 polypeptide.
PN WO200042189-A1.
PD 20-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.4%; Score 154.5; DB 3; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1200
ID AAE10950 standard; protein; 180 AA.
DE Human Zcyto7 protein #1.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 14.4%; Score 154.5; DB 4; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;

RESULT 1201
ID AAU12394 standard; protein; 180 AA.
DE Human PRO1031 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 4; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1202
ID AAU04950 standard; protein; 180 AA.
DE Human Interleukin 17B ligand, IL-17B.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 4; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1203
ID AAB49894 standard; protein; 180 AA.
DE Human PRO1031 protein sequence.
PN WO200070050-A1.
PD 23-NOV-2000.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 4; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1204
ID AAB50920 standard; protein; 180 AA.
DE Human PRO1031 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 4; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1205
ID AAG65242 standard; protein; 180 AA.
DE Human cell factor-CX1 protein related protein #1.
PN CN1299823-A.
PD 20-JUN-2001.
PA (SHAN-) SHANGHAI HUACHEN BIOLOGICAL TECHNOLOGY I.
Query Match 14.4%; Score 154.5; DB 4; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1206
ID ABB99361 standard; protein; 180 AA.
DE Amino acid sequence of human interleukin 17B (IL-17B).
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1207
ID ABO17838 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1208
ID ABO25264 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1209
ID ABU81092 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1210
ID ABU72270 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1211
ID ABU66792 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1212
ID ABU84950 standard; protein; 180 AA.
DE Human secreted and transmembrane PRO polypeptide #26.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1213
ID ABU59873 standard; protein; 180 AA.
DE Novel secreted and transmembrane protein PRO1031.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1214
ID ABU61148 standard; protein; 180 AA.
DE Human PRO1031 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1215
ID ABO25063 standard; protein; 180 AA.
DE Human secreted/transmembrane protein (PRO) #223.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1216
ID ABU89697 standard; protein; 180 AA.
DE Human interleukin 17 homologue h-IL17-B/PRO1031.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1217
ID ABU80417 standard; protein; 180 AA.
DE Human secreted/transmembrane protein PRO1031.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1218
ID ABU67068 standard; protein; 180 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 446.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1219

ID ABG71974 standard; protein; 180 AA.
DE Human full length Zcyto7 protein.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1220
ID ABU72592 standard; protein; 180 AA.
DE Human IL-17 family member, PRO1031, h-IL17B.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1221
ID ADA45965 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1222
ID ADA76396 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1223
ID ADA19046 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1224
ID ADA43225 standard; protein; 180 AA.
DE Human interleukin 17 related mammalian cytokine polypeptide #1.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1225
ID ADA61669 standard; protein; 180 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1226
ID ADB19454 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1227
ID ADB27995 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1228
ID ADA86474 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1229
ID ADB16038 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1230
ID ADA47824 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1231
ID ADA67619 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1232
ID ADB30626 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1233
ID ADA85922 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1234
ID ADA97134 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1235
ID ADA79438 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1236
ID ADA87577 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1237
ID ADB16779 standard; protein; 180 AA.

DE Human PRO polypeptide #223.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1238
ID ADA91871 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1239
ID ADB14934 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1240
ID ADA25009 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1241
ID ADB18895 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1242
ID ADA94110 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1243
ID ADB20006 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1244
ID ADB13318 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1245
ID ABO43371 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1246
ID ABO19719 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1247
ID ADA12670 standard; protein; 180 AA.
DE Human secreted/transmembrane polypeptide PRO1031.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1248
ID ADA74572 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1249
ID ADB24805 standard; protein; 180 AA.
DE Human PRO polypeptide SEQ ID NO 446.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1250
ID ADA82329 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1251
ID ADA75292 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1252
ID ADA85370 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1253
ID ADA84818 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1254
ID ADB30074 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1255
ID ADA80602 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082761-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1256
ID ADA75844 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1257
ID ADA47069 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1258
ID ADB25365 standard; protein; 180 AA.
DE Human PRO polypeptide SEQ ID NO 446.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1259
ID ADA93541 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1260
ID ADB26891 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1261
ID ADB31178 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1262
ID ADA61106 standard; protein; 180 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1263
ID ADB24253 standard; protein; 180 AA.
DE Human PRO polypeptide SEQ ID NO 446.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1264
ID ADA96582 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1265
ID ADA81154 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1266
ID ADA96030 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1267
ID ADB26339 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1268
ID ADB21824 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1269
ID ABO19610 standard; protein; 180 AA.
DE Novel human secreted and transmembrane polypeptide #78.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 14.4%; Score 154.5; DB 6; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1270
ID ADA77603 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1271
ID ADB18343 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1272
ID ADA87026 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1273
ID ADA88129 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;

Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1274
ID ADA46517 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1275
ID ADA49766 standard; protein; 180 AA.
DE Human interleukin-17/interleukin-17 receptor related PRO1031.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1276
ID ADB28547 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1277
ID ADB29099 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1278
ID ADA77051 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1279
ID ADA26959 standard; protein; 180 AA.
DE Human PRO polypeptide #1.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1280
ID ADA88681 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1281
ID ADA97686 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1282
ID ADB27443 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1283
ID ADB22376 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1284
ID ADA67067 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1285
ID ADB22928 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1286
ID ADB23701 standard; protein; 180 AA.
DE Human PRO polypeptide SEQ ID NO 446.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1287
ID ADA92423 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1288
ID ADB15486 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1289
ID ADB38738 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1290
ID ADB38186 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1291
ID ADB66658 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1292
ID ADB89738 standard; protein; 180 AA.
DE Human PRO polypeptide #223.

PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1293
ID ADB90470 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1294
ID ADB39571 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1295
ID ADB73976 standard; protein; 180 AA.
DE Human PRO polypeptide #78.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1296
ID ADB47194 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1297
ID ADB86801 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1298
ID ADB76692 standard; protein; 180 AA.
DE Human PRO polypeptide #78.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1299
ID ADB77406 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1300
ID ADB34563 standard; protein; 180 AA.
DE Human PRO polypeptide SEQ ID NO 446.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1301
ID ADB35667 standard; protein; 180 AA.
DE Human PRO polypeptide SEQ ID NO 446.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1302
ID ADB66893 standard; protein; 180 AA.
DE Human PRO polypeptide #1.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1303
ID ADB34011 standard; protein; 180 AA.
DE Human PRO polypeptide SEQ ID NO 446.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1304
ID ADB35115 standard; protein; 180 AA.
DE Human PRO polypeptide SEQ ID NO 446.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1305
ID ADB36219 standard; protein; 180 AA.
DE Human PRO polypeptide SEQ ID NO 446.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1306
ID ADB46614 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1307
ID ADC44118 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1308
ID ADC61878 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1309
ID ADC63842 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1310
ID ADC66942 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003060406-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1311
ID ADC69066 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1312
ID ADC63126 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1313
ID ADC68191 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1314
ID ADC41511 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1315
ID ADC67566 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1316
ID ADC62502 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1317
ID ADC42135 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1318
ID ADC50487 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1319
ID ADC72034 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1320
ID ADC60013 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1321
ID ADC53020 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein Seq ID446.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1322
ID ADC57374 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein Seq ID446.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1323
ID ADC60565 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1324
ID ADC51040 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1325
ID ADC65567 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1326
ID ADC54665 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein Seq ID446.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1327
ID ADC53626 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein Seq ID446.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1328
ID ADC59149 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein Seq ID446.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;

Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1329
ID ADC56027 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein Seq ID446.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1330
ID ADC58597 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein Seq ID446.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1331
ID ADD03271 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1332
ID ADC90263 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1333
ID ADC69682 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1334
ID ADC48571 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1335
ID ADD10100 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1336
ID ADD04675 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1337
ID ADC80631 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1338
ID ADD11138 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1339
ID ADC48019 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1340
ID ADC80079 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1341
ID ADD09548 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1342
ID ADD41261 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1343
ID ADD52400 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1344
ID ADD53140 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1345
ID ADD53692 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1346
ID ADD51848 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1347

ID ADD02647 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1348
ID ADD02081 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1349
ID ADD54263 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1350
ID ADE49504 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1351
ID ADD92580 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1352
ID ADD91476 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1353
ID ADE04090 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1354
ID ADE32387 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1355
ID ADE22319 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1356
ID ADD79543 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1357
ID ADE35558 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1358
ID ADE16672 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1359
ID ADD73287 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1360
ID ADE42079 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1361
ID ADE17896 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1362
ID ADD92028 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1363
ID ADE33491 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1364
ID ADE34043 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1365
ID ADD80095 standard; protein; 180 AA.
DE Human PRO polypeptide #223.

PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1366
ID ADD93132 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1367
ID ADD72645 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1368
ID ADE19552 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1369
ID ADE19000 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1370
ID ADE43196 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1371
ID ADD95985 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1372
ID ADE22871 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1373
ID ADD78989 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1374
ID ADE32939 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1375
ID ADE42631 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1376
ID ADE17296 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1377
ID ADD80647 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1378
ID ADD89675 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1379
ID ADE40959 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1380
ID ADE04758 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1381
ID ABW02053 standard; protein; 180 AA.
DE Human IL-17B ligand (PRO1031) protein.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1382
ID ADE92887 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1383
ID ADF47310 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003195333-A1.
PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1384
ID ADG21596 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1385
ID ADG23237 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1386
ID ADF97572 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1387
ID ADG87377 standard; protein; 180 AA.
DE Human PRO1031 protein from clone DNA59294-1381-1.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1388
ID ADG80636 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1389
ID ADG53067 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1390
ID ADG60387 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1391
ID ADG80084 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1392
ID ADH55376 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1393
ID ADH55928 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1394
ID ADI61147 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1395
ID ADI64147 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1396
ID ADI65096 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1397
ID ADH82009 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1398
ID ADH81457 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1399
ID ADL16673 standard; protein; 180 AA.
DE Human PRO1031 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1400
ID ADM82626 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1401
ID ADN16025 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;

Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1402
ID ADN16654 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1403
ID ADN15473 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1404
ID ADN14921 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1405
ID ADI63595 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 7; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1406
ID ADC81183 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1407
ID ADD76631 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1408
ID ADD87995 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1409
ID ADD86399 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1410
ID ADE75847 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1411
ID ADE48804 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1412
ID ADE23423 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1413
ID ADE23975 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1414
ID ADE24618 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1415
ID ADD87443 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1416
ID ADE89309 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1417
ID ADE18448 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1418
ID ADE88757 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1419
ID ADE89905 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.

PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1420
ID ADF61545 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1421
ID ADF40237 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1422
ID ADF46033 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1423
ID ADE94777 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1424
ID ADE91188 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1425
ID ADE95329 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1426
ID ADE93439 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1427
ID ADF24429 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1428
ID ADF40861 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1429
ID ADF23805 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1430
ID ADF33788 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1431
ID ADF35020 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1432
ID ADF27255 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1433
ID ADF27891 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1434
ID ADE92335 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1435

ID ADE90636 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1436
ID ADF41485 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1437
ID ADF33164 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1438
ID ADF25530 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1439
ID ADF26631 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1440
ID ADF34420 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1441
ID ADF46657 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1442
ID ADE91783 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1443
ID ADG02362 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1444
ID ADG22148 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1445
ID ADG20218 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1446
ID ADF98124 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1447
ID ADG24341 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1448
ID ADF98695 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1449
ID ADG03526 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1450
ID ADF99247 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1451
ID ADG16832 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1452
ID ADG05291 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1453
ID ADG19558 standard; protein; 180 AA.
DE Human PRO polypeptide #223.

PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1454
ID ADG13395 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1455
ID ADG08452 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1456
ID ADG15622 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1457
ID ADF97020 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1458
ID ADG06205 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1459
ID ADG23789 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1460
ID ADG04078 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1461
ID ADG24979 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1462
ID ADG07276 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1463
ID ADG07828 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1464
ID ADG55323 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1465
ID ADG60987 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1466
ID ADG62091 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1467
ID ADG82292 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1468
ID ADG57531 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1469
ID ADG56979 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1470
ID ADG55875 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1471
ID ADG58635 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207368-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1472
ID ADG71001 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1473
ID ADG58083 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1474
ID ADG53667 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1475
ID ADG71553 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1476
ID ADG50643 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1477
ID ADG81740 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1478
ID ADH30702 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1479
ID ADH12069 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1480
ID ADG50019 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1481
ID ADG51891 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1482
ID ADG52491 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1483
ID ADG54219 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1484
ID ADG49395 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1485
ID ADG81188 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1486
ID ADG56427 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1487
ID ADH12693 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1488
ID ADG48771 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1489
ID ADG61539 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;

RESULT 1490
ID ADH28626 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1491
ID ADG54771 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1492
ID ADG59811 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1493
ID ADG51267 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1494
ID ADG59211 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1495
ID ADG62667 standard; protein; 180 AA.
DE Human secreted/transmembrane protein, PRO1031.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1496
ID ADI81235 standard; protein; 180 AA.
DE Human PRO polypeptide #223.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1497
ID ADH25692 standard; protein; 180 AA.
DE Human neurotrimin homologue related protein sequence SEQ ID NO:470.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1498
ID ADG09978 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1499
ID ADI15449 standard; protein; 180 AA.
DE Novel human secreted and transmembrane protein PRO1031.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 14.4%; Score 154.5; DB 8; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;
RESULT 1500
ID ADW49704 standard; protein; 180 AA.
DE PRO1031 protein, SEQ ID 470.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 14.4%; Score 154.5; DB 9; Length 180;
Best Local Similarity 28.7%; Pred. No. 3.3e-08;

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OM protein - protein search, using sw model

Run on: April 27, 2006, 17:17:54 ; Search time 24 Seconds
(without alignments)
678.630 Million cell updates/sec

Title: US-09-854-280-3
Perfect score: 1073
Sequence: 1 MTLLPGLLFLTWLHTCLAHH.....FHTEFIHVPVGCTCVLPRSV 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1073	100.0	197	2	US-09-480-297A-23	Sequence 23, Appl
2	1073	100.0	197	2	US-09-747-259-4	Sequence 4, Appli
3	1073	100.0	197	2	US-09-816-744-4	Sequence 4, Appli
4	1073	100.0	213	2	US-09-949-016-11258	Sequence 11258, A
5	459	42.8	87	2	US-09-231-788-11	Sequence 11, Appl
6	446	41.6	123	2	US-09-480-297A-21	Sequence 21, Appl
7	199	18.5	202	2	US-09-480-297A-8	Sequence 8, Appli
8	197	18.4	202	2	US-09-747-259-8	Sequence 8, Appli
9	197	18.4	202	2	US-09-816-744-8	Sequence 8, Appli
10	193	18.0	169	2	US-09-480-297A-18	Sequence 18, Appl
11	193	18.0	169	2	US-09-836-385-4	Sequence 4, Appli
12	192	17.9	151	2	US-09-480-297A-6	Sequence 6, Appli
13	192	17.9	160	2	US-09-231-788-12	Sequence 12, Appl
14	183	17.1	205	2	US-09-724-864-37	Sequence 37, Appl
15	183	17.1	205	2	US-09-480-297A-12	Sequence 12, Appl
16	173	16.1	153	1	US-08-514-014-12	Sequence 12, Appl
17	173	16.1	153	1	US-08-833-823-12	Sequence 12, Appl
18	173	16.1	163	2	US-09-034-810-2	Sequence 2, Appli
19	173	16.1	163	2	US-08-685-239-2	Sequence 2, Appli
20	173	16.1	163	2	US-09-747-259-10	Sequence 10, Appl
21	173	16.1	163	2	US-09-816-744-10	Sequence 10, Appl
22	173	16.1	163	2	US-10-102-080-2	Sequence 2, Appli
23	168.5	15.7	179	2	US-09-794-705A-7	Sequence 7, Appli
24	168.5	15.7	180	2	US-09-620-956-12	Sequence 12, Appl
25	168.5	15.7	180	2	US-09-611-152-12	Sequence 12, Appl
26	168.5	15.7	180	2	US-09-480-297A-4	Sequence 4, Appli
27	168.5	15.7	180	2	US-09-631-531-12	Sequence 12, Appl
28	165.5	15.4	161	2	US-09-480-297A-14	Sequence 14, Appl
29	165.5	15.4	161	2	US-09-836-385-2	Sequence 2, Appli
30	165.5	15.4	177	2	US-09-747-259-6	Sequence 6, Appli
31	165.5	15.4	177	2	US-09-816-744-6	Sequence 6, Appli
32	165.5	15.4	233	2	US-09-949-016-9008	Sequence 9008, Ap
33	163.5	15.2	158	2	US-09-620-956-40	Sequence 40, Appl
34	163.5	15.2	158	2	US-09-611-152-40	Sequence 40, Appl
35	163.5	15.2	158	2	US-09-794-705A-25	Sequence 25, Appl
36	163.5	15.2	158	2	US-09-631-531-40	Sequence 40, Appl
37	163.5	15.2	160	2	US-09-620-956-39	Sequence 39, Appl
38	163.5	15.2	160	2	US-09-611-152-39	Sequence 39, Appl
39	163.5	15.2	160	2	US-09-794-705A-24	Sequence 24, Appl
40	163.5	15.2	160	2	US-09-631-531-39	Sequence 39, Appl
41	160.5	15.0	151	1	US-08-620-694A-8	Sequence 8, Appli
42	160.5	15.0	151	2	US-09-034-810-6	Sequence 6, Appli
43	160.5	15.0	151	2	US-09-022-255-8	Sequence 8, Appli
44	160.5	15.0	151	2	US-09-022-696-8	Sequence 8, Appli
45	160.5	15.0	151	2	US-08-685-239-6	Sequence 6, Appli
46	160.5	15.0	151	2	US-09-022-253-8	Sequence 8, Appli
47	160.5	15.0	151	2	US-09-022-260-8	Sequence 8, Appli
48	160.5	15.0	151	2	US-09-022-259-8	Sequence 8, Appli
49	160.5	15.0	151	2	US-09-022-257-8	Sequence 8, Appli
50	160.5	15.0	151	2	US-08-432-994A-4	Sequence 4, Appli
51	160.5	15.0	151	2	US-09-231-788-14	Sequence 14, Appl
52	160.5	15.0	151	2	US-08-250-846-4	Sequence 4, Appli
53	160.5	15.0	151	2	US-09-480-297A-34	Sequence 34, Appl
54	160.5	15.0	151	2	US-09-549-679-8	Sequence 8, Appli
55	160.5	15.0	151	2	US-09-929-612A-4	Sequence 4, Appli
56	160.5	15.0	151	2	US-10-102-080-6	Sequence 6, Appli
57	160.5	15.0	160	2	US-09-620-956-21	Sequence 21, Appl
58	160.5	15.0	160	2	US-09-611-152-21	Sequence 21, Appl
59	160.5	15.0	160	2	US-09-794-705A-16	Sequence 16, Appl
60	160.5	15.0	160	2	US-09-631-531-21	Sequence 21, Appl
61	158	14.7	155	2	US-08-432-994A-8	Sequence 8, Appli
62	158	14.7	155	2	US-09-231-788-3	Sequence 3, Appli
63	158	14.7	155	2	US-08-250-846-8	Sequence 8, Appli
64	158	14.7	155	2	US-09-480-297A-33	Sequence 33, Appl
65	158	14.7	155	2	US-09-929-612A-8	Sequence 8, Appli
66	158	14.7	160	2	US-09-949-016-7330	Sequence 7330, Ap
67	155.5	14.5	160	2	US-09-620-956-23	Sequence 23, Appl
68	155.5	14.5	160	2	US-09-611-152-23	Sequence 23, Appl
69	155.5	14.5	160	2	US-09-794-705A-18	Sequence 18, Appl
70	155.5	14.5	160	2	US-09-631-531-23	Sequence 23, Appl
71	154.5	14.4	151	2	US-09-620-956-38	Sequence 38, Appl
72	154.5	14.4	151	2	US-09-611-152-38	Sequence 38, Appl
73	154.5	14.4	151	2	US-09-794-705A-23	Sequence 23, Appl
74	154.5	14.4	151	2	US-09-631-531-38	Sequence 38, Appl
75	154.5	14.4	153	2	US-09-620-956-41	Sequence 41, Appl
76	154.5	14.4	153	2	US-09-611-152-41	Sequence 41, Appl
77	154.5	14.4	153	2	US-09-794-705A-26	Sequence 26, Appl
78	154.5	14.4	153	2	US-09-631-531-41	Sequence 41, Appl
79	154.5	14.4	154	2	US-09-620-956-37	Sequence 37, Appl
80	154.5	14.4	154	2	US-09-611-152-37	Sequence 37, Appl
81	154.5	14.4	154	2	US-09-794-705A-22	Sequence 22, Appl
82	154.5	14.4	154	2	US-09-631-531-37	Sequence 37, Appl
83	154.5	14.4	157	2	US-09-620-956-43	Sequence 43, Appl
84	154.5	14.4	157	2	US-09-611-152-43	Sequence 43, Appl
85	154.5	14.4	157	2	US-09-794-705A-28	Sequence 28, Appl
86	154.5	14.4	157	2	US-09-631-531-43	Sequence 43, Appl
87	154.5	14.4	158	2	US-09-620-956-36	Sequence 36, Appl
88	154.5	14.4	158	2	US-09-611-152-36	Sequence 36, Appl
89	154.5	14.4	158	2	US-09-794-705A-21	Sequence 21, Appl
90	154.5	14.4	158	2	US-09-631-531-36	Sequence 36, Appl
91	154.5	14.4	160	2	US-09-620-956-14	Sequence 14, Appl
92	154.5	14.4	160	2	US-09-620-956-15	Sequence 15, Appl
93	154.5	14.4	160	2	US-09-620-956-16	Sequence 16, Appl
94	154.5	14.4	160	2	US-09-620-956-17	Sequence 17, Appl
95	154.5	14.4	160	2	US-09-620-956-19	Sequence 19, Appl
96	154.5	14.4	160	2	US-09-620-956-20	Sequence 20, Appl
97	154.5	14.4	160	2	US-09-620-956-24	Sequence 24, Appl
98	154.5	14.4	160	2	US-09-620-956-25	Sequence 25, Appl
99	154.5	14.4	160	2	US-09-611-152-14	Sequence 14, Appl
100	154.5	14.4	160	2	US-09-611-152-15	Sequence 15, Appl

101	154.5	14.4	160	2	US-09-611-152-16	Sequence 16, Appl
102	154.5	14.4	160	2	US-09-611-152-17	Sequence 17, Appl
103	154.5	14.4	160	2	US-09-611-152-19	Sequence 19, Appl
104	154.5	14.4	160	2	US-09-611-152-20	Sequence 20, Appl
105	154.5	14.4	160	2	US-09-611-152-24	Sequence 24, Appl
106	154.5	14.4	160	2	US-09-611-152-25	Sequence 25, Appl
107	154.5	14.4	160	2	US-09-794-705A-9	Sequence 9, Appli
108	154.5	14.4	160	2	US-09-794-705A-10	Sequence 10, Appl
109	154.5	14.4	160	2	US-09-794-705A-11	Sequence 11, Appl
110	154.5	14.4	160	2	US-09-794-705A-12	Sequence 12, Appl
111	154.5	14.4	160	2	US-09-794-705A-14	Sequence 14, Appl
112	154.5	14.4	160	2	US-09-794-705A-15	Sequence 15, Appl
113	154.5	14.4	160	2	US-09-794-705A-19	Sequence 19, Appl
114	154.5	14.4	160	2	US-09-794-705A-20	Sequence 20, Appl
115	154.5	14.4	160	2	US-09-631-531-14	Sequence 14, Appl
116	154.5	14.4	160	2	US-09-631-531-15	Sequence 15, Appl
117	154.5	14.4	160	2	US-09-631-531-16	Sequence 16, Appl
118	154.5	14.4	160	2	US-09-631-531-17	Sequence 17, Appl
119	154.5	14.4	160	2	US-09-631-531-19	Sequence 19, Appl
120	154.5	14.4	160	2	US-09-631-531-20	Sequence 20, Appl
121	154.5	14.4	160	2	US-09-631-531-24	Sequence 24, Appl
122	154.5	14.4	160	2	US-09-631-531-25	Sequence 25, Appl
123	154.5	14.4	180	2	US-09-231-788-2	Sequence 2, Appli
124	154.5	14.4	180	2	US-09-620-956-2	Sequence 2, Appli
125	154.5	14.4	180	2	US-09-611-152-2	Sequence 2, Appli
126	154.5	14.4	180	2	US-09-794-705A-2	Sequence 2, Appli
127	154.5	14.4	180	2	US-09-747-259-2	Sequence 2, Appli
128	154.5	14.4	180	2	US-09-816-744-2	Sequence 2, Appli
129	154.5	14.4	180	2	US-09-631-531-2	Sequence 2, Appli
130	154.5	14.4	180	2	US-09-796-844-35	Sequence 35, Appl
131	154.5	14.4	180	2	US-09-999-833A-470	Sequence 470, App
132	154.5	14.4	180	2	US-10-020-445A-470	Sequence 470, App
133	154.5	14.4	193	2	US-09-949-016-10191	Sequence 10191, A
134	151.5	14.1	160	2	US-09-620-956-18	Sequence 18, Appl
135	151.5	14.1	160	2	US-09-611-152-18	Sequence 18, Appl
136	151.5	14.1	160	2	US-09-794-705A-13	Sequence 13, Appl
137	151.5	14.1	160	2	US-09-631-531-18	Sequence 18, Appl
138	150.5	14.0	158	1	US-08-620-694A-7	Sequence 7, Appli
139	150.5	14.0	158	2	US-09-022-255-7	Sequence 7, Appli
140	150.5	14.0	158	2	US-09-022-696-7	Sequence 7, Appli
141	150.5	14.0	158	2	US-09-022-253-7	Sequence 7, Appli
142	150.5	14.0	158	2	US-09-022-260-7	Sequence 7, Appli
143	150.5	14.0	158	2	US-09-022-259-7	Sequence 7, Appli
144	150.5	14.0	158	2	US-09-022-257-7	Sequence 7, Appli
145	150.5	14.0	158	2	US-09-549-679-7	Sequence 7, Appli
146	150.5	14.0	160	2	US-09-620-956-22	Sequence 22, Appl
147	150.5	14.0	160	2	US-09-611-152-22	Sequence 22, Appl
148	150.5	14.0	160	2	US-09-794-705A-17	Sequence 17, Appl
149	150.5	14.0	160	2	US-09-631-531-22	Sequence 22, Appl
150	150.5	14.0	180	2	US-09-480-297A-2	Sequence 2, Appli
151	148.5	13.8	147	2	US-09-480-297A-32	Sequence 32, Appl
152	148.5	13.8	150	2	US-09-034-810-4	Sequence 4, Appli
153	148.5	13.8	150	2	US-08-685-239-4	Sequence 4, Appli
154	148.5	13.8	150	2	US-08-432-994A-2	Sequence 2, Appli
155	148.5	13.8	150	2	US-08-250-846-2	Sequence 2, Appli
156	148.5	13.8	150	2	US-09-480-297A-31	Sequence 31, Appl
157	148.5	13.8	150	2	US-09-929-612A-2	Sequence 2, Appli
158	148.5	13.8	150	2	US-10-102-080-4	Sequence 4, Appli
159	148.5	13.8	158	2	US-08-432-994A-10	Sequence 10, Appl
160	148.5	13.8	158	2	US-09-231-788-13	Sequence 13, Appl
161	148.5	13.8	158	2	US-09-929-612A-10	Sequence 10, Appl
162	138.5	12.9	96	2	US-09-611-152-26	Sequence 26, Appl
163	138.5	12.9	97	2	US-09-620-956-26	Sequence 26, Appl
164	138.5	12.9	97	2	US-09-631-531-26	Sequence 26, Appl
165	138.5	12.9	128	2	US-09-620-956-42	Sequence 42, Appl
166	138.5	12.9	128	2	US-09-611-152-42	Sequence 42, Appl
167	138.5	12.9	128	2	US-09-794-705A-27	Sequence 27, Appl
168	138.5	12.9	128	2	US-09-631-531-42	Sequence 42, Appl
169	138.5	12.9	130	2	US-09-231-788-27	Sequence 27, Appl
170	138.5	12.9	144	2	US-09-480-297A-16	Sequence 16, Appl
171	125	11.6	78	2	US-09-929-612A-6	Sequence 6, Appli
172	125	11.6	79	2	US-08-432-994A-6	Sequence 6, Appli
173	125	11.6	79	2	US-08-250-846-6	Sequence 6, Appli
174	110.5	10.3	111	2	US-09-480-297A-26	Sequence 26, Appl
175	93.5	8.7	73	2	US-09-620-956-35	Sequence 35, Appl
176	93.5	8.7	73	2	US-09-611-152-35	Sequence 35, Appl
177	93.5	8.7	73	2	US-09-631-531-35	Sequence 35, Appl
178	87.5	8.2	493	2	US-09-252-991A-16925	Sequence 16925, A
179	87	8.1	326	2	US-09-252-991A-30438	Sequence 30438, A
180	85.5	8.0	1520	2	US-09-252-991A-17501	Sequence 17501, A
181	85	7.9	516	2	US-09-489-039A-7660	Sequence 7660, Ap
182	84.5	7.9	716	2	US-09-252-991A-30683	Sequence 30683, A
183	84	7.8	100	2	US-09-620-956-27	Sequence 27, Appl
184	84	7.8	100	2	US-09-611-152-27	Sequence 27, Appl
185	84	7.8	100	2	US-09-631-531-27	Sequence 27, Appl
186	84	7.8	529	2	US-09-252-991A-31840	Sequence 31840, A
187	83	7.7	430	1	US-08-318-947A-16	Sequence 16, Appl
188	83	7.7	430	1	US-08-795-303-16	Sequence 16, Appl
189	82.5	7.7	569	2	US-09-252-991A-25582	Sequence 25582, A
190	82	7.6	268	2	US-09-489-039A-12401	Sequence 12401, A
191	81.5	7.6	997	2	US-09-252-991A-30799	Sequence 30799, A
192	81	7.5	191	2	US-09-893-737-224	Sequence 224, App
193	81	7.5	601	2	US-09-252-991A-21824	Sequence 21824, A
194	81	7.5	774	2	US-09-252-991A-16789	Sequence 16789, A
195	80.5	7.5	254	2	US-09-252-991A-22771	Sequence 22771, A
196	80.5	7.5	511	2	US-09-252-991A-20054	Sequence 20054, A
197	80	7.5	407	2	US-10-104-047-3895	Sequence 3895, Ap
198	80	7.5	491	2	US-09-252-991A-31758	Sequence 31758, A
199	80	7.5	619	2	US-09-252-991A-21585	Sequence 21585, A
200	79	7.4	176	2	US-09-252-991A-24407	Sequence 24407, A
201	79	7.4	525	2	US-09-252-991A-31946	Sequence 31946, A
202	79	7.4	550	1	US-08-318-947A-4	Sequence 4, Appli
203	79	7.4	550	1	US-08-795-303-4	Sequence 4, Appli
204	79	7.4	556	2	US-09-252-991A-17793	Sequence 17793, A
205	78.5	7.3	569	2	US-09-902-540-10181	Sequence 10181, A
206	78	7.3	413	2	US-09-585-173B-44	Sequence 44, Appl
207	77.5	7.2	61	2	US-09-620-956-34	Sequence 34, Appl
208	77.5	7.2	61	2	US-09-611-152-34	Sequence 34, Appl
209	77.5	7.2	61	2	US-09-631-531-34	Sequence 34, Appl
210	77.5	7.2	472	2	US-09-489-039A-10123	Sequence 10123, A
211	77.5	7.2	567	1	US-08-261-822A-12	Sequence 12, Appl
212	77.5	7.2	567	4	PCT-US95-07744A-12	Sequence 12, Appl
213	77.5	7.2	742	2	US-09-252-991A-32659	Sequence 32659, A
214	77	7.2	44	2	US-09-480-297A-10	Sequence 10, Appl
215	77	7.2	535	2	US-09-252-991A-28410	Sequence 28410, A
216	77	7.2	636	2	US-09-252-991A-21770	Sequence 21770, A
217	77	7.2	760	2	US-09-252-991A-31917	Sequence 31917, A
218	76.5	7.1	220	2	US-09-252-991A-25709	Sequence 25709, A
219	76.5	7.1	526	2	US-09-252-991A-24326	Sequence 24326, A
220	76	7.1	385	2	US-10-029-180-42	Sequence 42, Appl
221	76	7.1	417	2	US-09-252-991A-20643	Sequence 20643, A
222	76	7.1	1798	2	US-09-270-767-60233	Sequence 60233, A
223	76	7.1	2410	2	US-09-270-767-44775	Sequence 44775, A
224	75.5	7.0	764	2	US-09-252-991A-22510	Sequence 22510, A
225	75	7.0	126	2	US-09-231-788-15	Sequence 15, Appl
226	75	7.0	316	2	US-09-252-991A-19764	Sequence 19764, A
227	75	7.0	416	2	US-09-252-991A-29541	Sequence 29541, A
228	75	7.0	509	2	US-09-902-540-12233	Sequence 12233, A
229	75	7.0	613	2	US-09-252-991A-28253	Sequence 28253, A
230	75	7.0	735	2	US-09-252-991A-32172	Sequence 32172, A
231	75	7.0	1043	2	US-09-252-991A-28885	Sequence 28885, A
232	75	7.0	3287	1	US-08-477-451-7	Sequence 7, Appli
233	74.5	6.9	307	1	US-08-918-206-1	Sequence 1, Appli
234	74.5	6.9	363	2	US-09-252-991A-18016	Sequence 18016, A
235	74.5	6.9	422	2	US-09-902-540-15649	Sequence 15649, A
236	74.5	6.9	555	1	US-08-484-044-6	Sequence 6, Appli
237	74.5	6.9	582	1	US-08-422-699A-9	Sequence 9, Appli
238	74.5	6.9	582	1	US-08-422-706B-9	Sequence 9, Appli
239	74.5	6.9	639	2	US-10-100-252-21	Sequence 21, Appl
240	74.5	6.9	657	2	US-09-252-991A-28001	Sequence 28001, A
241	74	6.9	260	2	US-09-006-353A-8	Sequence 8, Appli
242	74	6.9	260	2	US-09-573-986-8	Sequence 8, Appli
243	74	6.9	260	2	US-09-949-016-6047	Sequence 6047, Ap
244	74	6.9	293	2	US-09-949-016-7945	Sequence 7945, Ap
245	74	6.9	561	2	US-09-252-991A-31119	Sequence 31119, A
246	74	6.9	652	2	US-10-104-047-3364	Sequence 3364, Ap

247	74	6.9	984	1	US-08-449-645A-19	Sequence 19, Appl
248	74	6.9	984	1	US-08-702-367A-19	Sequence 19, Appl
249	74	6.9	984	4	PCT-US95-04681-19	Sequence 19, Appl
250	74	6.9	2289	2	US-09-051-019-2	Sequence 2, Appli
251	73.5	6.8	385	2	US-09-252-991A-18688	Sequence 18688, A
252	73.5	6.8	497	2	US-09-252-991A-31534	Sequence 31534, A
253	73.5	6.8	593	2	US-09-252-991A-17983	Sequence 17983, A
254	73.5	6.8	1418	2	US-09-252-991A-32367	Sequence 32367, A
255	73	6.8	305	2	US-09-902-540-12811	Sequence 12811, A
256	73	6.8	402	2	US-09-252-991A-29857	Sequence 29857, A
257	73	6.8	420	2	US-09-252-991A-29911	Sequence 29911, A
258	73	6.8	570	2	US-09-252-991A-26331	Sequence 26331, A
259	73	6.8	677	2	US-09-394-142B-6	Sequence 6, Appli
260	73	6.8	707	2	US-09-252-991A-18542	Sequence 18542, A
261	73	6.8	777	2	US-09-252-991A-27864	Sequence 27864, A
262	73	6.8	1216	2	US-09-949-016-9461	Sequence 9461, Ap
263	72.5	6.8	208	2	US-09-252-991A-23874	Sequence 23874, A
264	72.5	6.8	370	2	US-08-311-731A-203	Sequence 203, App
265	72.5	6.8	422	2	US-09-724-864-45	Sequence 45, Appl
266	72.5	6.8	434	2	US-09-543-681A-6266	Sequence 6266, Ap
267	72.5	6.8	457	2	US-09-252-991A-23463	Sequence 23463, A
268	72.5	6.8	514	2	US-09-252-991A-25281	Sequence 25281, A
269	72.5	6.8	533	2	US-09-252-991A-21549	Sequence 21549, A
270	72.5	6.8	591	2	US-09-252-991A-20700	Sequence 20700, A
271	72.5	6.8	625	2	US-09-771-161A-242	Sequence 242, App
272	72.5	6.8	625	2	US-09-771-161A-243	Sequence 243, App
273	72	6.7	508	2	US-09-252-991A-32651	Sequence 32651, A
274	72	6.7	521	2	US-09-252-991A-30311	Sequence 30311, A
275	72	6.7	543	2	US-09-252-991A-31103	Sequence 31103, A
276	72	6.7	719	2	US-09-252-991A-23660	Sequence 23660, A
277	72	6.7	817	2	US-09-252-991A-25598	Sequence 25598, A
278	72	6.7	834	2	US-09-252-991A-18401	Sequence 18401, A
279	72	6.7	1427	2	US-09-252-991A-20577	Sequence 20577, A
280	71.5	6.7	133	2	US-09-270-767-47500	Sequence 47500, A
281	71.5	6.7	298	2	US-09-252-991A-28705	Sequence 28705, A
282	71.5	6.7	444	2	US-09-252-991A-24777	Sequence 24777, A
283	71.5	6.7	460	2	US-09-270-767-46776	Sequence 46776, A
284	71.5	6.7	530	2	US-09-949-016-10017	Sequence 10017, A
285	71.5	6.7	565	2	US-09-252-991A-20122	Sequence 20122, A
286	71.5	6.7	664	2	US-09-902-540-16365	Sequence 16365, A
287	71.5	6.7	981	2	US-09-902-540-9848	Sequence 9848, Ap
288	71.5	6.7	1017	2	US-09-600-776-6	Sequence 6, Appli
289	71.5	6.7	1017	2	US-09-965-830-6	Sequence 6, Appli
290	71.5	6.7	1034	2	US-10-104-047-2343	Sequence 2343, Ap
291	71	6.6	169	2	US-08-630-172-11	Sequence 11, Appl
292	71	6.6	169	2	US-09-375-419-11	Sequence 11, Appl
293	71	6.6	259	2	US-09-270-767-44926	Sequence 44926, A
294	71	6.6	422	2	US-09-252-991A-25540	Sequence 25540, A
295	71	6.6	427	2	US-09-252-991A-22649	Sequence 22649, A
296	71	6.6	444	2	US-09-252-991A-23992	Sequence 23992, A
297	71	6.6	462	2	US-09-252-991A-20410	Sequence 20410, A
298	71	6.6	513	2	US-09-252-991A-21092	Sequence 21092, A
299	71	6.6	523	2	US-09-252-991A-17791	Sequence 17791, A
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302	71	6.6	607	2	US-09-567-969-9	Sequence 9, Appli
303	71	6.6	607	2	US-09-568-480-9	Sequence 9, Appli
304	71	6.6	607	2	US-09-568-486-9	Sequence 9, Appli
305	71	6.6	607	2	US-09-568-472-9	Sequence 9, Appli
306	71	6.6	607	2	US-09-567-899-9	Sequence 9, Appli
307	71	6.6	607	2	US-10-014-717-9	Sequence 9, Appli
308	71	6.6	2600	2	US-09-949-016-7309	Sequence 7309, Ap
309	70.5	6.6	340	2	US-09-252-991A-27116	Sequence 27116, A
310	70.5	6.6	366	2	US-09-252-991A-17018	Sequence 17018, A
311	70.5	6.6	387	2	US-09-252-991A-18477	Sequence 18477, A
312	70.5	6.6	440	2	US-09-252-991A-27594	Sequence 27594, A
313	70.5	6.6	441	2	US-09-270-767-45465	Sequence 45465, A
314	70.5	6.6	448	2	US-09-252-991A-24066	Sequence 24066, A
315	70.5	6.6	451	2	US-09-477-962-118	Sequence 118, App
316	70.5	6.6	553	2	US-09-252-991A-22589	Sequence 22589, A
317	70.5	6.6	640	2	US-09-949-016-8010	Sequence 8010, Ap
318	70.5	6.6	759	2	US-09-252-991A-29395	Sequence 29395, A
319	70.5	6.6	801	2	US-09-252-991A-20743	Sequence 20743, A
320	70	6.5	189	1	US-08-469-427A-15	Sequence 15, Appl
321	70	6.5	235	2	US-09-252-991A-30315	Sequence 30315, A
322	70	6.5	278	2	US-09-252-991A-22273	Sequence 22273, A
323	70	6.5	326	2	US-09-252-991A-30194	Sequence 30194, A
324	70	6.5	338	2	US-09-543-681A-6123	Sequence 6123, Ap
325	70	6.5	381	2	US-09-919-497-96	Sequence 96, Appl
326	70	6.5	417	2	US-09-252-991A-24041	Sequence 24041, A
327	70	6.5	453	2	US-09-252-991A-24830	Sequence 24830, A
328	70	6.5	516	2	US-09-252-991A-21880	Sequence 21880, A
329	70	6.5	520	2	US-09-252-991A-32505	Sequence 32505, A
330	70	6.5	536	2	US-09-252-991A-16754	Sequence 16754, A
331	70	6.5	546	2	US-09-252-991A-25851	Sequence 25851, A
332	70	6.5	612	2	US-09-252-991A-17516	Sequence 17516, A
333	70	6.5	959	2	US-09-252-991A-21747	Sequence 21747, A
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335	70	6.5	2584	2	US-08-936-135-4	Sequence 4, Appli
336	69.5	6.5	161	2	US-09-673-395A-248	Sequence 248, App
337	69.5	6.5	168	2	US-09-252-991A-19362	Sequence 19362, A
338	69.5	6.5	238	2	US-09-605-703B-404	Sequence 404, App
339	69.5	6.5	238	2	US-09-605-703B-406	Sequence 406, App
340	69.5	6.5	399	2	US-08-808-346-4	Sequence 4, Appli
341	69.5	6.5	593	2	US-09-252-991A-30673	Sequence 30673, A
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343	69.5	6.5	811	2	US-09-252-991A-28570	Sequence 28570, A
344	69.5	6.5	933	2	US-10-104-047-2299	Sequence 2299, Ap
345	69.5	6.5	1064	2	US-09-252-991A-17508	Sequence 17508, A
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347	69	6.4	84	2	US-08-648-322-10	Sequence 10, Appl
348	69	6.4	84	2	US-08-857-389-10	Sequence 10, Appl
349	69	6.4	84	2	US-09-766-396-10	Sequence 10, Appl
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351	69	6.4	109	2	US-08-857-389-5	Sequence 5, Appli
352	69	6.4	109	2	US-09-766-396-5	Sequence 5, Appli
353	69	6.4	121	2	US-08-828-683A-18	Sequence 18, Appl
354	69	6.4	169	2	US-09-252-991A-19719	Sequence 19719, A
355	69	6.4	213	2	US-09-252-991A-21254	Sequence 21254, A
356	69	6.4	215	2	US-09-252-991A-19142	Sequence 19142, A
357	69	6.4	316	2	US-09-252-991A-25345	Sequence 25345, A
358	69	6.4	325	2	US-09-252-991A-23890	Sequence 23890, A
359	69	6.4	332	2	US-09-270-767-42978	Sequence 42978, A
360	69	6.4	334	2	US-09-252-991A-22532	Sequence 22532, A
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363	69	6.4	406	2	US-09-252-991A-18731	Sequence 18731, A
364	69	6.4	439	2	US-09-252-991A-20570	Sequence 20570, A
365	69	6.4	451	2	US-10-012-231A-142	Sequence 142, App
366	69	6.4	451	2	US-10-015-389A-142	Sequence 142, App
367	69	6.4	451	2	US-10-006-768A-142	Sequence 142, App
368	69	6.4	451	2	US-10-015-671A-142	Sequence 142, App
369	69	6.4	451	2	US-10-015-393A-142	Sequence 142, App
370	69	6.4	451	2	US-10-011-833A-142	Sequence 142, App
371	69	6.4	451	2	US-10-006-041A-142	Sequence 142, App
372	69	6.4	451	2	US-10-012-064A-142	Sequence 142, App
373	69	6.4	508	2	US-09-111-730-2	Sequence 2, Appli
374	69	6.4	508	2	US-09-949-016-5994	Sequence 5994, Ap
375	69	6.4	523	2	US-09-949-016-10466	Sequence 10466, A
376	69	6.4	551	2	US-09-252-991A-23694	Sequence 23694, A
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379	68.5	6.4	191	2	US-09-021-715-4	Sequence 4, Appli
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394	68	6.3	70	2	US-09-611-152-33	Sequence 33, Appl
395	68	6.3	70	2	US-09-631-531-33	Sequence 33, Appl
396	68	6.3	160	2	US-10-104-047-2149	Sequence 2149, Ap
397	68	6.3	184	2	US-09-252-991A-27801	Sequence 27801, A
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409	68	6.3	726	2	US-09-252-991A-18271	Sequence 18271, A
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412	68	6.3	1185	2	US-09-041-886-23	Sequence 23, Appl
413	68	6.3	1185	2	US-09-538-092-1209	Sequence 1209, Ap
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427	67.5	6.3	507	2	US-09-249-003-12	Sequence 12, Appl
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431	67.5	6.3	520	2	US-09-949-002-558	Sequence 558, App
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437	67.5	6.3	769	2	US-10-010-720-44	Sequence 44, Appl
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442	67.5	6.3	922	2	US-10-010-720-38	Sequence 38, Appl
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444	67.5	6.3	982	2	US-10-010-720-6	Sequence 6, Appli
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447	67.5	6.3	1939	2	US-10-010-720-48	Sequence 48, Appl
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449	67.5	6.3	1999	2	US-10-010-720-16	Sequence 16, Appl
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451	67.5	6.3	2032	2	US-10-010-720-42	Sequence 42, Appl
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453	67.5	6.3	2076	2	US-10-010-720-46	Sequence 46, Appl
454	67.5	6.3	2092	2	US-09-854-856-10	Sequence 10, Appl
455	67.5	6.3	2092	2	US-10-010-720-10	Sequence 10, Appl
456	67.5	6.3	2136	2	US-09-854-856-14	Sequence 14, Appl
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458	67.5	6.3	2169	2	US-09-854-856-40	Sequence 40, Appl
459	67.5	6.3	2169	2	US-10-010-720-40	Sequence 40, Appl
460	67.5	6.3	2185	2	US-09-854-856-36	Sequence 36, Appl
461	67.5	6.3	2185	2	US-10-010-720-36	Sequence 36, Appl
462	67.5	6.3	2229	2	US-09-854-856-8	Sequence 8, Appli
463	67.5	6.3	2229	2	US-10-010-720-8	Sequence 8, Appli
464	67.5	6.3	2245	2	US-09-854-856-4	Sequence 4, Appli
465	67.5	6.3	2245	2	US-10-010-720-4	Sequence 4, Appli
466	67.5	6.3	2322	2	US-09-854-856-34	Sequence 34, Appl
467	67.5	6.3	2322	2	US-09-976-594-15	Sequence 15, Appl
468	67.5	6.3	2322	2	US-09-919-039-15	Sequence 15, Appl
469	67.5	6.3	2322	2	US-10-010-720-34	Sequence 34, Appl
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471	67.5	6.3	2382	2	US-10-010-720-2	Sequence 2, Appli
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476	67	6.2	245	2	US-08-467-344A-37	Sequence 37, Appl
477	67	6.2	245	2	US-08-424-550B-37	Sequence 37, Appl
478	67	6.2	278	2	US-09-724-864-63	Sequence 63, Appl
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484	67	6.2	461	2	US-09-990-444-314	Sequence 314, App
485	67	6.2	461	2	US-09-997-333-314	Sequence 314, App
486	67	6.2	461	2	US-09-992-598-314	Sequence 314, App
487	67	6.2	486	2	US-09-252-991A-30369	Sequence 30369, A
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495	67	6.2	1487	1	US-08-760-489-4	Sequence 4, Appli
496	67	6.2	1487	2	US-09-185-373-2	Sequence 2, Appli
497	67	6.2	1487	2	US-09-185-373-4	Sequence 4, Appli
498	67	6.2	2293	2	US-09-368-590-2	Sequence 2, Appli
499	67	6.2	2626	2	US-09-477-962-106	Sequence 106, App
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515	66.5	6.2	422	2	US-09-949-016-9592	Sequence 9592, Ap
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520	66.5	6.2	615	2	US-10-104-047-3203	Sequence 3203, Ap
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522	66.5	6.2	676	2	US-09-949-016-7426	Sequence 7426, Ap
523	66.5	6.2	680	2	US-09-949-016-10770	Sequence 10770, A
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528	66.5	6.2	912	2	US-09-252-991A-24163	Sequence 24163, A
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537	66.5	6.2	3798	2	US-09-568-102-6	Sequence 6, Appli
538	66.5	6.2	3798	2	US-09-567-969-6	Sequence 6, Appli

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541	66.5	6.2	3798	2	US-09-568-472-6	Sequence 6, Appli
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543	66.5	6.2	3798	2	US-10-014-717-6	Sequence 6, Appli
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550	66	6.2	375	2	US-09-690-359-50	Sequence 50, Appl
551	66	6.2	395	2	US-09-252-991A-26116	Sequence 26116, A
552	66	6.2	407	2	US-09-389-956-14	Sequence 14, Appl
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555	66	6.2	466	2	US-09-252-991A-17965	Sequence 17965, A
556	66	6.2	485	2	US-09-949-016-6557	Sequence 6557, Ap
557	66	6.2	491	2	US-09-252-991A-20136	Sequence 20136, A
558	66	6.2	504	2	US-09-949-016-7783	Sequence 7783, Ap
559	66	6.2	540	2	US-09-949-016-6358	Sequence 6358, Ap
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562	66	6.2	564	2	US-09-949-016-11234	Sequence 11234, A
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565	66	6.2	677	2	US-09-252-991A-28529	Sequence 28529, A
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572	66	6.2	1723	2	US-10-037-417-18	Sequence 18, Appl
573	66	6.2	1919	2	US-10-152-886-13	Sequence 13, Appl
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575	65.5	6.1	109	2	US-09-270-767-50381	Sequence 50381, A
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582	65.5	6.1	312	2	US-09-328-352-4439	Sequence 4439, Ap
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589	65.5	6.1	399	1	US-08-901-200A-2	Sequence 2, Appli
590	65.5	6.1	399	2	US-08-889-419-9	Sequence 9, Appli
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592	65.5	6.1	399	2	US-08-402-542-9	Sequence 9, Appli
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595	65.5	6.1	399	4	PCT-US93-10520-2	Sequence 2, Appli
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603	65.5	6.1	480	2	US-09-252-991A-26799	Sequence 26799, A
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606	65.5	6.1	521	2	US-09-252-991A-22686	Sequence 22686, A
607	65.5	6.1	525	2	US-09-976-594-64	Sequence 64, Appl
608	65.5	6.1	525	2	US-09-919-039-62	Sequence 62, Appl
609	65.5	6.1	557	2	US-09-252-991A-17824	Sequence 17824, A
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622	65.5	6.1	1178	2	US-08-663-731-2	Sequence 2, Appli
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624	65.5	6.1	1178	4	PCT-US95-02044-2	Sequence 2, Appli
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626	65	6.1	176	2	US-09-205-258-733	Sequence 733, App
627	65	6.1	176	2	US-10-004-860-733	Sequence 733, App
628	65	6.1	254	2	US-09-252-991A-17480	Sequence 17480, A
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653	65	6.1	570	2	US-09-543-681A-5889	Sequence 5889, Ap
654	65	6.1	580	2	US-09-252-991A-22036	Sequence 22036, A
655	65	6.1	580	2	US-09-949-016-9593	Sequence 9593, Ap
656	65	6.1	580	2	US-09-949-016-9594	Sequence 9594, Ap
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665	65	6.1	898	2	US-08-206-188B-12	Sequence 12, Appl
666	65	6.1	900	1	US-07-688-352C-12	Sequence 12, Appl
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684	64.5	6.0	257	2	US-08-928-694-10	Sequence 10, Appl

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729	64	6.0	216	1	US-08-424-826A-8	Sequence 8, Appli
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732	64	6.0	216	2	US-08-451-390-8	Sequence 8, Appli
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768	64	6.0	1029	2	US-10-033-301-22	Sequence 22, Appl
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771	64	6.0	1130	1	US-08-125-077-2	Sequence 2, Appli
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774	64	6.0	3070	2	US-09-961-403-7	Sequence 7, Appli
775	64	6.0	3088	2	US-09-562-702A-8	Sequence 8, Appli
776	64	6.0	3089	2	US-09-562-702A-4	Sequence 4, Appli
777	64	6.0	3110	2	US-09-562-702A-2	Sequence 2, Appli
778	64	6.0	3110	2	US-09-562-702A-6	Sequence 6, Appli
779	64	6.0	3110	2	US-09-561-709B-7	Sequence 7, Appli
780	64	6.0	3110	2	US-09-917-254-86	Sequence 86, Appl
781	64	6.0	3110	2	US-09-949-016-5937	Sequence 5937, Ap
782	64	6.0	3111	1	US-08-460-309-4	Sequence 4, Appli
783	64	6.0	3111	1	US-08-125-077-4	Sequence 4, Appli
784	63.5	5.9	164	2	US-10-104-047-3407	Sequence 3407, Ap
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787	63.5	5.9	176	2	US-09-739-852-14	Sequence 14, Appl
788	63.5	5.9	186	2	US-09-252-991A-21982	Sequence 21982, A
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790	63.5	5.9	200	2	US-10-004-860-588	Sequence 588, App
791	63.5	5.9	201	2	US-09-252-991A-25745	Sequence 25745, A
792	63.5	5.9	207	2	US-09-252-991A-20253	Sequence 20253, A
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806	63.5	5.9	421	2	US-09-248-796A-19591	Sequence 19591, A
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814	63.5	5.9	575	2	US-08-922-865-2	Sequence 2, Appli
815	63.5	5.9	575	2	US-09-510-949-2	Sequence 2, Appli
816	63.5	5.9	634	2	US-09-252-991A-24400	Sequence 24400, A
817	63.5	5.9	646	2	US-09-252-991A-16819	Sequence 16819, A
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826	63.5	5.9	1115	2	US-10-015-671A-58	Sequence 58, Appl
827	63.5	5.9	1115	2	US-10-015-393A-58	Sequence 58, Appl
828	63.5	5.9	1115	2	US-10-011-833A-58	Sequence 58, Appl
829	63.5	5.9	1115	2	US-10-006-041A-58	Sequence 58, Appl
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839	63	5.9	231	2	US-09-252-991A-17819	Sequence 17819, A
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841	63	5.9	249	2	US-09-154-083-2	Sequence 2, Appli
842	63	5.9	250	1	US-08-460-309-11	Sequence 11, Appl
843	63	5.9	250	1	US-08-125-077-11	Sequence 11, Appl
844	63	5.9	314	2	US-09-270-767-43294	Sequence 43294, A
845	63	5.9	317	2	US-09-902-540-15080	Sequence 15080, A
846	63	5.9	331	2	US-10-010-580-2	Sequence 2, Appli
847	63	5.9	341	2	US-09-252-991A-28938	Sequence 28938, A
848	63	5.9	361	1	US-08-483-926A-9	Sequence 9, Appli
849	63	5.9	364	2	US-09-902-540-12780	Sequence 12780, A
850	63	5.9	372	2	US-09-252-991A-20108	Sequence 20108, A
851	63	5.9	399	2	US-09-252-991A-16821	Sequence 16821, A
852	63	5.9	411	2	US-09-252-991A-25526	Sequence 25526, A
853	63	5.9	412	2	US-09-252-991A-25522	Sequence 25522, A
854	63	5.9	420	2	US-09-252-991A-27610	Sequence 27610, A
855	63	5.9	428	2	US-09-423-340-4	Sequence 4, Appli
856	63	5.9	428	2	US-09-820-155-4	Sequence 4, Appli
857	63	5.9	430	2	US-09-252-991A-18226	Sequence 18226, A
858	63	5.9	430	2	US-09-252-991A-18437	Sequence 18437, A
859	63	5.9	431	2	US-09-252-991A-20267	Sequence 20267, A
860	63	5.9	451	2	US-09-252-991A-30465	Sequence 30465, A
861	63	5.9	484	2	US-09-949-016-9440	Sequence 9440, Ap
862	63	5.9	485	2	US-09-252-991A-26680	Sequence 26680, A
863	63	5.9	491	2	US-09-489-039A-11014	Sequence 11014, A
864	63	5.9	503	2	US-10-104-047-3266	Sequence 3266, Ap
865	63	5.9	575	2	US-09-252-991A-17187	Sequence 17187, A
866	63	5.9	605	2	US-09-252-991A-27220	Sequence 27220, A
867	63	5.9	623	2	US-09-252-991A-23930	Sequence 23930, A
868	63	5.9	693	2	US-09-252-991A-20348	Sequence 20348, A
869	63	5.9	750	2	US-09-902-540-15485	Sequence 15485, A
870	63	5.9	804	2	US-09-949-016-7337	Sequence 7337, Ap
871	63	5.9	837	2	US-09-252-991A-26362	Sequence 26362, A
872	63	5.9	891	2	US-09-252-991A-30624	Sequence 30624, A
873	63	5.9	913	2	US-09-489-039A-7615	Sequence 7615, Ap
874	63	5.9	968	1	US-08-434-730-14	Sequence 14, Appl
875	63	5.9	1338	2	US-10-680-730-1	Sequence 1, Appli
876	63	5.9	1371	2	US-09-902-540-16024	Sequence 16024, A
877	63	5.9	2310	2	US-09-874-923-120	Sequence 120, App
878	63	5.9	2887	2	US-08-462-467B-8	Sequence 8, Appli
879	63	5.9	3712	2	US-10-037-417-48	Sequence 48, Appl
880	63	5.9	3712	2	US-10-037-417-51	Sequence 51, Appl
881	62.5	5.8	199	2	US-09-252-991A-23002	Sequence 23002, A
882	62.5	5.8	201	2	US-09-252-991A-25691	Sequence 25691, A
883	62.5	5.8	202	2	US-08-388-852B-38	Sequence 38, Appl
884	62.5	5.8	210	2	US-09-252-991A-29908	Sequence 29908, A
885	62.5	5.8	244	2	US-09-252-991A-26246	Sequence 26246, A
886	62.5	5.8	244	2	US-09-252-991A-31668	Sequence 31668, A
887	62.5	5.8	251	2	US-09-091-725-21	Sequence 21, Appl
888	62.5	5.8	251	2	US-08-737-319-1	Sequence 1, Appli
889	62.5	5.8	255	2	US-09-252-991A-22733	Sequence 22733, A
890	62.5	5.8	258	2	US-09-252-991A-23325	Sequence 23325, A
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892	62.5	5.8	269	2	US-10-104-047-3593	Sequence 3593, Ap
893	62.5	5.8	285	2	US-10-272-490-44	Sequence 44, Appl
894	62.5	5.8	287	2	US-09-252-991A-19966	Sequence 19966, A
895	62.5	5.8	302	2	US-09-599-360B-75	Sequence 75, Appl
896	62.5	5.8	306	2	US-09-538-092-262	Sequence 262, App
897	62.5	5.8	358	2	US-09-252-991A-28757	Sequence 28757, A
898	62.5	5.8	363	2	US-09-252-991A-23199	Sequence 23199, A
899	62.5	5.8	365	2	US-09-252-991A-17925	Sequence 17925, A
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901	62.5	5.8	369	2	US-09-252-991A-24423	Sequence 24423, A
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904	62.5	5.8	390	2	US-09-252-991A-24124	Sequence 24124, A
905	62.5	5.8	393	2	US-09-252-991A-24171	Sequence 24171, A
906	62.5	5.8	406	2	US-09-252-991A-22730	Sequence 22730, A
907	62.5	5.8	415	2	US-09-252-991A-31846	Sequence 31846, A
908	62.5	5.8	417	2	US-09-252-991A-27213	Sequence 27213, A
909	62.5	5.8	425	2	US-09-252-991A-17186	Sequence 17186, A
910	62.5	5.8	427	2	US-09-252-991A-24995	Sequence 24995, A
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912	62.5	5.8	443	2	US-09-252-991A-29446	Sequence 29446, A
913	62.5	5.8	448	2	US-09-252-991A-33055	Sequence 33055, A
914	62.5	5.8	476	2	US-09-252-991A-27078	Sequence 27078, A
915	62.5	5.8	487	2	US-09-949-016-7797	Sequence 7797, Ap
916	62.5	5.8	487	2	US-10-033-301-18	Sequence 18, Appl
917	62.5	5.8	508	2	US-09-252-991A-32269	Sequence 32269, A
918	62.5	5.8	525	2	US-09-252-991A-23870	Sequence 23870, A
919	62.5	5.8	526	2	US-09-252-991A-23688	Sequence 23688, A
920	62.5	5.8	547	2	US-09-252-991A-26732	Sequence 26732, A
921	62.5	5.8	611	2	US-09-252-991A-17597	Sequence 17597, A
922	62.5	5.8	629	2	US-10-104-047-2289	Sequence 2289, Ap
923	62.5	5.8	638	2	US-09-252-991A-26597	Sequence 26597, A
924	62.5	5.8	653	1	US-08-339-152A-16	Sequence 16, Appl
925	62.5	5.8	653	1	US-08-007-999B-3	Sequence 3, Appli
926	62.5	5.8	653	1	US-08-689-276A-3	Sequence 3, Appli
927	62.5	5.8	659	2	US-09-562-737-17	Sequence 17, Appl
928	62.5	5.8	663	2	US-09-270-767-61220	Sequence 61220, A
929	62.5	5.8	684	2	US-09-252-991A-18416	Sequence 18416, A
930	62.5	5.8	696	2	US-10-237-551-238	Sequence 238, App
931	62.5	5.8	730	2	US-09-578-063-21	Sequence 21, Appl
932	62.5	5.8	761	2	US-09-578-063-19	Sequence 19, Appl
933	62.5	5.8	761	2	US-10-012-231A-277	Sequence 277, App
934	62.5	5.8	761	2	US-10-015-389A-277	Sequence 277, App
935	62.5	5.8	761	2	US-10-006-768A-277	Sequence 277, App
936	62.5	5.8	761	2	US-10-015-671A-277	Sequence 277, App
937	62.5	5.8	761	2	US-10-015-393A-277	Sequence 277, App
938	62.5	5.8	761	2	US-10-011-833A-277	Sequence 277, App
939	62.5	5.8	761	2	US-10-006-041A-277	Sequence 277, App
940	62.5	5.8	761	2	US-10-012-064A-277	Sequence 277, App
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943	62.5	5.8	1178	2	US-09-949-016-7163	Sequence 7163, Ap
944	62.5	5.8	1281	2	US-09-702-216-2	Sequence 2, Appli
945	62.5	5.8	1281	2	US-09-949-016-6860	Sequence 6860, Ap
946	62.5	5.8	1296	2	US-09-949-016-7378	Sequence 7378, Ap
947	62.5	5.8	1362	2	US-09-902-540-14577	Sequence 14577, A
948	62.5	5.8	1591	2	US-09-270-767-45698	Sequence 45698, A
949	62.5	5.8	2942	2	US-09-902-540-9733	Sequence 9733, Ap
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951	62	5.8	127	2	US-09-461-325-460	Sequence 460, App
952	62	5.8	127	2	US-10-012-542-460	Sequence 460, App
953	62	5.8	127	2	US-10-115-123-460	Sequence 460, App
954	62	5.8	135	2	US-09-252-991A-18756	Sequence 18756, A
955	62	5.8	140	2	US-09-270-767-45327	Sequence 45327, A
956	62	5.8	168	2	US-08-946-329A-67	Sequence 67, Appl
957	62	5.8	168	2	US-09-562-914-67	Sequence 67, Appl
958	62	5.8	177	1	US-08-700-013B-8	Sequence 8, Appli
959	62	5.8	201	2	US-09-350-852A-1	Sequence 1, Appli
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961	62	5.8	217	2	US-09-252-991A-25979	Sequence 25979, A
962	62	5.8	225	2	US-09-252-991A-17464	Sequence 17464, A
963	62	5.8	233	2	US-09-311-021-46	Sequence 46, Appl
964	62	5.8	251	2	US-09-270-767-46744	Sequence 46744, A
965	62	5.8	258	2	US-09-252-991A-21053	Sequence 21053, A
966	62	5.8	281	2	US-09-252-991A-18840	Sequence 18840, A
967	62	5.8	282	2	US-10-027-736A-66	Sequence 66, Appl
968	62	5.8	285	2	US-09-252-991A-26665	Sequence 26665, A
969	62	5.8	295	2	US-09-252-991A-22439	Sequence 22439, A
970	62	5.8	301	2	US-09-252-991A-17405	Sequence 17405, A
971	62	5.8	310	2	US-10-027-736A-15	Sequence 15, Appl
972	62	5.8	314	2	US-09-252-991A-31938	Sequence 31938, A
973	62	5.8	352	2	US-09-252-991A-24482	Sequence 24482, A
974	62	5.8	355	2	US-09-252-991A-22326	Sequence 22326, A
975	62	5.8	355	2	US-09-252-991A-25895	Sequence 25895, A
976	62	5.8	362	2	US-09-513-838-2	Sequence 2, Appli

977	62	5.8	362	2	US-09-364-425B-47	Sequence 47, Appl
978	62	5.8	379	2	US-08-311-731A-268	Sequence 268, App
979	62	5.8	390	2	US-09-252-991A-17829	Sequence 17829, A
980	62	5.8	396	2	US-09-538-092-1303	Sequence 1303, Ap
981	62	5.8	403	1	US-08-474-379C-14	Sequence 14, Appl
982	62	5.8	403	2	US-09-146-249A-14	Sequence 14, Appl
983	62	5.8	403	2	US-08-206-188B-14	Sequence 14, Appl
984	62	5.8	405	1	US-07-688-352C-14	Sequence 14, Appl
985	62	5.8	405	4	PCT-US91-02714-14	Sequence 14, Appl
986	62	5.8	418	2	US-09-252-991A-17796	Sequence 17796, A
987	62	5.8	422	2	US-09-252-991A-27632	Sequence 27632, A
988	62	5.8	423	2	US-09-252-991A-22774	Sequence 22774, A
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991	62	5.8	434	2	US-08-558-135-2	Sequence 2, Appli
992	62	5.8	435	2	US-09-794-422-2	Sequence 2, Appli
993	62	5.8	457	2	US-10-029-180-24	Sequence 24, Appl
994	62	5.8	463	2	US-09-252-991A-29731	Sequence 29731, A
995	62	5.8	466	2	US-09-902-540-13514	Sequence 13514, A
996	62	5.8	480	2	US-09-252-991A-23424	Sequence 23424, A
997	62	5.8	485	2	US-09-252-991A-21664	Sequence 21664, A
998	62	5.8	494	2	US-09-489-039A-9940	Sequence 9940, Ap
999	62	5.8	494	2	US-09-949-016-7790	Sequence 7790, Ap
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1001	62	5.8	556	2	US-08-462-467B-26	Sequence 26, Appl
1002	62	5.8	560	1	US-08-095-728B-6	Sequence 6, Appli
1003	62	5.8	560	4	PCT-US92-02320A-6	Sequence 6, Appli
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1005	62	5.8	576	2	US-09-252-991A-30245	Sequence 30245, A
1006	62	5.8	633	2	US-09-949-016-6259	Sequence 6259, Ap
1007	62	5.8	655	2	US-09-949-016-11676	Sequence 11676, A
1008	62	5.8	681	2	US-09-252-991A-24567	Sequence 24567, A
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1011	62	5.8	790	2	US-09-543-681A-6059	Sequence 6059, Ap
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1013	62	5.8	797	1	US-08-700-013B-19	Sequence 19, Appl
1014	62	5.8	797	2	US-09-191-468-124	Sequence 124, App
1015	62	5.8	797	4	PCT-US92-02320A-2	Sequence 2, Appli
1016	62	5.8	802	2	US-09-252-991A-25050	Sequence 25050, A
1017	62	5.8	882	2	US-09-538-092-1036	Sequence 1036, Ap
1018	62	5.8	958	2	US-09-706-594-5	Sequence 5, Appli
1019	62	5.8	966	2	US-09-964-956-32	Sequence 32, Appl
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1023	62	5.8	1601	2	US-09-862-027-40	Sequence 40, Appl
1024	62	5.8	1618	2	US-08-462-467B-4	Sequence 4, Appli
1025	62	5.8	1690	2	US-09-595-684B-39	Sequence 39, Appl
1026	62	5.8	1690	2	US-09-949-016-6474	Sequence 6474, Ap
1027	62	5.8	1695	2	US-09-949-016-9887	Sequence 9887, Ap
1028	62	5.8	1723	2	US-09-194-612A-31	Sequence 31, Appl
1029	62	5.8	1838	2	US-09-120-663-2	Sequence 2, Appli
1030	62	5.8	1838	2	US-09-431-614-8	Sequence 8, Appli
1031	62	5.8	1838	2	US-09-596-784-2	Sequence 2, Appli
1032	62	5.8	1838	2	US-09-412-100-28	Sequence 28, Appl
1033	62	5.8	2336	2	US-09-268-163-10	Sequence 10, Appl
1034	62	5.8	2887	2	US-08-462-467B-2	Sequence 2, Appli
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1037	61.5	5.7	116	2	US-09-270-767-56208	Sequence 56208, A
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1043	61.5	5.7	191	2	US-09-252-991A-23902	Sequence 23902, A
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1048	61.5	5.7	253	2	US-09-252-991A-19036	Sequence 19036, A
1049	61.5	5.7	258	2	US-09-252-991A-27264	Sequence 27264, A
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1053	61.5	5.7	291	2	US-09-252-991A-17495	Sequence 17495, A
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1055	61.5	5.7	292	2	US-09-414-453A-18	Sequence 18, Appl
1056	61.5	5.7	307	2	US-09-949-016-8453	Sequence 8453, Ap
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1058	61.5	5.7	313	2	US-09-345-468-16	Sequence 16, Appl
1059	61.5	5.7	313	2	US-09-414-453A-16	Sequence 16, Appl
1060	61.5	5.7	313	2	US-09-498-520A-16	Sequence 16, Appl
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1062	61.5	5.7	316	2	US-09-252-991A-21525	Sequence 21525, A
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1069	61.5	5.7	405	2	US-09-902-540-11789	Sequence 11789, A
1070	61.5	5.7	412	2	US-09-079-030-124	Sequence 124, App
1071	61.5	5.7	415	2	US-09-252-991A-24962	Sequence 24962, A
1072	61.5	5.7	416	2	US-09-252-991A-18079	Sequence 18079, A
1073	61.5	5.7	420	2	US-09-949-016-11701	Sequence 11701, A
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1076	61.5	5.7	478	2	US-09-252-991A-28496	Sequence 28496, A
1077	61.5	5.7	480	2	US-09-252-991A-26866	Sequence 26866, A
1078	61.5	5.7	495	2	US-09-252-991A-21489	Sequence 21489, A
1079	61.5	5.7	501	2	US-09-902-540-12135	Sequence 12135, A
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1084	61.5	5.7	546	2	US-09-808-387-28	Sequence 28, Appl
1085	61.5	5.7	551	2	US-09-252-991A-20014	Sequence 20014, A
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1088	61.5	5.7	566	2	US-09-252-991A-16790	Sequence 16790, A
1089	61.5	5.7	567	2	US-09-252-991A-28435	Sequence 28435, A
1090	61.5	5.7	580	2	US-08-665-259-21	Sequence 21, Appl
1091	61.5	5.7	580	2	US-08-762-500-21	Sequence 21, Appl
1092	61.5	5.7	596	2	US-09-252-991A-32193	Sequence 32193, A
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ALIGNMENTS

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RESULT 1
US-09-480-297A-23
; Sequence 23, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11 (no seq.)
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-480-297A-23

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RESULT 2
US-09-747-259-4
; Sequence 4, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Chen, Jian
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
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;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Li,Hanzhong
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  VanLookeren,Menno
;  APPLICANT:  Vandlen,Richard
;  APPLICANT:  Watanabe,Colin
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William
;  APPLICANT:  Yansura,Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P1(US)
;  CURRENT APPLICATION NUMBER: US/09/747,259
;  CURRENT FILING DATE:  2000-12-20
;  PRIOR APPLICATION NUMBER: US 09/311,832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US 60/172,096
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: PCT/US99/31274
;  PRIOR FILING DATE: 1999-12-30
;  PRIOR APPLICATION NUMBER: US 60/175,481
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/191,007
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/07532
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/15264
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: US 60/213,087
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: US 09/644,848
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/242,837
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: PCT/US00/30873
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: US 60/253,646
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 39
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;   ORGANISM: Homo Sapien
US-09-747-259-4

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RESULT 3
US-09-816-744-4
; Sequence 4, Application US/09816744
; Patent No. 6579520
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Li,Hanzhong
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  VanLookeren,Menno
;  APPLICANT:  Vandlen,Richard
;  APPLICANT:  Watanabe,Colin
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William
;  APPLICANT:  Yansura,Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P2(US)
;  CURRENT APPLICATION NUMBER: US/09/816,744
;  CURRENT FILING DATE:  2001-03-22
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 4
;   LENGTH: 197
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-816-744-4

  Query Match             100.0%;  Score 1073;  DB 2;  Length 197;
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RESULT 4
US-09-949-016-11258
; Sequence 11258, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
```

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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11258
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11258

  Query Match             100.0%;  Score 1073;  DB 2;  Length 213;
  Best Local Similarity   100.0%;  Pred. No. 9e-119;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 76

Qy         61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY 136

Qy        121 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 PQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHT 196

Qy        181 EFIHVPVGCTCVLPRSV 197
              |||||||||||||||||
Db        197 EFIHVPVGCTCVLPRSV 213


RESULT 5
US-09-231-788-11
; Sequence 11, Application US/09231788A
; Patent No. 6486301
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  TITLE OF INVENTION: Interleukin-20
;  FILE REFERENCE: PF399P1
;  CURRENT APPLICATION NUMBER: US/09/231,788A
;  CURRENT FILING DATE: 1999-01-15
;  EARLIER APPLICATION NUMBER: 60/052,870
;  EARLIER FILING DATE: 1997-07-16
;  EARLIER APPLICATION NUMBER: 60/055,952
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/060,140
;  EARLIER FILING DATE: 1997-09-26
;  EARLIER APPLICATION NUMBER: 09/115,832
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 87
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-231-788-11

  Query Match             42.8%;  Score 459;  DB 2;  Length 87;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-46;
  Matches   86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        112 RVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLP 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 RVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLP 61

Qy        172 TPGAFAFHTEFIHVPVGCTCVLPRSV 197
              ||||||||||||||||||||||||||
Db         62 TPGAFAFHTEFIHVPVGCTCVLPRSV 87


RESULT 6
US-09-480-297A-21
; Sequence 21, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (94)..(94)
;   OTHER INFORMATION: The 'Xaa' at location 94 stands for Asp, Gly, Ala, or Val.
;   NAME/KEY: misc_feature
;   LOCATION: (123)..(123)
;   OTHER INFORMATION: The 'Xaa' at location 123 stands for Ser, Gly, Arg, or Cys.
;   NAME/KEY: misc_feature
;   LOCATION: (281)..(281)
;   OTHER INFORMATION: unkown amino
;   NAME/KEY: misc_feature
;   LOCATION: (367)..(367)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (437)..(437)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (462)..(462)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (468)..(468)
;   OTHER INFORMATION: unknown amino
US-09-480-297A-21

  Query Match             41.6%;  Score 446;  DB 2;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-45;
  Matches   83;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        114 DTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTP 173
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTP 60

Qy        174 GAFAFHTEFIHVPVGCTCVLPRS 196
              |||||||||||||||||||||||
Db         61 GAFAFHTEFIHVPVGCTCVLPRS 83


RESULT 7
US-09-480-297A-8
; Sequence 8, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 202
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-480-297A-8
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```
  Query Match           18.5%;  Score 199;  DB 2;  Length 202;
  Best Local Similarity   30.6%;  Pred. No. 3.1e-15;
  Matches   57;  Conservative   14;  Mismatches   49;  Indels   66;  Gaps    7;

Qy         51 LLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLE------------ 98
              |||    |   | |           ||  ||:    |   ||||:||
Db          7 LLALPPSWAAGAPRA-----------GR--RPARPRGC-ADRPEELLEQLYGRLAAGVLS 52

Qy         99 -------------------------AD------THQRSISPWRYRVDTDEDRYPQKLAFA 127
                                       ||      |: ||:||| ||:  |  |||: |  |
Db         53 AFHHTLQLGPREQARNASCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEA 112

Qy        128 ECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTE-FIHVP 186
              ||||||:    | |     |  :    :|||| |    |  :        :|| :: :|
Db        113 YCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSV--------YTEAYVTIP 164

Qy        187 VGCTCV 192
              ||||||
Db        165 VGCTCV 170


RESULT 8
US-09-747-259-8
; Sequence 8, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Chen, Jian
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Li,Hanzhong
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  VanLookeren,Menno
;  APPLICANT:  Vandlen,Richard
;  APPLICANT:  Watanabe,Colin
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William
;  APPLICANT:  Yansura,Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P1(US)
;  CURRENT APPLICATION NUMBER: US/09/747,259
;  CURRENT FILING DATE:  2000-12-20
;  PRIOR APPLICATION NUMBER: US 09/311,832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US 60/172,096
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: PCT/US99/31274
;  PRIOR FILING DATE: 1999-12-30
;  PRIOR APPLICATION NUMBER: US 60/175,481
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/191,007
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/07532
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/15264
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: US 60/213,087
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: US 09/644,848
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/242,837
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: PCT/US00/30873
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: US 60/253,646
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 8
;   LENGTH: 202
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-747-259-8

  Query Match           18.4%;  Score 197;  DB 2;  Length 202;
  Best Local Similarity   29.6%;  Pred. No. 5.4e-15;
  Matches   55;  Conservative   14;  Mismatches   51;  Indels   66;  Gaps    6;

Qy         51 LLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLE------------ 98
              |||    |   | |           ||  ||:    |   ||||:||
Db          7 LLALPPSWAAGAPRA-----------GR--RPARPRGC-ADRPEELLEQLYGRLAAGVLS 52

Qy         99 ------------------------------ADTHQRSISPWRYRVDTDEDRYPQKLAFA 127
                                             |: ||:||| ||:  |  |||: |  |
Db         53 AFHHTLQLGPREQARNASCPAGGRPGDRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEA 112

Qy        128 ECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTE-FIHVP 186
              ||||||:    | |     |  :    :|||| |    |  :        :|| :: :|
Db        113 YCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSV--------YTEAYVTIP 164

Qy        187 VGCTCV 192
              ||||||
Db        165 VGCTCV 170


RESULT 9
US-09-816-744-8
; Sequence 8, Application US/09816744
; Patent No. 6579520
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Li,Hanzhong
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  VanLookeren,Menno
;  APPLICANT:  Vandlen,Richard
;  APPLICANT:  Watanabe,Colin
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William
;  APPLICANT:  Yansura,Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P2(US)
;  CURRENT APPLICATION NUMBER: US/09/816,744
;  CURRENT FILING DATE:  2001-03-22
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 8
;   LENGTH: 202
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-816-744-8

  Query Match           18.4%;  Score 197;  DB 2;  Length 202;
  Best Local Similarity   29.6%;  Pred. No. 5.4e-15;
  Matches   55;  Conservative   14;  Mismatches   51;  Indels   66;  Gaps    6;

Qy         51 LLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLE------------ 98
              |||    |   | |           ||  ||:    |   ||||:||
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```
Db          7 LLALPPSWAAGAPRA-----------GR--RPARPRGC-ADRPEELLEQLYGRLAAGVLS 52

Qy         99 ------------------------------ADTHQRSISPWRYRVDTDEDRYPQKLAFA 127
                                            |: ||:||| ||:  |  |||: |  |
Db         53 AFHHTLQLGPREQARNASCPAGGRPGDRRFRPPTNLRSVSPWAYRISYDPARYPRYLPEA 112

Qy        128 ECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTE-FIHVP 186
              ||||||:    | |     |  :    :|||| |    |  :        :|| :: :|
Db        113 YCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSV--------YTEAYVTIP 164

Qy        187 VGCTCV 192
              ||||||
Db        165 VGCTCV 170


RESULT 10
US-09-480-297A-18
; Sequence 18, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-480-297A-18

  Query Match             18.0%;  Score 193;  DB 2;  Length 169;
  Best Local Similarity   31.0%;  Pred. No. 1.2e-14;
  Matches   58;  Conservative   17;  Mismatches   86;  Indels   26;  Gaps    6;

Qy         10 LTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVSS 69
              : :|   :  | |||        | |  ::|    | ||       ||      | ||
Db          5 VAFLAMIVGTHTVSLRIQEGCSHLPSCCPSKE----QEPPE---EWLKWSS----ASVSP 53

Qy         70 LEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAEC 129
              |  ||    |   |:   |:          : |:|||| | :| | :| || |  | |
Db         54 PEPLSHTHHAESCRASKDGPL----------NSRAISPWSYELDRDLNRVPQDLYHARC 102

Qy        130 LCRGCIDARTGRETAAL-NSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVG 188
              ||  |:  :||     | ||| |  :  |  ||||  :     |   :        | :
Db        103 LCPHCVSLQTGSHMDPLGNSVPLYHNQTVFYRRPCHGEEG---THRRYCLERRLYRVSLA 159

Qy        189 CTCVLPR 195
              | || ||
Db        160 CVCVRPR 166


RESULT 11
US-09-836-385-4
; Sequence 4, Application US/09836385
; Patent No. 6676939
; GENERAL INFORMATION:
;  APPLICANT: Hurst, Stephen D.
;  APPLICANT:  Zurawski, Sandra M.
;  APPLICANT:  Rennick, Donna M.
;  TITLE OF INVENTION: Cytokine Uses; Compositions; Methods
;  FILE REFERENCE: DX01088K
;  CURRENT APPLICATION NUMBER: US/09/836,385
;  CURRENT FILING DATE:  2001-04-17
;  PRIOR APPLICATION NUMBER: US 60/198,488
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: rodent
US-09-836-385-4

  Query Match             18.0%;  Score 193;  DB 2;  Length 169;
  Best Local Similarity   31.0%;  Pred. No. 1.2e-14;
  Matches   58;  Conservative   17;  Mismatches   86;  Indels   26;  Gaps    6;

Qy         10 LTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVSS 69
              : :|   :  | |||        | |  ::|    | ||       ||      | ||
Db          5 VAFLAMIVGTHTVSLRIQEGCSHLPSCCPSKE----QEPPE---EWLKWSS----ASVSP 53

Qy         70 LEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKLAFAEC 129
              |  ||    |   |:   |:          : |:|||| | :| | :| || |  | |
Db         54 PEPLSHTHHAESCRASKDGPL----------NSRAISPWSYELDRDLNRVPQDLYHARC 102

Qy        130 LCRGCIDARTGRETAAL-NSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVG 188
              ||  |:  :||     | ||| |  :  |  ||||  :     |   :        | :
Db        103 LCPHCVSLQTGSHMDPLGNSVPLYHNQTVFYRRPCHGEEG---THRRYCLERRLYRVSLA 159

Qy        189 CTCVLPR 195
              | || ||
Db        160 CVCVRPR 166


RESULT 12
US-09-480-297A-6
; Sequence 6, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 151
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-480-297A-6

  Query Match             17.9%;  Score 192;  DB 2;  Length 151;
  Best Local Similarity   34.3%;  Pred. No. 1.4e-14;
  Matches   46;  Conservative   18;  Mismatches   58;  Indels   12;  Gaps    5;

Qy         62 LPVALVSSLEAASHRGRHERPSATTQCPV-LRP-EEVLEADTHQRSISPWRYRVDTDEDR 119
              |   ::|:        |  |: :    ||   || :      |: ||:||| ||:  |  |
Db         16 LAAGVLSAFHHTLQLGPREQ-ARNASCPAGGRPADRRFRTPTNLRSVSPWAYRISYDPAR 74

Qy        120 YPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFH 179
              ||: |  | ||||||:    | |     |  :    :|||| |    | :       :
Db         75 YPRYLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSV--------Y 126

Qy        180 TE-FIHVPVGCTCV 192
              || :: :|||||||
Db        127 TEAYVTIPVGCTCV 140


RESULT 13
US-09-231-788-12
; Sequence 12, Application US/09231788A
; Patent No. 6486301
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
```

```
;  TITLE OF INVENTION: Interleukin-20
;  FILE REFERENCE: PF399P1
;  CURRENT APPLICATION NUMBER: US/09/231,788A
;  CURRENT FILING DATE: 1999-01-15
;  EARLIER APPLICATION NUMBER: 60/052,870
;  EARLIER FILING DATE: 1997-07-16
;  EARLIER APPLICATION NUMBER: 60/055,952
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/060,140
;  EARLIER FILING DATE: 1997-09-26
;  EARLIER APPLICATION NUMBER: 09/115,832
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 160
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-231-788-12

  Query Match             17.9%;  Score 192;  DB 2;  Length 160;
  Best Local Similarity   35.1%;  Pred. No. 1.5e-14;
  Matches   46;  Conservative   18;  Mismatches   55;  Indels   12;  Gaps    5;

Qy         65 ALVSSLEAASHRGRHERPSATTQCPV-LRP-EEVLEADTHQRSISPWRYRVDTDEDRYPQ 122
              |::|:       |  |: :    ||   || :      |: ||:||| ||:  |  |||:
Db          7 AVLSAFHHTLQLGPREQ-ARNASCPAGGRPADRRFRPPTNLRSVSPWAYRISYDPARYPR 65

Qy        123 KLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTE- 181
              | | ||||||:   | |     |  :   :|||| |    |  :      :||
Db         66 YLPEAYCLCRGCLTGLFGEEDVRFRSAPVYMPTVVLRRTPACAGGRSV--------YTEA 117

Qy        182 FIHVPVGCTCV 192
              :: :|||||||
Db        118 YVTIPVGCTCV 128


RESULT 14
US-09-724-864-37
; Sequence 37, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
;  APPLICANT:  Watson, James D
;  APPLICANT:  Murison, James G.
;  TITLE OF INVENTION:  Polynucleotides, polypeptides expressed
;  TITLE OF INVENTION:  by the polynucleotides and methods for their use.
;  FILE REFERENCE:  11000.1050U1
;  CURRENT APPLICATION NUMBER: US/09/724,864
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER:  U.S. No. 6380362 60/171,678
;  PRIOR FILING DATE:  1999-12-23
;  NUMBER OF SEQ ID NOS:  72
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 37
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-724-864-37

  Query Match             17.1%;  Score 183;  DB 2;  Length 205;
  Best Local Similarity   31.2%;  Pred. No. 2.5e-13;
  Matches   54;  Conservative   16;  Mismatches   49;  Indels   54;  Gaps    7;

Qy         64 VALVSSLEAASHR-GRHERPSATTQCPVLRPEEVLE----------------------- 98
              :||     | : | ||  ||:    |   ||||:||
Db         15 LALAPGRAAGALRTGR--RPARPRDC-ADRPEELLEQLYGRLAAGVLSAFHHTLQLGPRE 71

Qy         99 -------------AD------THQRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDART 139
                           ||      |: ||:||| ||:  |  |:|: |  | ||||||:
Db         72 QARNASCPAGGRAADRRFRPPTNLRSVSPWAYRISYDPARFPRYLPEAYCLCRGCLTGLY 131

Qy        140 GRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCV 192
              | |     |  :    :||||     |  :     :| |  :| :|||||||
Db        132 GEEDFRFRSTPVFSPAVVLRRTAACAGGRSV-----YAEH--YITIPVGCTCV 177


RESULT 15
US-09-480-297A-12
; Sequence 12, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-480-297A-12

  Query Match             17.1%;  Score 183;  DB 2;  Length 205;
  Best Local Similarity   31.2%;  Pred. No. 2.5e-13;
  Matches   54;  Conservative   16;  Mismatches   49;  Indels   54;  Gaps    7;

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Search completed: April 27, 2006, 17:18:39
Job time : 32 secs
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OM protein - protein search, using sw model

Run on: April 27, 2006, 17:37:16 ; Search time 27 Seconds
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331.820 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 232119

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Post-processing: Minimum Match 0%
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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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19	173	16.1	163	7	US-11-103-195-160	Sequence 160, App
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252	66	6.2	345	7	US-11-096-568A-11332	Sequence 11332, A
253	66	6.2	345	7	US-11-188-298-10932	Sequence 10932, A
254	66	6.2	360	7	US-11-096-568A-15133	Sequence 15133, A
255	66	6.2	374	7	US-11-188-298-8192	Sequence 8192, Ap
256	66	6.2	399	7	US-11-096-568A-15132	Sequence 15132, A
257	66	6.2	414	7	US-11-096-568A-15131	Sequence 15131, A
258	66	6.2	442	7	US-11-096-568A-23131	Sequence 23131, A
259	66	6.2	551	7	US-11-188-298-5035	Sequence 5035, Ap
260	66	6.2	678	7	US-11-188-298-11543	Sequence 11543, A
261	66	6.2	710	7	US-11-072-512-3402	Sequence 3402, Ap
262	66	6.2	898	7	US-11-174-150-43	Sequence 43, Appl
263	66	6.2	1681	7	US-11-019-711-20	Sequence 20, Appl
264	66	6.2	1697	7	US-11-019-711-68	Sequence 68, Appl
265	66	6.2	1723	7	US-11-019-711-18	Sequence 18, Appl
266	65.5	6.1	118	7	US-11-072-512-3051	Sequence 3051, Ap
267	65.5	6.1	136	7	US-11-264-096-461	Sequence 461, App
268	65.5	6.1	218	6	US-10-667-295-151	Sequence 151, App

269	65.5	6.1	269	7	US-11-096-568A-16358	Sequence 16358, A
270	65.5	6.1	279	6	US-10-506-454-1425	Sequence 1425, Ap
271	65.5	6.1	324	7	US-11-096-568A-14996	Sequence 14996, A
272	65.5	6.1	365	7	US-11-096-568A-18844	Sequence 18844, A
273	65.5	6.1	414	7	US-11-096-568A-18843	Sequence 18843, A
274	65.5	6.1	502	7	US-11-072-512-2388	Sequence 2388, Ap
275	65.5	6.1	954	7	US-11-188-298-16512	Sequence 16512, A
276	65.5	6.1	2911	7	US-11-090-617-706	Sequence 706, App
277	65	6.1	133	7	US-11-072-512-2167	Sequence 2167, Ap
278	65	6.1	208	7	US-11-096-568A-21877	Sequence 21877, A
279	65	6.1	359	6	US-10-467-657-1898	Sequence 1898, Ap
280	65	6.1	504	7	US-11-087-099-11155	Sequence 11155, A
281	65	6.1	601	7	US-11-079-463-9471	Sequence 9471, Ap
282	65	6.1	807	7	US-11-079-463-6963	Sequence 6963, Ap
283	65	6.1	1515	7	US-11-124-367A-402	Sequence 402, App
284	65	6.1	1516	7	US-11-124-367A-401	Sequence 401, App
285	65	6.1	1518	7	US-11-124-367A-406	Sequence 406, App
286	65	6.1	1532	7	US-11-124-367A-403	Sequence 403, App
287	65	6.1	1532	7	US-11-124-367A-404	Sequence 404, App
288	65	6.1	1532	7	US-11-124-367A-405	Sequence 405, App
289	65	6.1	1532	7	US-11-124-367A-407	Sequence 407, App
290	65	6.1	1535	7	US-11-124-367A-408	Sequence 408, App
291	65	6.1	2764	6	US-10-995-561-691	Sequence 691, App
292	65	6.1	2813	6	US-10-995-561-688	Sequence 688, App
293	65	6.1	2919	6	US-10-821-234-1133	Sequence 1133, Ap
294	64.5	6.0	188	7	US-11-096-568A-21419	Sequence 21419, A
295	64.5	6.0	328	7	US-11-096-568A-21832	Sequence 21832, A
296	64.5	6.0	382	7	US-11-054-281-104	Sequence 104, App
297	64.5	6.0	547	7	US-11-087-099-11351	Sequence 11351, A
298	64.5	6.0	579	7	US-11-096-568A-24333	Sequence 24333, A
299	64.5	6.0	602	6	US-10-453-372-1064	Sequence 1064, Ap
300	64.5	6.0	668	7	US-11-072-512-2308	Sequence 2308, Ap
301	64.5	6.0	717	7	US-11-121-438-10	Sequence 10, Appl
302	64.5	6.0	749	7	US-11-054-281-103	Sequence 103, App
303	64.5	6.0	752	7	US-11-080-991-52	Sequence 52, Appl
304	64.5	6.0	752	7	US-11-054-281-101	Sequence 101, App
305	64.5	6.0	755	6	US-10-453-372-1108	Sequence 1108, Ap
306	64.5	6.0	755	7	US-11-054-281-26	Sequence 26, Appl
307	64.5	6.0	755	7	US-11-054-281-102	Sequence 102, App
308	64	6.0	275	7	US-11-096-568A-15894	Sequence 15894, A
309	64	6.0	282	7	US-11-096-568A-19165	Sequence 19165, A
310	64	6.0	285	7	US-11-096-568A-19164	Sequence 19164, A
311	64	6.0	312	6	US-10-714-887-54	Sequence 54, Appl
312	64	6.0	344	7	US-11-087-099-11544	Sequence 11544, A
313	64	6.0	579	6	US-10-524-750-4	Sequence 4, Appli
314	64	6.0	679	6	US-10-507-876A-2	Sequence 2, Appli
315	64	6.0	747	6	US-10-492-835-8	Sequence 8, Appli
316	64	6.0	747	6	US-10-492-835-27	Sequence 27, Appl
317	64	6.0	748	7	US-11-072-512-2336	Sequence 2336, Ap
319	64	6.0	1198	6	US-10-451-375-4	Sequence 4, Appli
320	64	6.0	2392	6	US-10-330-773-907	Sequence 907, App
321	63.5	5.9	164	7	US-11-072-512-3407	Sequence 3407, Ap
322	63.5	5.9	208	7	US-11-079-463-8297	Sequence 8297, Ap
323	63.5	5.9	260	7	US-11-096-568A-26540	Sequence 26540, A
324	63.5	5.9	275	7	US-11-096-568A-26539	Sequence 26539, A
325	63.5	5.9	298	6	US-10-821-234-1240	Sequence 1240, Ap
326	63.5	5.9	360	7	US-11-188-298-1516	Sequence 1516, Ap
327	63.5	5.9	368	7	US-11-096-568A-11631	Sequence 11631, A
328	63.5	5.9	406	7	US-11-096-568A-11630	Sequence 11630, A
329	63.5	5.9	421	7	US-11-096-568A-11629	Sequence 11629, A
330	63.5	5.9	481	7	US-11-188-298-14771	Sequence 14771, A
331	63.5	5.9	534	7	US-11-096-568A-24457	Sequence 24457, A
332	63.5	5.9	545	7	US-11-188-298-2157	Sequence 2157, Ap
333	63.5	5.9	548	7	US-11-096-568A-24456	Sequence 24456, A
334	63.5	5.9	552	7	US-11-096-568A-18755	Sequence 18755, A
335	63.5	5.9	561	7	US-11-096-568A-18754	Sequence 18754, A
336	63.5	5.9	567	7	US-11-096-568A-18753	Sequence 18753, A
337	63.5	5.9	580	7	US-11-087-099-1273	Sequence 1273, Ap
338	63.5	5.9	580	7	US-11-087-099-6034	Sequence 6034, Ap
339	63.5	5.9	580	7	US-11-087-099-6200	Sequence 6200, Ap
340	63.5	5.9	580	7	US-11-087-099-9615	Sequence 9615, Ap
341	63.5	5.9	581	7	US-11-087-099-4940	Sequence 4940, Ap
342	63.5	5.9	581	7	US-11-087-099-10168	Sequence 10168, A
343	63.5	5.9	582	7	US-11-087-099-1734	Sequence 1734, Ap
344	63.5	5.9	585	7	US-11-205-109-26	Sequence 26, Appl
345	63.5	5.9	590	7	US-11-087-099-2105	Sequence 2105, Ap
346	63.5	5.9	618	7	US-11-078-735-18	Sequence 18, Appl
347	63.5	5.9	618	7	US-11-050-346-63	Sequence 63, Appl
348	63.5	5.9	618	7	US-11-103-077-18	Sequence 18, Appl
349	63.5	5.9	618	7	US-11-058-066-18	Sequence 18, Appl
354	63	5.9	244	7	US-11-087-099-3319	Sequence 3319, Ap
355	63	5.9	257	7	US-11-096-568A-9050	Sequence 9050, Ap
356	63	5.9	268	7	US-11-096-568A-18549	Sequence 18549, A
357	63	5.9	269	7	US-11-188-298-11965	Sequence 11965, A
358	63	5.9	333	7	US-11-096-568A-18548	Sequence 18548, A
359	63	5.9	345	7	US-11-096-568A-18547	Sequence 18547, A
360	63	5.9	388	7	US-11-043-788-465	Sequence 465, App
361	63	5.9	424	7	US-11-188-298-12163	Sequence 12163, A
362	63	5.9	448	6	US-10-967-527A-16	Sequence 16, Appl
363	63	5.9	496	7	US-11-096-568A-29371	Sequence 29371, A
364	63	5.9	503	7	US-11-072-512-3266	Sequence 3266, Ap
365	63	5.9	513	7	US-11-188-298-21012	Sequence 21012, A
366	63	5.9	548	7	US-11-096-568A-29370	Sequence 29370, A
367	63	5.9	548	7	US-11-188-298-6464	Sequence 6464, Ap
368	63	5.9	634	7	US-11-096-568A-15357	Sequence 15357, A
369	63	5.9	635	7	US-11-096-568A-15356	Sequence 15356, A
370	63	5.9	642	7	US-11-188-298-18861	Sequence 18861, A
371	63	5.9	650	7	US-11-096-568A-19944	Sequence 19944, A
372	63	5.9	664	7	US-11-096-568A-19943	Sequence 19943, A
373	63	5.9	669	7	US-11-096-568A-19942	Sequence 19942, A
374	63	5.9	684	7	US-11-096-568A-29369	Sequence 29369, A
375	63	5.9	830	6	US-10-995-561-899	Sequence 899, App
376	63	5.9	890	7	US-11-182-016-34	Sequence 34, Appl
377	63	5.9	1068	7	US-11-045-004-931	Sequence 931, App
378	63	5.9	1075	7	US-11-079-463-6009	Sequence 6009, Ap
379	63	5.9	1184	7	US-11-065-695-10	Sequence 10, Appl
380	63	5.9	3712	7	US-11-019-711-48	Sequence 48, Appl
381	63	5.9	3712	7	US-11-019-711-51	Sequence 51, Appl
382	62.5	5.8	84	7	US-11-138-642-9	Sequence 9, Appli
383	62.5	5.8	84	7	US-11-138-882-9	Sequence 9, Appli
384	62.5	5.8	84	7	US-11-138-757-10	Sequence 10, Appl
385	62.5	5.8	213	7	US-11-188-298-21703	Sequence 21703, A
386	62.5	5.8	221	7	US-11-096-568A-5302	Sequence 5302, Ap
387	62.5	5.8	237	7	US-11-079-463-5990	Sequence 5990, Ap
388	62.5	5.8	253	7	US-11-096-568A-5301	Sequence 5301, Ap
389	62.5	5.8	269	7	US-11-072-512-3593	Sequence 3593, Ap
390	62.5	5.8	275	7	US-11-096-568A-20259	Sequence 20259, A
391	62.5	5.8	282	7	US-11-096-568A-5300	Sequence 5300, Ap
392	62.5	5.8	300	7	US-11-096-568A-20258	Sequence 20258, A
393	62.5	5.8	302	5	US-09-978-360A-407	Sequence 407, App
394	62.5	5.8	336	7	US-11-188-298-7857	Sequence 7857, Ap
395	62.5	5.8	366	6	US-10-215-245A-2	Sequence 2, Appli
396	62.5	5.8	374	7	US-11-096-568A-31576	Sequence 31576, A
397	62.5	5.8	391	7	US-11-096-568A-8794	Sequence 8794, Ap
398	62.5	5.8	393	7	US-11-096-568A-31575	Sequence 31575, A
399	62.5	5.8	407	7	US-11-079-463-10130	Sequence 10130, A
400	62.5	5.8	408	7	US-11-096-568A-8793	Sequence 8793, Ap
401	62.5	5.8	409	7	US-11-096-568A-9548	Sequence 9548, Ap
402	62.5	5.8	432	7	US-11-096-568A-8792	Sequence 8792, Ap
403	62.5	5.8	449	6	US-10-506-454-1070	Sequence 1070, Ap
405	62.5	5.8	487	6	US-10-973-115B-528	Sequence 528, App
414	62.5	5.8	487	7	US-11-290-153-528	Sequence 528, App
415	62.5	5.8	551	6	US-10-491-468-38	Sequence 38, Appl
416	62.5	5.8	609	7	US-11-087-099-7286	Sequence 7286, Ap
417	62.5	5.8	629	7	US-11-072-512-2289	Sequence 2289, Ap
418	62.5	5.8	762	6	US-10-501-841-48	Sequence 48, Appl
419	62.5	5.8	837	6	US-10-995-561-698	Sequence 698, App
420	62.5	5.8	1017	7	US-11-156-300-8	Sequence 8, Appli
421	62.5	5.8	1049	7	US-11-051-720-1565	Sequence 1565, Ap
422	62.5	5.8	1174	6	US-10-995-561-697	Sequence 697, App
423	62.5	5.8	1281	7	US-11-072-175-253	Sequence 253, App
424	62.5	5.8	1526	7	US-11-051-720-1566	Sequence 1566, Ap
425	62	5.8	96	7	US-11-096-568A-11778	Sequence 11778, A
426	62	5.8	194	7	US-11-172-740-878	Sequence 878, App
427	62	5.8	209	6	US-10-518-701-6	Sequence 6, Appli
428	62	5.8	221	7	US-11-096-568A-17196	Sequence 17196, A

429	62	5.8	233	7	US-11-096-568A-17195	Sequence 17195, A
430	62	5.8	235	6	US-10-455-772-200	Sequence 200, App
431	62	5.8	292	7	US-11-096-568A-24228	Sequence 24228, A
432	62	5.8	301	7	US-11-096-568A-24227	Sequence 24227, A
433	62	5.8	330	7	US-11-055-822-524	Sequence 524, App
434	62	5.8	362	7	US-11-110-274-5	Sequence 5, Appli
435	62	5.8	362	7	US-11-040-218-43	Sequence 43, Appl
436	62	5.8	376	7	US-11-040-218-45	Sequence 45, Appl
437	62	5.8	380	7	US-11-188-298-17662	Sequence 17662, A
438	62	5.8	386	7	US-11-043-788-398	Sequence 398, App
439	62	5.8	392	7	US-11-043-788-469	Sequence 469, App
440	62	5.8	409	7	US-11-096-568A-24736	Sequence 24736, A
441	62	5.8	419	7	US-11-096-568A-24735	Sequence 24735, A
442	62	5.8	439	7	US-11-096-568A-24734	Sequence 24734, A
443	62	5.8	508	6	US-10-784-004-414	Sequence 414, App
444	62	5.8	571	7	US-11-188-298-1313	Sequence 1313, Ap
445	62	5.8	572	7	US-11-087-099-4593	Sequence 4593, Ap
446	62	5.8	572	7	US-11-087-099-7113	Sequence 7113, Ap
447	62	5.8	572	7	US-11-188-298-15206	Sequence 15206, A
448	62	5.8	572	7	US-11-188-298-17546	Sequence 17546, A
449	62	5.8	637	7	US-11-087-099-12363	Sequence 12363, A
450	62	5.8	748	6	US-10-492-835-12	Sequence 12, Appl
451	62	5.8	748	6	US-10-492-835-28	Sequence 28, Appl
452	62	5.8	797	6	US-10-469-469-48	Sequence 48, Appl
453	62	5.8	797	6	US-10-469-469-208	Sequence 208, App
454	62	5.8	837	7	US-11-079-463-6900	Sequence 6900, Ap
455	62	5.8	864	7	US-11-079-463-5554	Sequence 5554, Ap
456	62	5.8	882	7	US-11-169-041-137	Sequence 137, App
457	62	5.8	925	6	US-10-453-372-1124	Sequence 1124, Ap
458	62	5.8	966	6	US-10-877-346-32	Sequence 32, Appl
459	62	5.8	972	6	US-10-453-372-1128	Sequence 1128, Ap
460	62	5.8	1097	6	US-10-995-561-781	Sequence 781, App
461	62	5.8	1353	7	US-11-296-294-16	Sequence 16, Appl
462	62	5.8	1378	7	US-11-296-294-18	Sequence 18, Appl
463	62	5.8	1669	6	US-10-330-773-392	Sequence 392, App
464	62	5.8	1690	6	US-10-330-773-389	Sequence 389, App
465	62	5.8	2333	7	US-11-096-281-13	Sequence 13, Appl
466	61.5	5.7	170	7	US-11-096-568A-25	Sequence 25, Appl
467	61.5	5.7	185	7	US-11-188-298-11319	Sequence 11319, A
468	61.5	5.7	201	6	US-10-821-234-1645	Sequence 1645, Ap
469	61.5	5.7	241	7	US-11-096-568A-16952	Sequence 16952, A
470	61.5	5.7	261	7	US-11-072-512-2586	Sequence 2586, Ap
471	61.5	5.7	265	7	US-11-096-568A-21567	Sequence 21567, A
472	61.5	5.7	274	7	US-11-096-568A-1420	Sequence 1420, Ap
473	61.5	5.7	278	7	US-11-188-298-20907	Sequence 20907, A
474	61.5	5.7	365	7	US-11-188-298-3896	Sequence 3896, Ap
475	61.5	5.7	371	7	US-11-096-568A-8795	Sequence 8795, Ap
476	61.5	5.7	382	7	US-11-096-568A-26984	Sequence 26984, A
477	61.5	5.7	416	7	US-11-096-568A-21786	Sequence 21786, A
478	61.5	5.7	441	7	US-11-096-568A-18629	Sequence 18629, A
479	61.5	5.7	468	7	US-11-096-568A-18628	Sequence 18628, A
480	61.5	5.7	486	7	US-11-188-298-8697	Sequence 8697, Ap
481	61.5	5.7	487	6	US-10-784-004-785	Sequence 785, App
482	61.5	5.7	487	6	US-10-784-004-1113	Sequence 1113, Ap
483	61.5	5.7	499	6	US-10-714-995-42	Sequence 42, Appl
484	61.5	5.7	509	7	US-11-188-298-3151	Sequence 3151, Ap
485	61.5	5.7	509	7	US-11-188-298-10034	Sequence 10034, A
486	61.5	5.7	562	7	US-11-072-512-3214	Sequence 3214, Ap
487	61.5	5.7	580	7	US-11-183-136-6	Sequence 6, Appli
488	61.5	5.7	580	7	US-11-046-653-2	Sequence 2, Appli
489	61.5	5.7	617	7	US-11-087-099-9501	Sequence 9501, Ap
490	61.5	5.7	628	7	US-11-080-991-108	Sequence 108, App
491	61.5	5.7	672	7	US-11-188-298-6914	Sequence 6914, Ap
492	61.5	5.7	932	6	US-10-511-989-20	Sequence 20, Appl
493	61.5	5.7	950	6	US-10-511-989-18	Sequence 18, Appl
494	61.5	5.7	959	6	US-10-467-962B-4	Sequence 4, Appli
495	61.5	5.7	1023	7	US-11-188-298-5228	Sequence 5228, Ap
496	61.5	5.7	1168	6	US-10-970-750-5	Sequence 5, Appli
497	61	5.7	140	7	US-11-234-786-477	Sequence 477, App
498	61	5.7	155	7	US-11-172-740-879	Sequence 879, App
499	61	5.7	189	7	US-11-264-096-1629	Sequence 1629, Ap
500	61	5.7	251	7	US-11-096-568A-22969	Sequence 22969, A
501	61	5.7	256	7	US-11-096-568A-22968	Sequence 22968, A
502	61	5.7	260	7	US-11-183-261-25	Sequence 25, Appl
503	61	5.7	261	7	US-11-096-568A-22967	Sequence 22967, A
504	61	5.7	268	7	US-11-096-568A-17766	Sequence 17766, A
505	61	5.7	269	7	US-11-079-463-7300	Sequence 7300, Ap
506	61	5.7	271	6	US-10-506-454-729	Sequence 729, App
507	61	5.7	354	6	US-10-506-454-517	Sequence 517, App
508	61	5.7	362	7	US-11-072-512-3160	Sequence 3160, Ap
509	61	5.7	388	7	US-11-188-298-9549	Sequence 9549, Ap
510	61	5.7	424	7	US-11-232-440-23	Sequence 23, Appl
511	61	5.7	459	7	US-11-188-298-16200	Sequence 16200, A
512	61	5.7	541	7	US-11-096-568A-20889	Sequence 20889, A
513	61	5.7	543	7	US-11-072-512-3761	Sequence 3761, Ap
514	61	5.7	548	7	US-11-188-298-2620	Sequence 2620, Ap
515	61	5.7	550	7	US-11-188-298-4393	Sequence 4393, Ap
516	61	5.7	578	7	US-11-087-099-11496	Sequence 11496, A
517	61	5.7	594	7	US-11-087-099-1679	Sequence 1679, Ap
518	61	5.7	617	7	US-11-143-980-35	Sequence 35, Appl
519	61	5.7	625	7	US-11-154-673-7	Sequence 7, Appli
520	61	5.7	884	6	US-10-453-372-58	Sequence 58, Appl
521	61	5.7	1361	7	US-11-089-508-10	Sequence 10, Appl
522	60.5	5.6	38	6	US-10-957-351-183	Sequence 183, App
523	60.5	5.6	144	7	US-11-096-568A-12659	Sequence 12659, A
524	60.5	5.6	188	7	US-11-087-099-8568	Sequence 8568, Ap
525	60.5	5.6	188	7	US-11-188-298-17509	Sequence 17509, A
526	60.5	5.6	190	7	US-11-249-422-7	Sequence 7, Appli
527	60.5	5.6	208	7	US-11-096-568A-18675	Sequence 18675, A
528	60.5	5.6	227	7	US-11-072-512-3269	Sequence 3269, Ap
529	60.5	5.6	235	7	US-11-172-740-563	Sequence 563, App
530	60.5	5.6	235	7	US-11-172-740-2225	Sequence 2225, Ap
531	60.5	5.6	235	7	US-11-188-298-22491	Sequence 22491, A
532	60.5	5.6	237	7	US-11-172-740-568	Sequence 568, App
533	60.5	5.6	237	7	US-11-188-298-22170	Sequence 22170, A
534	60.5	5.6	257	7	US-11-156-516-30	Sequence 30, Appl
535	60.5	5.6	265	7	US-11-188-298-9289	Sequence 9289, Ap
536	60.5	5.6	282	7	US-11-188-298-3766	Sequence 3766, Ap
537	60.5	5.6	305	7	US-11-080-091-13	Sequence 13, Appl
538	60.5	5.6	305	7	US-11-087-177-11	Sequence 11, Appl
539	60.5	5.6	305	7	US-11-087-177-13	Sequence 13, Appl
540	60.5	5.6	312	7	US-11-072-512-3588	Sequence 3588, Ap
541	60.5	5.6	330	7	US-11-072-512-2839	Sequence 2839, Ap
542	60.5	5.6	332	7	US-11-079-463-9376	Sequence 9376, Ap
543	60.5	5.6	347	7	US-11-079-463-6594	Sequence 6594, Ap
544	60.5	5.6	374	6	US-10-513-269-5	Sequence 5, Appli
545	60.5	5.6	382	7	US-11-134-795-19	Sequence 19, Appl
546	60.5	5.6	400	7	US-11-186-284-155	Sequence 155, App
547	60.5	5.6	489	7	US-11-096-568A-31950	Sequence 31950, A
548	60.5	5.6	522	7	US-11-045-004-1066	Sequence 1066, Ap
549	60.5	5.6	524	7	US-11-072-512-3318	Sequence 3318, Ap
550	60.5	5.6	547	7	US-11-156-003-16	Sequence 16, Appl
551	60.5	5.6	652	7	US-11-299-182-4	Sequence 4, Appli
552	60.5	5.6	662	7	US-11-188-298-16369	Sequence 16369, A
553	60.5	5.6	838	7	US-11-031-737A-11	Sequence 11, Appl
554	60.5	5.6	838	7	US-11-031-482-11	Sequence 11, Appl
555	60.5	5.6	1019	6	US-10-455-772-1120	Sequence 1120, Ap
556	60.5	5.6	1062	6	US-10-821-234-1079	Sequence 1079, Ap
557	60.5	5.6	1618	6	US-10-984-645-2	Sequence 2, Appli
558	60.5	5.6	1618	7	US-11-132-687-2	Sequence 2, Appli
559	60.5	5.6	2011	7	US-11-080-991-56	Sequence 56, Appl
560	60.5	5.6	2767	7	US-11-100-640-38	Sequence 38, Appl
561	60.5	5.6	2768	6	US-10-510-101-72	Sequence 72, Appl
562	60.5	5.6	3588	6	US-10-995-561-672	Sequence 672, App
563	60.5	5.6	4346	6	US-10-995-561-671	Sequence 671, App
564	60.5	5.6	4347	6	US-10-995-561-670	Sequence 670, App
565	60.5	5.6	4390	7	US-11-169-041-169	Sequence 169, App
566	60	5.6	206	7	US-11-015-546A-7	Sequence 7, Appli
567	60	5.6	208	7	US-11-096-568A-9963	Sequence 9963, Ap
568	60	5.6	212	7	US-11-015-546A-5	Sequence 5, Appli
569	60	5.6	219	7	US-11-015-546A-4	Sequence 4, Appli
570	60	5.6	238	7	US-11-050-857-606	Sequence 606, App
571	60	5.6	238	7	US-11-051-720-1288	Sequence 1288, Ap
572	60	5.6	253	7	US-11-015-546A-2	Sequence 2, Appli
573	60	5.6	257	7	US-11-087-099-3858	Sequence 3858, Ap
574	60	5.6	283	7	US-11-050-857-603	Sequence 603, App

575	60	5.6	283	7	US-11-051-720-1285	Sequence 1285, Ap
576	60	5.6	287	7	US-11-096-568A-5037	Sequence 5037, Ap
577	60	5.6	295	7	US-11-096-568A-5906	Sequence 5906, Ap
578	60	5.6	317	7	US-11-096-568A-5036	Sequence 5036, Ap
579	60	5.6	327	7	US-11-096-568A-12914	Sequence 12914, A
580	60	5.6	329	7	US-11-072-512-3709	Sequence 3709, Ap
581	60	5.6	345	7	US-11-079-463-7015	Sequence 7015, Ap
582	60	5.6	353	7	US-11-096-568A-22016	Sequence 22016, A
583	60	5.6	355	7	US-11-096-568A-22015	Sequence 22015, A
584	60	5.6	357	7	US-11-096-568A-15568	Sequence 15568, A
585	60	5.6	363	7	US-11-050-857-605	Sequence 605, App
586	60	5.6	363	7	US-11-051-720-1287	Sequence 1287, Ap
587	60	5.6	363	7	US-11-096-568A-22583	Sequence 22583, A
588	60	5.6	369	7	US-11-188-298-13388	Sequence 13388, A
589	60	5.6	372	7	US-11-096-568A-22014	Sequence 22014, A
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591	60	5.6	402	6	US-10-650-326B-21	Sequence 21, Appl
592	60	5.6	402	6	US-10-921-793-24	Sequence 24, Appl
593	60	5.6	402	6	US-10-931-198-24	Sequence 24, Appl
594	60	5.6	402	6	US-10-942-042-24	Sequence 24, Appl
595	60	5.6	402	7	US-11-051-568-29	Sequence 29, Appl
596	60	5.6	402	7	US-11-226-555-21	Sequence 21, Appl
597	60	5.6	407	7	US-11-096-568A-22582	Sequence 22582, A
598	60	5.6	413	7	US-11-096-568A-5905	Sequence 5905, Ap
599	60	5.6	414	7	US-11-096-568A-5904	Sequence 5904, Ap
600	60	5.6	417	7	US-11-072-175-233	Sequence 233, App
601	60	5.6	447	7	US-11-050-857-604	Sequence 604, App
602	60	5.6	447	7	US-11-051-720-1286	Sequence 1286, Ap
603	60	5.6	459	7	US-11-096-568A-15566	Sequence 15566, A
604	60	5.6	461	6	US-10-523-328-5	Sequence 5, Appli
605	60	5.6	461	7	US-11-132-285-6	Sequence 6, Appli
606	60	5.6	461	7	US-11-182-946-4	Sequence 4, Appli
607	60	5.6	461	7	US-11-183-205-32	Sequence 32, Appl
608	60	5.6	461	7	US-11-260-192-2	Sequence 2, Appli
609	60	5.6	467	7	US-11-037-243-63	Sequence 63, Appl
610	60	5.6	478	7	US-11-177-506-51	Sequence 51, Appl
611	60	5.6	478	7	US-11-050-857-602	Sequence 602, App
612	60	5.6	478	7	US-11-050-857-1000	Sequence 1000, Ap
613	60	5.6	478	7	US-11-051-720-1418	Sequence 1418, Ap
614	60	5.6	478	7	US-11-051-720-1696	Sequence 1696, Ap
615	60	5.6	494	7	US-11-087-099-3900	Sequence 3900, Ap
616	60	5.6	495	7	US-11-182-016-31	Sequence 31, Appl
617	60	5.6	519	7	US-11-080-991-106	Sequence 106, App
628	60	5.6	550	7	US-11-096-568A-18775	Sequence 18775, A
629	60	5.6	550	7	US-11-188-298-1128	Sequence 1128, Ap
630	60	5.6	552	7	US-11-072-512-3426	Sequence 3426, Ap
631	60	5.6	645	7	US-11-072-512-3227	Sequence 3227, Ap
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634	60	5.6	1745	7	US-11-264-096-2222	Sequence 2222, Ap
635	60	5.6	2339	7	US-11-096-281-11	Sequence 11, Appl
636	60	5.6	3116	6	US-10-995-561-826	Sequence 826, App
637	59.5	5.5	141	7	US-11-124-367A-295	Sequence 295, App
638	59.5	5.5	153	6	US-10-821-234-1355	Sequence 1355, Ap
639	59.5	5.5	181	7	US-11-096-568A-26261	Sequence 26261, A
640	59.5	5.5	233	7	US-11-096-568A-14586	Sequence 14586, A
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642	59.5	5.5	250	7	US-11-087-099-10619	Sequence 10619, A
643	59.5	5.5	250	7	US-11-096-568A-19825	Sequence 19825, A
644	59.5	5.5	252	7	US-11-096-568A-17418	Sequence 17418, A
645	59.5	5.5	271	7	US-11-172-740-737	Sequence 737, App
646	59.5	5.5	299	7	US-11-124-367A-298	Sequence 298, App
647	59.5	5.5	324	7	US-11-096-568A-17416	Sequence 17416, A
648	59.5	5.5	333	7	US-11-188-298-17774	Sequence 17774, A
649	59.5	5.5	349	7	US-11-096-568A-17688	Sequence 17688, A
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651	59.5	5.5	378	7	US-11-096-568A-12584	Sequence 12584, A
652	59.5	5.5	387	7	US-11-124-367A-294	Sequence 294, App
653	59.5	5.5	392	7	US-11-096-568A-22314	Sequence 22314, A
654	59.5	5.5	392	7	US-11-188-298-10095	Sequence 10095, A
655	59.5	5.5	412	7	US-11-124-367A-296	Sequence 296, App
656	59.5	5.5	417	7	US-11-087-099-9165	Sequence 9165, Ap
657	59.5	5.5	417	7	US-11-079-463-9205	Sequence 9205, Ap
658	59.5	5.5	442	7	US-11-096-568A-19628	Sequence 19628, A
659	59.5	5.5	448	7	US-11-124-367A-297	Sequence 297, App
660	59.5	5.5	448	7	US-11-124-367A-299	Sequence 299, App
661	59.5	5.5	449	7	US-11-096-568A-22313	Sequence 22313, A
662	59.5	5.5	453	7	US-11-096-568A-17494	Sequence 17494, A
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665	59.5	5.5	509	7	US-11-087-099-12404	Sequence 12404, A
666	59.5	5.5	519	7	US-11-033-039-442	Sequence 442, App
667	59.5	5.5	522	7	US-11-096-568A-17492	Sequence 17492, A
668	59.5	5.5	522	7	US-11-188-298-17607	Sequence 17607, A
669	59.5	5.5	543	7	US-11-087-099-1220	Sequence 1220, Ap
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671	59.5	5.5	755	7	US-11-087-099-8307	Sequence 8307, Ap
672	59.5	5.5	1056	7	US-11-044-111-22	Sequence 22, Appl
673	59.5	5.5	1159	7	US-11-113-751-27	Sequence 27, Appl
674	59.5	5.5	1200	7	US-11-207-078-612	Sequence 612, App
675	59.5	5.5	1230	7	US-11-188-298-21082	Sequence 21082, A
676	59.5	5.5	1250	6	US-10-531-036-37	Sequence 37, Appl
677	59.5	5.5	1642	7	US-11-183-261-40	Sequence 40, Appl
678	59.5	5.5	1700	6	US-10-453-372-398	Sequence 398, App
679	59.5	5.5	1700	6	US-10-453-372-412	Sequence 412, App
680	59.5	5.5	1700	6	US-10-453-372-414	Sequence 414, App
681	59.5	5.5	1700	6	US-10-453-372-416	Sequence 416, App
682	59.5	5.5	1700	6	US-10-453-372-418	Sequence 418, App
683	59.5	5.5	2145	7	US-11-087-099-10331	Sequence 10331, A
684	59.5	5.5	3396	7	US-11-183-261-39	Sequence 39, Appl
685	59.5	5.5	5689	6	US-10-784-004-709	Sequence 709, App
686	59	5.5	171	7	US-11-096-568A-2131	Sequence 2131, Ap
687	59	5.5	184	7	US-11-087-099-3811	Sequence 3811, Ap
688	59	5.5	207	7	US-11-072-512-2278	Sequence 2278, Ap
689	59	5.5	213	7	US-11-264-096-1852	Sequence 1852, Ap
690	59	5.5	231	7	US-11-096-568A-933	Sequence 933, App
691	59	5.5	237	7	US-11-087-099-5073	Sequence 5073, Ap
692	59	5.5	243	7	US-11-096-568A-17767	Sequence 17767, A
693	59	5.5	244	6	US-10-524-647-102	Sequence 102, App
694	59	5.5	244	6	US-10-524-972-86	Sequence 86, Appl
695	59	5.5	246	6	US-10-793-626-542	Sequence 542, App
696	59	5.5	246	6	US-10-793-626-814	Sequence 814, App
697	59	5.5	270	7	US-11-296-294-21	Sequence 21, Appl
698	59	5.5	275	7	US-11-188-298-6923	Sequence 6923, Ap
699	59	5.5	297	6	US-10-967-527A-17	Sequence 17, Appl
700	59	5.5	310	6	US-10-501-841-58	Sequence 58, Appl
701	59	5.5	317	7	US-11-072-512-3036	Sequence 3036, Ap
702	59	5.5	340	7	US-11-072-512-2841	Sequence 2841, Ap
703	59	5.5	342	7	US-11-094-519A-39	Sequence 39, Appl
704	59	5.5	343	7	US-11-096-568A-15572	Sequence 15572, A
705	59	5.5	352	7	US-11-096-568A-15571	Sequence 15571, A
706	59	5.5	359	7	US-11-096-568A-9000	Sequence 9000, Ap
707	59	5.5	361	7	US-11-096-568A-24045	Sequence 24045, A
708	59	5.5	384	7	US-11-188-298-11646	Sequence 11646, A
710	59	5.5	390	6	US-10-973-115B-338	Sequence 338, App
713	59	5.5	390	7	US-11-290-153-338	Sequence 338, App
714	59	5.5	408	7	US-11-288-493-54	Sequence 54, Appl
715	59	5.5	414	7	US-11-096-568A-20654	Sequence 20654, A
716	59	5.5	432	7	US-11-188-298-14127	Sequence 14127, A
717	59	5.5	480	7	US-11-087-099-6825	Sequence 6825, Ap
718	59	5.5	484	7	US-11-096-568A-22965	Sequence 22965, A
719	59	5.5	485	7	US-11-188-298-16768	Sequence 16768, A
720	59	5.5	492	7	US-11-188-298-16236	Sequence 16236, A
721	59	5.5	503	7	US-11-013-247A-4	Sequence 4, Appli
722	59	5.5	514	6	US-10-821-234-998	Sequence 998, App
723	59	5.5	543	7	US-11-096-568A-12653	Sequence 12653, A
724	59	5.5	574	7	US-11-169-041-199	Sequence 199, App
725	59	5.5	578	6	US-10-821-234-1039	Sequence 1039, Ap
726	59	5.5	578	7	US-11-087-099-359	Sequence 359, App
727	59	5.5	593	7	US-11-087-099-3921	Sequence 3921, Ap
728	59	5.5	593	7	US-11-087-099-5800	Sequence 5800, Ap
729	59	5.5	596	7	US-11-203-526-28	Sequence 28, Appl
730	59	5.5	634	7	US-11-188-298-396	Sequence 396, App
731	59	5.5	861	7	US-11-188-298-6586	Sequence 6586, Ap
732	59	5.5	863	6	US-10-793-626-2010	Sequence 2010, Ap
733	59	5.5	1236	6	US-10-912-971-8	Sequence 8, Appli

734	59	5.5	1236	7	US-11-080-991-68	Sequence 68, Appl
735	59	5.5	1275	6	US-10-724-598-49	Sequence 49, Appl
736	59	5.5	1433	7	US-11-094-519A-40	Sequence 40, Appl
737	59	5.5	1609	7	US-11-087-099-4181	Sequence 4181, Ap
738	59	5.5	1649	6	US-10-995-561-974	Sequence 974, App
739	59	5.5	1694	7	US-11-135-855-36	Sequence 36, Appl
740	59	5.5	1709	6	US-10-995-561-973	Sequence 973, App
741	59	5.5	1709	6	US-10-453-372-410	Sequence 410, App
742	59	5.5	1709	7	US-11-135-855-35	Sequence 35, Appl
743	59	5.5	2804	7	US-11-120-925-3	Sequence 3, Appli
744	58.5	5.5	154	6	US-10-330-773-763	Sequence 763, App
745	58.5	5.5	154	6	US-10-330-773-765	Sequence 765, App
746	58.5	5.5	162	7	US-11-096-568A-4283	Sequence 4283, Ap
747	58.5	5.5	179	7	US-11-096-568A-17741	Sequence 17741, A
748	58.5	5.5	189	6	US-10-995-561-643	Sequence 643, App
749	58.5	5.5	191	6	US-10-995-561-642	Sequence 642, App
750	58.5	5.5	191	7	US-11-064-774A-2	Sequence 2, Appli
751	58.5	5.5	191	7	US-11-075-400-2	Sequence 2, Appli
752	58.5	5.5	191	7	US-11-226-005-4	Sequence 4, Appli
753	58.5	5.5	191	7	US-11-129-076-9	Sequence 9, Appli
754	58.5	5.5	191	7	US-11-145-494-2	Sequence 2, Appli
755	58.5	5.5	191	7	US-11-075-047A-81	Sequence 81, Appl
756	58.5	5.5	191	7	US-11-208-288-7	Sequence 7, Appli
757	58.5	5.5	191	7	US-11-204-554-4	Sequence 4, Appli
758	58.5	5.5	209	6	US-10-995-561-640	Sequence 640, App
759	58.5	5.5	211	7	US-11-096-568A-24824	Sequence 24824, A
760	58.5	5.5	212	6	US-10-330-773-761	Sequence 761, App
761	58.5	5.5	215	6	US-10-995-561-645	Sequence 645, App
762	58.5	5.5	215	6	US-10-995-561-646	Sequence 646, App
763	58.5	5.5	215	6	US-10-921-793-64	Sequence 64, Appl
764	58.5	5.5	215	6	US-10-931-198-64	Sequence 64, Appl
765	58.5	5.5	215	6	US-10-942-042-64	Sequence 64, Appl
766	58.5	5.5	215	7	US-11-149-462-3	Sequence 3, Appli
767	58.5	5.5	220	6	US-10-506-454-1038	Sequence 1038, Ap
768	58.5	5.5	229	7	US-11-096-568A-23258	Sequence 23258, A
769	58.5	5.5	229	7	US-11-188-298-16805	Sequence 16805, A
770	58.5	5.5	232	6	US-10-995-561-641	Sequence 641, App
771	58.5	5.5	232	6	US-10-995-561-644	Sequence 644, App
772	58.5	5.5	232	7	US-11-153-880-7	Sequence 7, Appli
773	58.5	5.5	232	7	US-11-064-774A-147	Sequence 147, App
774	58.5	5.5	232	7	US-11-211-724-5	Sequence 5, Appli
775	58.5	5.5	232	7	US-11-233-119-7	Sequence 7, Appli
776	58.5	5.5	232	7	US-11-075-047A-91	Sequence 91, Appl
777	58.5	5.5	240	7	US-11-096-568A-80	Sequence 80, Appl
778	58.5	5.5	247	7	US-11-096-568A-23257	Sequence 23257, A
779	58.5	5.5	250	7	US-11-087-099-6352	Sequence 6352, Ap
780	58.5	5.5	253	7	US-11-096-568A-23256	Sequence 23256, A
781	58.5	5.5	258	6	US-10-055-877-2	Sequence 2, Appli
782	58.5	5.5	264	7	US-11-188-298-3181	Sequence 3181, Ap
783	58.5	5.5	274	7	US-11-096-568A-23575	Sequence 23575, A
784	58.5	5.5	293	7	US-11-096-568A-16425	Sequence 16425, A
785	58.5	5.5	295	7	US-11-188-298-4291	Sequence 4291, Ap
786	58.5	5.5	342	7	US-11-096-568A-7858	Sequence 7858, Ap
787	58.5	5.5	360	7	US-11-096-568A-7857	Sequence 7857, Ap
788	58.5	5.5	360	7	US-11-096-568A-15012	Sequence 15012, A
789	58.5	5.5	387	7	US-11-188-298-8419	Sequence 8419, Ap
790	58.5	5.5	387	7	US-11-188-298-9530	Sequence 9530, Ap
791	58.5	5.5	397	7	US-11-188-298-20463	Sequence 20463, A
792	58.5	5.5	398	7	US-11-190-188-5	Sequence 5, Appli
793	58.5	5.5	399	6	US-10-650-326B-23	Sequence 23, Appl
794	58.5	5.5	399	7	US-11-051-568-27	Sequence 27, Appl
795	58.5	5.5	399	7	US-11-226-555-23	Sequence 23, Appl
796	58.5	5.5	406	7	US-11-096-568A-18614	Sequence 18614, A
797	58.5	5.5	410	7	US-11-096-568A-7856	Sequence 7856, Ap
798	58.5	5.5	453	7	US-11-096-568A-18613	Sequence 18613, A
799	58.5	5.5	455	7	US-11-096-568A-18612	Sequence 18612, A
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801	58.5	5.5	536	7	US-11-096-568A-17759	Sequence 17759, A
802	58.5	5.5	566	6	US-10-491-468-21	Sequence 21, Appl
803	58.5	5.5	576	7	US-11-087-099-10787	Sequence 10787, A
804	58.5	5.5	576	7	US-11-172-740-973	Sequence 973, App
805	58.5	5.5	740	7	US-11-096-568A-14594	Sequence 14594, A
806	58.5	5.5	758	7	US-11-072-175-242	Sequence 242, App
807	58.5	5.5	807	7	US-11-207-078-5	Sequence 5, Appli
808	58.5	5.5	1119	7	US-11-188-298-642	Sequence 642, App
809	58.5	5.5	1121	7	US-11-113-751-24	Sequence 24, Appl
810	58.5	5.5	1132	7	US-11-120-544B-3	Sequence 3, Appli
811	58.5	5.5	1132	7	US-11-207-078-2	Sequence 2, Appli
812	58.5	5.5	1132	7	US-11-207-078-344	Sequence 344, App
813	58.5	5.5	1132	7	US-11-219-419-2	Sequence 2, Appli
814	58.5	5.5	1154	7	US-11-207-078-611	Sequence 611, App
815	58.5	5.5	1166	7	US-11-188-298-11021	Sequence 11021, A
817	58.5	5.5	1184	6	US-10-973-115B-412	Sequence 412, App
820	58.5	5.5	1184	7	US-11-290-153-412	Sequence 412, App
821	58.5	5.5	1189	7	US-11-207-078-613	Sequence 613, App
822	58.5	5.5	1285	7	US-11-207-078-600	Sequence 600, App
823	58.5	5.5	1394	7	US-11-188-298-13354	Sequence 13354, A
824	58.5	5.5	1407	7	US-11-207-078-628	Sequence 628, App
825	58.5	5.5	1493	7	US-11-004-057-21	Sequence 21, Appl
826	58.5	5.5	1519	7	US-11-182-016-5	Sequence 5, Appli
827	58.5	5.5	1566	7	US-11-188-298-9022	Sequence 9022, Ap
828	58.5	5.5	1663	6	US-10-055-877-148	Sequence 148, App
829	58.5	5.5	3333	6	US-10-766-317-4	Sequence 4, Appli
830	58.5	5.5	3635	7	US-11-019-711-47	Sequence 47, Appl
831	58.5	5.5	3655	7	US-11-075-185-5	Sequence 5, Appli
832	58.5	5.5	4374	7	US-11-128-572-2	Sequence 2, Appli
833	58	5.4	85	6	US-10-966-648-6	Sequence 6, Appli
834	58	5.4	85	7	US-11-126-772-6	Sequence 6, Appli
835	58	5.4	103	6	US-10-966-648-27	Sequence 27, Appl
836	58	5.4	112	6	US-10-966-648-2	Sequence 2, Appli
837	58	5.4	112	7	US-11-072-512-3778	Sequence 3778, Ap
838	58	5.4	112	7	US-11-126-772-2	Sequence 2, Appli
839	58	5.4	114	7	US-11-072-512-3339	Sequence 3339, Ap
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841	58	5.4	144	7	US-11-188-298-13642	Sequence 13642, A
842	58	5.4	148	7	US-11-096-568A-10185	Sequence 10185, A
843	58	5.4	164	7	US-11-072-512-2888	Sequence 2888, Ap
844	58	5.4	175	7	US-11-096-568A-10183	Sequence 10183, A
845	58	5.4	204	7	US-11-087-099-12123	Sequence 12123, A
846	58	5.4	204	7	US-11-188-298-16921	Sequence 16921, A
847	58	5.4	218	7	US-11-188-298-3633	Sequence 3633, Ap
848	58	5.4	219	7	US-11-096-568A-18567	Sequence 18567, A
849	58	5.4	221	7	US-11-096-568A-21257	Sequence 21257, A
850	58	5.4	237	6	US-10-330-773-9	Sequence 9, Appli
851	58	5.4	264	7	US-11-096-568A-30608	Sequence 30608, A
852	58	5.4	281	7	US-11-096-568A-18279	Sequence 18279, A
853	58	5.4	290	7	US-11-013-592-2	Sequence 2, Appli
854	58	5.4	306	7	US-11-188-298-4837	Sequence 4837, Ap
855	58	5.4	310	7	US-11-087-099-11274	Sequence 11274, A
856	58	5.4	320	7	US-11-096-568A-18072	Sequence 18072, A
857	58	5.4	320	7	US-11-096-568A-18278	Sequence 18278, A
858	58	5.4	335	7	US-11-087-099-3023	Sequence 3023, Ap
859	58	5.4	345	7	US-11-087-099-5483	Sequence 5483, Ap
860	58	5.4	352	7	US-11-096-568A-4744	Sequence 4744, Ap
861	58	5.4	355	7	US-11-188-298-2022	Sequence 2022, Ap
862	58	5.4	355	7	US-11-188-298-7348	Sequence 7348, Ap
863	58	5.4	355	7	US-11-188-298-22014	Sequence 22014, A
864	58	5.4	357	7	US-11-188-298-9062	Sequence 9062, Ap
865	58	5.4	357	7	US-11-188-298-12873	Sequence 12873, A
866	58	5.4	360	7	US-11-087-099-11236	Sequence 11236, A
867	58	5.4	363	7	US-11-092-140-39	Sequence 39, Appl
868	58	5.4	363	7	US-11-096-568A-4743	Sequence 4743, Ap
869	58	5.4	363	7	US-11-096-568A-22297	Sequence 22297, A
870	58	5.4	364	7	US-11-096-568A-15334	Sequence 15334, A
871	58	5.4	380	6	US-10-506-454-898	Sequence 898, App
872	58	5.4	381	7	US-11-188-298-15196	Sequence 15196, A
873	58	5.4	390	7	US-11-096-568A-15333	Sequence 15333, A
874	58	5.4	412	7	US-11-188-298-21806	Sequence 21806, A
875	58	5.4	421	7	US-11-188-298-7320	Sequence 7320, Ap
876	58	5.4	433	6	US-10-506-454-922	Sequence 922, App
877	58	5.4	464	7	US-11-087-099-7240	Sequence 7240, Ap
878	58	5.4	483	6	US-10-467-657-2894	Sequence 2894, Ap
879	58	5.4	494	7	US-11-188-298-3608	Sequence 3608, Ap
880	58	5.4	494	7	US-11-188-298-10180	Sequence 10180, A
881	58	5.4	555	7	US-11-024-959-270	Sequence 270, App
882	58	5.4	614	7	US-11-072-512-3276	Sequence 3276, Ap

883	58	5.4	678	7	US-11-072-512-3295	Sequence 3295, Ap
884	58	5.4	802	6	US-10-510-386-2	Sequence 2, Appli
885	58	5.4	935	7	US-11-188-298-20909	Sequence 20909, A
886	58	5.4	1051	6	US-10-330-773-268	Sequence 268, App
887	58	5.4	1212	6	US-10-979-095-9	Sequence 9, Appli
888	58	5.4	1346	7	US-11-060-005-2	Sequence 2, Appli
889	58	5.4	1596	7	US-11-060-005-4	Sequence 4, Appli
890	57.5	5.4	122	6	US-10-667-295-177	Sequence 177, App
891	57.5	5.4	163	7	US-11-188-298-7696	Sequence 7696, Ap
892	57.5	5.4	169	6	US-10-821-234-1234	Sequence 1234, Ap
893	57.5	5.4	173	7	US-11-096-568A-19799	Sequence 19799, A
894	57.5	5.4	175	7	US-11-188-298-8130	Sequence 8130, Ap
895	57.5	5.4	176	7	US-11-072-512-2419	Sequence 2419, Ap
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897	57.5	5.4	203	7	US-11-096-568A-22000	Sequence 22000, A
898	57.5	5.4	214	7	US-11-188-298-6258	Sequence 6258, Ap
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900	57.5	5.4	265	7	US-11-096-568A-16359	Sequence 16359, A
901	57.5	5.4	266	7	US-11-188-298-15832	Sequence 15832, A
902	57.5	5.4	270	6	US-10-821-234-1348	Sequence 1348, Ap
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904	57.5	5.4	298	7	US-11-096-568A-21999	Sequence 21999, A
905	57.5	5.4	313	7	US-11-096-568A-25916	Sequence 25916, A
906	57.5	5.4	319	7	US-11-096-568A-25915	Sequence 25915, A
907	57.5	5.4	321	7	US-11-188-298-16892	Sequence 16892, A
908	57.5	5.4	331	7	US-11-096-568A-25219	Sequence 25219, A
909	57.5	5.4	333	7	US-11-087-099-6214	Sequence 6214, Ap
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913	57.5	5.4	398	7	US-11-188-298-2155	Sequence 2155, Ap
914	57.5	5.4	404	7	US-11-072-175-194	Sequence 194, App
915	57.5	5.4	408	7	US-11-188-298-7393	Sequence 7393, Ap
916	57.5	5.4	423	7	US-11-096-568A-25217	Sequence 25217, A
917	57.5	5.4	424	7	US-11-096-568A-22088	Sequence 22088, A
918	57.5	5.4	447	6	US-10-467-657-4034	Sequence 4034, Ap
919	57.5	5.4	447	6	US-10-467-657-7050	Sequence 7050, Ap
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921	57.5	5.4	525	7	US-11-138-642-2	Sequence 2, Appli
922	57.5	5.4	525	7	US-11-138-882-2	Sequence 2, Appli
923	57.5	5.4	525	7	US-11-138-757-3	Sequence 3, Appli
924	57.5	5.4	550	7	US-11-072-512-3416	Sequence 3416, Ap
925	57.5	5.4	556	7	US-11-072-512-3914	Sequence 3914, Ap
926	57.5	5.4	560	7	US-11-096-568A-23990	Sequence 23990, A
927	57.5	5.4	579	7	US-11-087-099-1986	Sequence 1986, Ap
928	57.5	5.4	579	7	US-11-172-740-970	Sequence 970, App
929	57.5	5.4	601	6	US-10-330-773-379	Sequence 379, App
930	57.5	5.4	607	7	US-11-188-298-1216	Sequence 1216, Ap
931	57.5	5.4	611	7	US-11-079-463-10057	Sequence 10057, A
932	57.5	5.4	613	7	US-11-087-099-5132	Sequence 5132, Ap
933	57.5	5.4	650	6	US-10-895-011-2	Sequence 2, Appli
934	57.5	5.4	650	6	US-10-722-371-2	Sequence 2, Appli
935	57.5	5.4	650	7	US-11-038-372-2	Sequence 2, Appli
936	57.5	5.4	729	7	US-11-130-821-4	Sequence 4, Appli
937	57.5	5.4	761	6	US-10-204-639-19	Sequence 19, Appl
938	57.5	5.4	792	7	US-11-200-296B-65	Sequence 65, Appl
939	57.5	5.4	898	7	US-11-188-298-9833	Sequence 9833, Ap
940	57.5	5.4	903	7	US-11-124-367A-450	Sequence 450, App
941	57.5	5.4	1114	6	US-10-469-469-277	Sequence 277, App
942	57.5	5.4	1197	6	US-10-055-877-8	Sequence 8, Appli
943	57.5	5.4	1247	6	US-10-055-877-10	Sequence 10, Appl
944	57.5	5.4	1349	6	US-10-531-036-34	Sequence 34, Appl
945	57.5	5.4	1823	6	US-10-995-561-988	Sequence 988, App
946	57.5	5.4	2102	6	US-10-995-561-990	Sequence 990, App
947	57.5	5.4	2108	6	US-10-995-561-989	Sequence 989, App
948	57.5	5.4	2157	6	US-10-995-561-991	Sequence 991, App
949	57	5.3	132	7	US-11-072-512-3844	Sequence 3844, Ap
950	57	5.3	151	7	US-11-072-512-2708	Sequence 2708, Ap
951	57	5.3	153	6	US-10-506-454-388	Sequence 388, App
952	57	5.3	168	6	US-10-467-657-1878	Sequence 1878, Ap
953	57	5.3	185	7	US-11-188-298-9775	Sequence 9775, Ap
954	57	5.3	188	7	US-11-096-568A-23885	Sequence 23885, A
955	57	5.3	200	6	US-10-667-295-180	Sequence 180, App
956	57	5.3	202	7	US-11-098-662-8	Sequence 8, Appli
957	57	5.3	202	7	US-11-193-955-8	Sequence 8, Appli
958	57	5.3	202	7	US-11-266-626-9	Sequence 9, Appli
959	57	5.3	209	7	US-11-072-512-1978	Sequence 1978, Ap
960	57	5.3	231	7	US-11-096-568A-327	Sequence 327, App
961	57	5.3	231	7	US-11-096-568A-329	Sequence 329, App
962	57	5.3	238	7	US-11-096-568A-31912	Sequence 31912, A
963	57	5.3	261	7	US-11-096-568A-13815	Sequence 13815, A
964	57	5.3	264	7	US-11-072-512-2242	Sequence 2242, Ap
965	57	5.3	290	7	US-11-096-568A-15287	Sequence 15287, A
966	57	5.3	298	7	US-11-172-740-736	Sequence 736, App
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968	57	5.3	319	7	US-11-096-568A-10469	Sequence 10469, A
969	57	5.3	324	7	US-11-096-568A-10468	Sequence 10468, A
970	57	5.3	327	6	US-10-506-454-33	Sequence 33, Appl
971	57	5.3	331	7	US-11-185-877-8	Sequence 8, Appli
972	57	5.3	338	7	US-11-096-568A-13588	Sequence 13588, A
973	57	5.3	345	7	US-11-096-568A-13587	Sequence 13587, A
974	57	5.3	360	7	US-11-194-246-307	Sequence 307, App
975	57	5.3	360	7	US-11-087-099-5803	Sequence 5803, Ap
976	57	5.3	366	7	US-11-087-099-11191	Sequence 11191, A
977	57	5.3	371	7	US-11-096-568A-16234	Sequence 16234, A
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979	57	5.3	388	7	US-11-087-099-8387	Sequence 8387, Ap
980	57	5.3	388	7	US-11-096-568A-13586	Sequence 13586, A
981	57	5.3	388	7	US-11-079-463-6897	Sequence 6897, Ap
982	57	5.3	390	7	US-11-096-568A-19403	Sequence 19403, A
983	57	5.3	424	7	US-11-096-568A-24510	Sequence 24510, A
984	57	5.3	437	7	US-11-087-099-6573	Sequence 6573, Ap
985	57	5.3	441	7	US-11-174-150-48	Sequence 48, Appl
986	57	5.3	450	6	US-10-506-454-1537	Sequence 1537, Ap
987	57	5.3	458	7	US-11-096-568A-21678	Sequence 21678, A
988	57	5.3	466	7	US-11-110-082-33	Sequence 33, Appl
989	57	5.3	479	7	US-11-096-568A-12989	Sequence 12989, A
990	57	5.3	490	7	US-11-188-298-4872	Sequence 4872, Ap
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992	57	5.3	506	7	US-11-188-298-2861	Sequence 2861, Ap
993	57	5.3	537	7	US-11-188-298-9322	Sequence 9322, Ap
994	57	5.3	564	7	US-11-124-367A-263	Sequence 263, App
995	57	5.3	643	7	US-11-096-568A-27797	Sequence 27797, A
996	57	5.3	647	6	US-10-501-841-121	Sequence 121, App
997	57	5.3	654	7	US-11-087-099-10545	Sequence 10545, A
998	57	5.3	681	7	US-11-072-512-3586	Sequence 3586, Ap
999	57	5.3	835	7	US-11-186-283-2	Sequence 2, Appli
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1001	57	5.3	917	7	US-11-188-298-3936	Sequence 3936, Ap
1002	57	5.3	955	7	US-11-188-298-21615	Sequence 21615, A
1004	57	5.3	1006	7	US-11-203-251A-90	Sequence 90, Appl
1005	57	5.3	1073	7	US-11-096-568A-31289	Sequence 31289, A
1006	57	5.3	1122	7	US-11-096-568A-31288	Sequence 31288, A
1007	57	5.3	1206	7	US-11-096-568A-31287	Sequence 31287, A
1008	57	5.3	1270	6	US-10-501-841-120	Sequence 120, App
1009	57	5.3	1363	7	US-11-043-693-32	Sequence 32, Appl
1010	57	5.3	1995	7	US-11-069-834-60	Sequence 60, Appl
1011	57	5.3	4419	6	US-10-821-234-1155	Sequence 1155, Ap
1012	57	5.3	7968	7	US-11-186-731-5	Sequence 5, Appli
1013	56.5	5.3	141	7	US-11-264-096-1084	Sequence 1084, Ap
1014	56.5	5.3	147	7	US-11-072-512-2835	Sequence 2835, Ap
1015	56.5	5.3	176	7	US-11-264-096-2029	Sequence 2029, Ap
1016	56.5	5.3	178	7	US-11-172-740-1308	Sequence 1308, Ap
1017	56.5	5.3	229	7	US-11-096-568A-26892	Sequence 26892, A
1018	56.5	5.3	255	7	US-11-096-568A-9816	Sequence 9816, Ap
1019	56.5	5.3	270	7	US-11-096-568A-9666	Sequence 9666, Ap
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1024	56.5	5.3	330	7	US-11-072-512-1985	Sequence 1985, Ap
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1031	56.5	5.3	377	7	US-11-146-428-72	Sequence 72, Appl
1032	56.5	5.3	378	7	US-11-096-568A-26057	Sequence 26057, A
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1034	56.5	5.3	393	7	US-11-096-568A-26989	Sequence 26989, A
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1036	56.5	5.3	411	7	US-11-096-568A-10858	Sequence 10858, A
1037	56.5	5.3	413	5	US-09-978-360A-710	Sequence 710, App
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1042	56.5	5.3	441	7	US-11-087-084-22	Sequence 22, Appl
1043	56.5	5.3	441	7	US-11-087-085-22	Sequence 22, Appl
1044	56.5	5.3	452	7	US-11-188-298-8926	Sequence 8926, Ap
1045	56.5	5.3	454	7	US-11-096-568A-20795	Sequence 20795, A
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1047	56.5	5.3	478	7	US-11-096-568A-11893	Sequence 11893, A
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1056	56.5	5.3	543	7	US-11-055-822-494	Sequence 494, App
1057	56.5	5.3	543	7	US-11-055-822-874	Sequence 874, App
1058	56.5	5.3	558	7	US-11-096-568A-26217	Sequence 26217, A
1059	56.5	5.3	565	7	US-11-096-568A-12973	Sequence 12973, A
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1061	56.5	5.3	579	7	US-11-172-740-971	Sequence 971, App
1062	56.5	5.3	593	7	US-11-188-298-13670	Sequence 13670, A
1063	56.5	5.3	600	7	US-11-055-822-228	Sequence 228, App
1064	56.5	5.3	600	7	US-11-055-822-716	Sequence 716, App
1065	56.5	5.3	600	7	US-11-055-822-758	Sequence 758, App
1066	56.5	5.3	600	7	US-11-239-674-106	Sequence 106, App
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1087	56.5	5.3	745	7	US-11-055-822-756	Sequence 756, App
1088	56.5	5.3	745	7	US-11-168-476-2	Sequence 2, Appli
1089	56.5	5.3	745	7	US-11-239-674-104	Sequence 104, App
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1318	55.5	5.2	1342	7	US-11-149-003-24	Sequence 24, Appl
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1335	55	5.1	217	7	US-11-166-340-3	Sequence 3, Appli
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1338	55	5.1	220	7	US-11-054-515-3233	Sequence 3233, Ap
1339	55	5.1	220	7	US-11-096-568A-21946	Sequence 21946, A
1340	55	5.1	220	7	US-11-266-444-3233	Sequence 3233, Ap

1341	55	5.1	220	7	US-11-232-439-178	Sequence 178, App
1342	55	5.1	234	7	US-11-096-568A-9312	Sequence 9312, Ap
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1344	55	5.1	239	7	US-11-096-568A-621	Sequence 621, App
1345	55	5.1	239	7	US-11-172-740-2230	Sequence 2230, Ap
1346	55	5.1	244	7	US-11-096-568A-620	Sequence 620, App
1347	55	5.1	249	7	US-11-264-096-1757	Sequence 1757, Ap
1348	55	5.1	249	7	US-11-264-096-1759	Sequence 1759, Ap
1349	55	5.1	260	7	US-11-087-099-5033	Sequence 5033, Ap
1350	55	5.1	266	7	US-11-096-568A-17804	Sequence 17804, A
1351	55	5.1	280	7	US-11-096-568A-23041	Sequence 23041, A
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1354	55	5.1	306	7	US-11-188-298-10056	Sequence 10056, A
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1373	55	5.1	367	7	US-11-096-568A-18566	Sequence 18566, A
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1381	55	5.1	412	7	US-11-096-568A-21979	Sequence 21979, A
1382	55	5.1	431	7	US-11-096-568A-9649	Sequence 9649, Ap
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1388	55	5.1	475	7	US-11-087-099-2233	Sequence 2233, Ap
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1394	55	5.1	491	7	US-11-024-959-363	Sequence 363, App
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1412	55	5.1	641	7	US-11-094-519A-29	Sequence 29, Appl
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1415	55	5.1	702	7	US-11-096-568A-14646	Sequence 14646, A
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1437	55	5.1	2351	7	US-11-244-087-3	Sequence 3, Appli
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1497	54.5	5.1	395	7	US-11-172-740-435	Sequence 435, App
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Job time : 39 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2006, 23:48:28 ; Search time 3875 Seconds
(without alignments)
2378.595 Million cell updates/sec

Title: US-09-854-280-3
Perfect score: 1073
Sequence: 1 MTLLPGLLFLTWLHTCLAHH.....FHTEFIHVPVGCTCVLPRSV 197

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	1063	99.1	588	11	DQ030711	DQ030711 Homo sapi
	2	1059	98.7	1027	4	BC069410	BC069410 Homo sapi
	3	905	84.3	586	11	DQ030712	DQ030712 Pan trogl
	4	543	50.6	466	5	BX281422	BX281422 BX281422
c	5	318	29.6	669	10	AG139411	AG139411 Pan trogl
	6	209	19.5	664	8	DN989597	DN989597 TC108206
	7	197.5	18.4	728	7	CV112574	CV112574 AGENCOURT
	8	192.5	17.9	441	1	AI275406	AI275406 ql63c10.x
	9	192.5	17.9	600	6	CA526593	CA526593 8013-66 M
	10	187.5	17.5	718	3	BI561289	BI561289 603256441
	11	187.5	17.5	836	3	BI828970	BI828970 603074846
	12	186.5	17.4	666	6	CB418976	CB418976 591812 MA
	13	183.5	17.1	742	8	DT096353	DT096353 JGI_ANNN2
c	14	179	16.7	627	5	BW006143	BW006143 BW006143
	15	179	16.7	649	5	BW035020	BW035020 BW035020
c	16	179	16.7	663	5	BW005398	BW005398 BW005398
	17	179	16.7	669	5	BW055597	BW055597 BW055597
	18	179	16.7	673	5	BW034283	BW034283 BW034283
c	19	179	16.7	737	5	BW022098	BW022098 BW022098
c	20	179	16.7	737	5	BW026536	BW026536 BW026536
	21	179	16.7	754	8	CX960534	CX960534 JGI_CAAO1
	22	177.5	16.5	524	1	AI430337	AI430337 mf68b10.y
	23	177.5	16.5	622	7	CN232484	CN232484 WLB074F04
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	25	175.5	16.4	526	5	BX517868	BX517868 BX517868
	26	175	16.3	715	6	CD639406	CD639406 AGENCOURT
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	28	173.5	16.2	870	3	BI413156	BI413156 602990024
	29	173	16.1	579	1	AA763404	AA763404 vw53h08.r
	30	173	16.1	1026	6	CB196478	CB196478 AGENCOURT
	31	172	16.0	891	6	CB566097	CB566097 AGENCOURT
	32	171	15.9	625	6	CD559601	CD559601 AGENCOURT
c	33	169.5	15.8	608	6	CD559447	CD559447 AGENCOURT
	34	169	15.8	534	11	DQ036975	DQ036975 Homo sapi
	35	169	15.8	534	11	DQ036976	DQ036976 Pan trogl
	36	168.5	15.7	522	10	AY417008	AY417008 Mus muscu
	37	168.5	15.7	569	6	CF740872	CF740872 UI-M-HC0-
c	38	168	15.7	684	6	CB325148	CB325148 UI-R-DZ0-
	39	166	15.5	749	4	AK003506	AK003506 Mus muscu
c	40	165.5	15.4	633	6	CB326948	CB326948 UI-R-FS0-
c	41	165.5	15.4	719	6	CB323112	CB323112 UI-R-DY0-
c	42	164.5	15.3	561	3	BQ209760	BQ209760 UI-R-DZ1-
	43	164	15.3	717	3	BI408737	BI408737 602964519
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	45	162	15.1	476	6	CB432107	CB432107 608210 MA
	46	162	15.1	721	6	CB205000	CB205000 AGENCOURT
	47	161.5	15.1	626	6	CD559597	CD559597 AGENCOURT
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	51	161	15.0	591	6	CD559596	CD559596 AGENCOURT
	52	161	15.0	592	6	CD559595	CD559595 AGENCOURT
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c	55	161	15.0	607	6	CD559441	CD559441 AGENCOURT
c	56	161	15.0	607	6	CD559446	CD559446 AGENCOURT
c	57	161	15.0	609	6	CD559443	CD559443 AGENCOURT
	58	161	15.0	620	7	CK130280	CK130280 AGENCOURT
	59	161	15.0	624	6	CD559600	CD559600 AGENCOURT
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	61	159.5	14.9	629	3	BM826445	BM826445 K-EST0098
c	62	159	14.8	633	2	BF682066	BF682066 602117154
c	63	159	14.8	703	5	BU753501	BU753501 UI-1-BC1-
	64	158.5	14.8	514	10	CG633935	CG633935 OST354225
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	68	156.5	14.6	678	8	CX148911	CX148911 1289050 N
c	69	156.5	14.6	707	8	CX148912	CX148912 1289051 N
c	70	156.5	14.6	707	8	CX149536	CX149536 1289749 N
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c	72	156	14.5	533	3	BQ211497	BQ211497 UI-R-DY1-
	73	156	14.5	659	7	CK655027	CK655027 AGENCOURT
	74	155	14.4	441	10	AY409000	AY409000 Pan trogl
	75	154.5	14.4	543	10	AY417006	AY417006 Homo sapi
c	76	154.5	14.4	590	2	BF510968	BF510968 UI-H-BI4-
	77	154	14.4	592	6	CD559598	CD559598 AGENCOURT
c	78	154	14.4	609	6	CD559444	CD559444 AGENCOURT
c	79	153.5	14.3	432	2	BE108127	BE108127 UI-R-CA0-
c	80	153.5	14.3	511	2	BF409208	BF409208 UI-R-BT1-

	81	153	14.3	662	2	BE307772 BE307772 601097115
c	82	152.5	14.2	490	7	CN544209 UI-R-DY1-
	83	152.5	14.2	595	6	CF366793 CF366793 841494 MA
c	84	152.5	14.2	596	6	CA413832 CA413832 UI-H-EZ0-
	85	152.5	14.2	731	6	CF523193 AGENCOURT
	86	152	14.2	398	7	CR568241 CR568241 CR568241
	87	152	14.2	704	7	CK654312 CK654312 AGENCOURT
	88	152	14.2	710	5	BX711802 BX711802
	89	152	14.2	753	6	CF219120 CF219120 AGENCOURT
	90	152	14.2	772	8	CX972860 CX972860 JGI_CAAP7
	91	152	14.2	827	8	CX983520 CX983520 JGI_CAAP1
	92	152	14.2	862	8	CX968241 CX968241 JGI_CAAP2
	93	152	14.2	875	8	DR854059 DR854059 JGI_CABG1
	94	152	14.2	877	8	CX383794 CX383794 JGI_XZT63
	95	152	14.2	884	8	DR857682 DR857682 JGI_CABG3
	96	152	14.2	886	5	BX741494 BX741494 BX741494
	97	152	14.2	887	5	BX741492 BX741492 BX741492
	98	152	14.2	910	5	BX712262 BX712262 BX712262
	99	151.5	14.1	428	6	CB050776 CB050776 NISC_gj19
	100	151	14.1	420	8	W88186 W88186 mf68b10.r1
	101	151	14.1	691	2	BF682781 BF682781 602117154
c	102	150.5	14.0	504	1	AI645992 AI645992 vw53h08.x
	103	150.5	14.0	590	5	BX302846 BX302846 BX302846
c	104	149.5	13.9	568	5	BQ574994 BQ574994 UI-H-EZ1-
	105	149.5	13.9	722	9	BH277943 BH277943 CH230-24D
	106	149.5	13.9	1172	4	AK040420 AK040420 Mus muscu
	107	148.5	13.8	444	10	AY409001 AY409001 Mus muscu
	108	148.5	13.8	660	2	BB635986 BB635986 BB635986
	109	148.5	13.8	811	6	CD099069 CD099069 AGENCOURT
	110	147.5	13.7	474	5	BW051217 BW051217 BW051217
c	111	147.5	13.7	502	2	BF408277 BF408277 UI-R-BJ2-
c	112	144	13.4	468	1	AA780147 AA780147 af37c02.s
c	113	144	13.4	600	8	DN109583 DN109583 1107185 M
	114	144	13.4	600	8	DN109934 DN109934 1107569 M
c	115	144	13.4	812	5	BW004858 BW004858 BW004858
c	116	143.5	13.4	366	1	AA960023 AA960023 vw53h08.s
c	117	143.5	13.4	583	6	CF368206 CF368206 852830 MA
	118	143.5	13.4	587	5	BX668894 BX668894 BX668894
c	119	142.5	13.3	373	1	AI867949 AI867949 wb90b08.x
c	120	142.5	13.3	405	1	AI375735 AI375735 ta64c02.x
c	121	142.5	13.3	467	1	AI370793 AI370793 ta58a04.x
	122	142	13.2	839	7	CK019128 CK019128 AGENCOURT
	123	142	13.2	842	7	CO812710 CO812710 AGENCOURT
c	124	141.5	13.2	369	2	BI274883 BI274883 UI-R-CW0-
	125	141.5	13.2	391	5	BW442148 BW442148 BW442148
	126	141.5	13.2	811	6	CB199287 CB199287 AGENCOURT
c	127	139.5	13.0	396	1	AA680405 AA680405 zi38h02.s
	128	139.5	13.0	499	8	W83241 W83241 mf23g06.r1
c	129	139.5	13.0	680	5	BU475623 BU475623 603843432
	130	138.5	12.9	319	11	DQ048062 DQ048062 Homo sapi
	131	138.5	12.9	319	11	DQ048063 DQ048063 Pan trogl
	132	136.5	12.7	889	11	CNS03HZZ AL244952 Tetraodon
	133	135.5	12.6	497	1	AA044549 AA044549 mj12c03.r
	134	135.5	12.6	811	3	BI601695 BI601695 603249937
	135	134	12.5	437	8	W89980 W89980 mf39h11.r1
	136	134	12.5	1015	1	AV087488 AV087488 AV087488
	137	132.5	12.3	482	10	CG666110 OST455757
	138	132.5	12.3	487	10	CG522134 OST91289
	139	132.5	12.3	496	10	CG623938 OST326695
	140	132.5	12.3	497	10	CG620814 OST318326
	141	132.5	12.3	512	10	CG640273 OST372828
	142	132.5	12.3	520	10	CG647579 OST397369
	143	132.5	12.3	532	10	CG530477 OST112200
	144	132.5	12.3	556	10	CG638056 OST366719
c	145	132	12.3	755	7	CJ383802 CJ383802
c	146	132	12.3	771	7	CJ384102 CJ384102
	147	132	12.3	927	11	CNS04KBZ AL294632 Tetraodon
	148	131.5	12.3	488	8	W87101 W87101 mf38e01.r1
	149	131.5	12.3	616	5	BW033416 BW033416 BW033416
	150	130.5	12.2	439	10	CG633928 CG633928 OST354191
	151	130.5	12.2	607	5	BW705967 BW705967 BW705967
	152	129.5	12.1	615	5	BW048414 BW048414 BW048414
	153	129.5	12.1	637	5	BW030987 BW030987 BW030987
	154	128	11.9	460	10	AY417007 AY417007 Pan trogl
	155	128	11.9	592	9	AQ426529 AQ426529 CITBI-E1-
	156	127.5	11.9	514	10	CG591420 CG591420 OST245959
c	157	126	11.7	622	8	DT096352 DT096352 JGI_ANNN2
	158	126	11.7	717	7	CJ413102 CJ413102 CJ413102
c	159	126	11.7	817	7	CJ429465 CJ429465 CJ429465
	160	124.5	11.6	452	10	CG506565 CG506565 OST56172
	161	124.5	11.6	469	1	AA015563 AA015563 mi61d10.r
	162	123.5	11.5	512	10	CG660447 CG660447 OST440201
	163	123.5	11.5	836	7	CN237189 CN237189 WLB116H10
c	164	122.5	11.4	397	1	AA443286 AA443286 zw87h02.s
	165	122.5	11.4	708	5	BW052287 BW052287 BW052287
	166	121.5	11.3	474	5	BX919226 BX919226 BX919226
	167	121.5	11.3	479	5	BX925466 BX925466 BX925466
	168	121.5	11.3	671	5	BX082888 BX082888 BX082888
	169	120	11.2	587	3	BP025580 BP025580 BP025580
	170	119	11.1	435	9	BZ097034 BZ097034 CH230-142
	171	117.5	11.0	1017	10	CNS01XI4 AL171733 Tetraodon
	172	115	10.7	506	10	CG650427 CG650427 OST407543
	173	115	10.7	569	3	BP010394 BP010394 BP010394
	174	115	10.7	4030	4	AK045928 AK045928 Mus muscu
c	175	113.5	10.6	460	8	W74664 W74664 zd56d05.s1
	176	111.5	10.4	463	10	CG603777 CG603777 OST278818
	177	111.5	10.4	726	5	BX727236 BX727236 BX727236
	178	111	10.3	543	3	BM719497 BM719497 UI-E-EJ1-
	179	111	10.3	615	3	BM724859 BM724859 UI-E-EJ0-
c	180	111	10.3	620	3	BM682816 BM682816 UI-E-EJ1-
c	181	111	10.3	623	5	BU741486 BU741486 UI-E-EJ0-
	182	110.5	10.3	294	10	CW917017 CW917017 CMHD-GT_1
	183	110.5	10.3	583	5	BY703767 BY703767 BY703767
c	184	110.5	10.3	882	2	BF677715 BF677715 602085408
c	185	110	10.3	415	6	CB397570 CB397570 OSTR192F7
c	186	110	10.3	415	6	CB397622 CB397622 OSTR192F7
	187	110	10.3	420	6	CB401283 CB401283 OSTF192F7
	188	110	10.3	539	7	CR927646 CR927646 CR927646
	189	108.5	10.1	330	10	CG487489 CG487489 OST23008
	190	108.5	10.1	575	10	CG564078 CG564078 OST187894
	191	108	10.1	344	2	BG609875 BG609875 324181 MA
	192	108	10.1	489	2	BE680108 BE680108 df61h10.y
	193	108	10.1	1406	2	BE871984 BE871984 601448034
	194	108	10.1	1564	3	BQ051951 BQ051951 AGENCOURT
	195	107.5	10.0	511	1	AU196616 AU196616 AU196616
c	196	107	10.0	663	6	CF753271 CF753271 EST-Conti
	197	106.5	9.9	683	8	CX854436 CX854436 JGI_CAAL9
	198	106.5	9.9	913	5	BQ670380 BQ670380 AGENCOURT
c	199	106	9.9	900	9	CC407080 CC407080 PUHIP43TD
c	200	105.5	9.8	467	1	AJ684641 AJ684641 AJ684641
c	201	105.5	9.8	2000	4	AK017743 AK017743 Mus muscu
c	202	105.5	9.8	2079	4	AK044559 AK044559 Mus muscu
c	203	105.5	9.8	2171	4	BC021810 BC021810 Mus muscu
	204	105.5	9.8	2288	2	BF106959 BF106959 601823256
c	205	105	9.8	724	1	AA698300 AA698300 HL04239.5
c	206	105	9.8	817	7	CR456182 CR456182 CR456182
c	207	105	9.8	930	5	BX712263 BX712263 BX712263
c	208	105	9.8	1265	5	BU539369 BU539369 AGENCOURT
c	209	104.5	9.7	788	2	BG746523 BG746523 602703822
	210	104.5	9.7	832	9	BZ656233 BZ656233 OGAOK20TM
	211	104.5	9.7	910	2	BG966609 BG966609 602834447
c	212	104	9.7	557	2	BE235532 BE235532 143055 MA
	213	104	9.7	604	7	CR369979 CR369979 CR369979
	214	104	9.7	848	10	CL936887 CL936887 OA_ABa004
c	215	103.5	9.6	505	9	CC721723 CC721723 OGWHL91TV
c	216	103.5	9.6	575	2	BG366316 BG366316 HVSMEi000
	217	103.5	9.6	983	10	CZ371834 CZ371834 ZMMBF0127
c	218	103	9.6	364	9	AQ901927 AQ901927 LMAJFV1_1
c	219	103	9.6	471	7	CO600707 CO600707 DG8-207E2
c	220	103	9.6	520	7	CO598691 CO598691 DG8-169h9
	221	103	9.6	618	7	CN066444 CN066444 G08_Ag2_p
	222	103	9.6	894	2	BF135759 BF135759 601781124
c	223	102.5	9.6	347	1	AI375503 AI375503 tc30h08.x
c	224	102.5	9.6	584	3	BI346103 BI346103 375124 MA
c	225	102.5	9.6	649	1	AJ448553 AJ448553 AJ448553
c	226	102.5	9.6	667	7	CJ376999 CJ376999 CJ376999

c 227	102.5	9.6	687	1	AJ448545	AJ448545 AJ448545
228	102.5	9.6	1015	5	BU438679	BU438679 603210205
229	102.5	9.6	2298	7	CN248187	CN248187 EST014089
230	102	9.5	641	7	CN065188	CN065188 C05_Ag2_p
c 231	102	9.5	666	1	AI107415	AI107415 GH04583.5
232	102	9.5	680	5	BX106288	BX106288 BX106288
c 233	102	9.5	869	10	CG009225	CG009225 ZUAHQ24TV
c 234	102	9.5	898	2	BG282024	BG282024 602402730
c 235	102	9.5	1015	2	BG753749	BG753749 602732954
236	101.5	9.5	642	7	CK604581	CK604581 UT01293.5
c 237	101.5	9.5	652	2	BE430844	BE430844 SUN006.D1
238	101.5	9.5	679	7	CK604917	CK604917 UT01536.5
239	101.5	9.5	690	7	CK604843	CK604843 UT01480.5
240	101.5	9.5	723	1	AW323707	AW323707 uo75f04.y
241	101.5	9.5	828	3	BI772466	BI772466 603058624
242	101.5	9.5	1078	2	BG175765	BG175765 602335168
c 243	101.5	9.5	1929	11	DQ046439	DQ046439 Homo sapi
244	101	9.4	484	10	CG533022	CG533022 OST117812
245	101	9.4	651	3	BM998205	BM998205 UI-H-DT1-
246	101	9.4	654	6	CA126655	CA126655 SCUTLR105
247	101	9.4	956	9	BZ550459	BZ550459 pacs1-60_
248	100.5	9.4	713	6	CA229855	CA229855 SCJFFL3C0
249	100.5	9.4	800	2	BG843015	BG843015 1024001B0
250	100.5	9.4	821	7	CK596034	CK596034 AGENCOURT
251	100.5	9.4	822	7	CK596922	CK596922 AGENCOURT
c 252	100.5	9.4	852	8	DR856410	DR856410 JGI_CABG2
253	100.5	9.4	1186	2	BI103856	BI103856 602889237
c 254	100.5	9.4	1269	10	CL967019	CL967019 OsIFCC014
c 255	100.5	9.4	4610	4	CR861419	CR861419 Pongo pyg
c 256	100	9.3	571	9	CC008745	CC008745 PUECR15TD
257	100	9.3	813	9	CC617459	CC617459 OGUHP63TH
258	99.5	9.3	497	7	CO968625	CO968625 BeE90N22B
259	99.5	9.3	530	7	CO963238	CO963238 BeE30N03C
260	99.5	9.3	538	7	CO961898	CO961898 BeE120N08
c 261	99.5	9.3	551	3	BI775001	BI775001 467342 MA
262	99.5	9.3	591	7	CO972784	CO972784 BeG60N02C
263	99.5	9.3	597	7	CO971893	CO971893 BeG30N11H
264	99.5	9.3	601	7	CO963794	CO963794 BeE30N09D
265	99.5	9.3	601	7	CO972636	CO972636 BeG30N20B
c 266	99.5	9.3	742	10	CE610806	CE610806 tigr-gss-
267	99.5	9.3	765	8	DN427407	DN427407 LIB4216-0
268	99.5	9.3	831	10	CNS01WZM	AL171067 Tetraodon
269	99.5	9.3	853	9	BZ651412	BZ651412 OGCCR14TM
270	99.5	9.3	880	9	BZ638786	BZ638786 OGCBV76TM
271	99.5	9.3	968	2	BF984512	BF984512 602307882
272	99.5	9.3	1067	3	BM925494	BM925494 AGENCOURT
273	99.5	9.3	1111	5	BQ876877	BQ876877 AGENCOURT
c 274	99	9.2	595	7	CR986173	CR986173 CR986173
c 275	99	9.2	818	3	BI821019	BI821019 603035675
276	99	9.2	1034	10	CW918627	CW918627 EDCA638TF
c 277	99	9.2	1150	3	BM918864	BM918864 AGENCOURT
c 278	99	9.2	1165	8	DN707803	DN707803 CLJ73-E09
279	99	9.2	1235	6	CA792743	CA792743 AGENCOURT
280	99	9.2	1241	2	BE904378	BE904378 601496283
281	99	9.2	1662	4	BC031286	BC031286 Homo sapi
282	99	9.2	1662	4	BC048010	BC048010 Homo sapi
283	99	9.2	1911	4	CR857739	CR857739 Pongo pyg
c 284	98.5	9.2	476	2	BG366636	BG366636 HVSMEi000
c 285	98.5	9.2	574	5	BU437388	BU437388 604144143
286	98.5	9.2	854	8	CV782157	CV782157 FGAS07657
287	98.5	9.2	862	5	BX387263	BX387263 BX387263
c 288	98.5	9.2	868	3	BI519349	BI519349 603062142
289	98.5	9.2	869	10	AG852234	AG852234 Oryza sat
c 290	98.5	9.2	873	3	BP141911	BP141911 BP141911
291	98.5	9.2	978	5	BQ688915	BQ688915 AGENCOURT
292	98.5	9.2	1017	5	BU571267	BU571267 AGENCOURT
293	98	9.1	650	11	LBAF050C09	BX543295 Leishmani
c 294	98	9.1	748	8	DR804948	DR804948 ZM_BFb003
c 295	98	9.1	758	7	CJ021293	CJ021293 CJ021293
296	98	9.1	846	8	CV771910	CV771910 FGAS06630
c 297	98	9.1	851	7	CK769875	CK769875 957984 MA
298	98	9.1	931	10	CL489231	CL489231 SAIL_51_E
c 299	98	9.1	972	8	DN457914	DN457914 EST953713
300	98	9.1	995	5	BU838983	BU838983 AGENCOURT
301	98	9.1	996	3	BM923840	BM923840 AGENCOURT
c 302	98	9.1	1037	2	BG679499	BG679499 602627514
c 303	98	9.1	1202	9	CC295850	CC295850 CH261-176
304	98	9.1	1339	8	DN738297	DN738297 CNB97-G09
305	98	9.1	1423	5	BQ715426	BQ715426 AGENCOURT
306	98	9.1	12798	11	DQ050682	DQ050682 Homo sapi
307	97.5	9.1	474	10	CG610801	CG610801 OST294925
c 308	97.5	9.1	506	1	AI515253	AI515253 LD46992.5
c 309	97.5	9.1	527	1	AI388275	AI388275 GH19111.5
c 310	97.5	9.1	576	1	AI546454	AI546454 LD48032.5
c 311	97.5	9.1	585	1	AJ448032	AJ448032 AJ448032
c 312	97.5	9.1	585	1	AJ448062	AJ448062 AJ448062
313	97.5	9.1	594	10	CE771159	CE771159 tigr-gss-
c 314	97.5	9.1	600	11	CNS033CV	AL225976 Tetraodon
c 315	97.5	9.1	619	5	BU392867	BU392867 603512807
c 316	97.5	9.1	629	1	AJ447372	AJ447372 AJ447372
c 317	97.5	9.1	643	1	AJ451745	AJ451745 AJ451745
318	97.5	9.1	673	5	BX604948	BX604948 BX604948
c 319	97.5	9.1	697	1	AI517162	AI517162 GH27812.5
320	97.5	9.1	730	10	CG358862	CG358862 OGXFH94TH
321	97.5	9.1	756	7	CF865715	CF865715 tric002xn
322	97.5	9.1	779	6	CB166859	CB166859 BTU602600
323	97.5	9.1	790	5	BX926144	BX926144 BX926144
324	97.5	9.1	799	9	BZ733888	BZ733888 OGFBU96TC
325	97.5	9.1	812	6	CB895630	CB895630 tric002xn
326	97.5	9.1	834	5	BX607380	BX607380 BX607380
327	97.5	9.1	887	5	BX606179	BX606179 BX606179
c 328	97.5	9.1	923	3	BI948247	BI948247 HVSMEl000
c 329	97.5	9.1	1051	1	AL551229	AL551229 AL551229
c 330	97.5	9.1	1187	8	DN657351	DN657351 CEC28-D01
c 331	97.5	9.1	1203	4	AK003004	AK003004 Mus muscu
c 332	97.5	9.1	1419	2	BF317078	BF317078 601903477
333	97.5	9.1	1467	2	BF235650	BF235650 602025581
334	97.5	9.1	3669	4	HSM805593	AL834206 Homo sapi
335	97	9.0	515	2	BE479599	BE479599 164361 BA
c 336	97	9.0	517	7	CO333462	CO333462 EK307009.
c 337	97	9.0	630	2	BI193682	BI193682 602946611
c 338	97	9.0	751	8	DR805377	DR805377 ZM_BFb003
339	97	9.0	863	11	CNS04BGC	AL283125 Tetraodon
340	97	9.0	888	10	CG246033	CG246033 OG1DS26TV
341	97	9.0	1020	1	AL565602	AL565602 AL565602
c 342	97	9.0	1085	2	BE741722	BE741722 601594792
c 343	97	9.0	1209	8	DN667422	DN667422 CFW38-A07
344	97	9.0	1371	8	DN665115	DN665115 CFW24-B09
c 345	97	9.0	1417	8	DN677742	DN677742 CFW95-A09
c 346	96.5	9.0	463	5	BQ467073	BQ467073 HS02I02r
c 347	96.5	9.0	477	2	BG366611	BG366611 HVSMEi000
c 348	96.5	9.0	489	5	BQ467686	BQ467686 HS04I24r
c 349	96.5	9.0	502	2	BG368837	BG368837 HVSMEi002
c 350	96.5	9.0	511	2	BG366823	BG366823 HVSMEi000
c 351	96.5	9.0	511	2	BG366896	BG366896 HVSMEi000
c 352	96.5	9.0	511	2	BG367195	BG367195 HVSMEi001
c 353	96.5	9.0	528	2	BG368186	BG368186 HVSMEi001
354	96.5	9.0	535	9	BH371659	BH371659 AG-ND-130
c 355	96.5	9.0	572	5	BQ466761	BQ466761 HS01I02T
356	96.5	9.0	579	3	BI874604	BI874604 963116G08
c 357	96.5	9.0	624	2	BG368598	BG368598 HVSMEi001
358	96.5	9.0	627	9	AZ212631	AZ212631 Sheared D
c 359	96.5	9.0	680	2	BB280046	BB280046 BB280046
360	96.5	9.0	684	5	BU379420	BU379420 603812914
c 361	96.5	9.0	689	2	BG369638	BG369638 HVSMEi002
362	96.5	9.0	712	2	BG850886	BG850886 1024029F0
363	96.5	9.0	729	3	BM251488	BM251488 BOTL01000
364	96.5	9.0	749	8	CX845944	CX845944 JGI_CAAK1
c 365	96.5	9.0	750	2	BG365661	BG365661 HVSMEi000
c 366	96.5	9.0	759	2	BG368328	BG368328 HVSMEi001
c 367	96.5	9.0	777	11	CR869299	CR869299 Sus scrof
c 368	96.5	9.0	802	2	BG369093	BG369093 HVSMEi002
c 369	96.5	9.0	823	2	BG369072	BG369072 HVSMEi002
370	96.5	9.0	843	5	BU367698	BU367698 603585622
c 371	96.5	9.0	861	3	BI547786	BI547786 603191960
c 372	96.5	9.0	876	10	CG295823	CG295823 OG0EY13TH

c 373	96.5	9.0	896	2	BG368930	BG368930 HVSMEi002
374	96.5	9.0	924	5	BQ619232	BQ619232 RNOSEQ5C0
c 375	96.5	9.0	940	2	BG365938	BG365938 HVSMEi000
c 376	96.5	9.0	964	5	BQ641625	BQ641625 AGENCOURT
377	96.5	9.0	1055	5	BX355042	BX355042 BX355042
c 378	96.5	9.0	1189	3	BQ278764	BQ278764 AGENCOURT
379	96.5	9.0	1331	8	DN652948	DN652948 CEC02-G04
c 380	96.5	9.0	1677	2	BE559557	BE559557 601347219
381	96.5	9.0	1751	3	BM043267	BM043267 603619506
382	96.5	9.0	2198	2	BG568017	BG568017 602586880
c 383	96	8.9	550	5	BQ571144	BQ571144 UI-M-FB0-
384	96	8.9	555	10	CG570028	CG570028 OST198562
385	96	8.9	593	6	CA229712	CA229712 SCAGFL302
c 386	96	8.9	640	8	DN351253	DN351253 LIB3579-0
387	96	8.9	691	3	BI413421	BI413421 602986784
388	96	8.9	739	10	CL449072	CL449072 ZMMBBb046
389	96	8.9	741	3	BI768889	BI768889 603058005
c 390	96	8.9	824	2	BE970382	BE970382 601679558
c 391	96	8.9	877	10	CG372163	CG372163 OGWLH84TV
392	96	8.9	925	5	BX397239	BX397239 BX397239
c 393	96	8.9	985	11	CNS04RIZ	AL303956 Tetraodon
394	96	8.9	1007	3	BM906017	BM906017 AGENCOURT
395	96	8.9	1074	3	BM922895	BM922895 AGENCOURT
396	96	8.9	1266	4	BC020441	BC020441 Homo sapi
397	96	8.9	1391	8	DN674731	DN674731 CFW82-B11
398	96	8.9	1734	4	CR625712	CR625712 full-leng
c 399	95.5	8.9	417	10	BX908220	BX908220 Leishmani
c 400	95.5	8.9	451	7	CK606961	CK606961 Controlb_
401	95.5	8.9	471	3	BI528277	BI528277 1024089A1
c 402	95.5	8.9	484	11	LBWF8D2	BX530539 Leishmani
c 403	95.5	8.9	519	9	BH778121	BH778121 fzmb013f0
404	95.5	8.9	605	5	BQ813315	BQ813315 1030035D1
c 405	95.5	8.9	618	8	DN420668	DN420668 LIB4216-0
406	95.5	8.9	640	9	CE066607	CE066607 tigr-gss-
407	95.5	8.9	686	10	CW588532	CW588532 OA_ABa012
408	95.5	8.9	691	2	BE413934	BE413934 SCU004.E0
409	95.5	8.9	757	5	BX768557	BX768557 BX768557
410	95.5	8.9	760	9	CE003486	CE003486 tigr-gss-
411	95.5	8.9	781	2	BF981573	BF981573 602309455
412	95.5	8.9	788	8	DN545180	DN545180 1394224 M
413	95.5	8.9	793	8	DR787209	DR787209 ZM_BFb000
414	95.5	8.9	799	10	CG437472	CG437472 OG7AD63TH
415	95.5	8.9	802	9	AQ865320	AQ865320 nbeb0025K
416	95.5	8.9	853	5	BU340456	BU340456 603519946
c 417	95.5	8.9	890	10	CG438125	CG438125 OG7AD64TV
c 418	95.5	8.9	954	2	BF304533	BF304533 601887916
419	95.5	8.9	956	5	BQ654230	BQ654230 AGENCOURT
420	95.5	8.9	984	6	CD251974	CD251974 AGENCOURT
421	95.5	8.9	989	1	AL560831	AL560831 AL560831
422	95.5	8.9	1019	10	CW920863	CW920863 EDCAJ09TR
423	95.5	8.9	1026	3	BM050044	BM050044 603632337
c 424	95.5	8.9	2748	4	CR857540	CR857540 Pongo pyg
c 425	95	8.9	388	9	BH385248	BH385248 AG-ND-152
426	95	8.9	541	7	CK009114	CK009114 24948rsic
427	95	8.9	634	10	CE655755	CE655755 tigr-gss-
428	95	8.9	644	7	CK072253	CK072253 65649rsic
c 429	95	8.9	652	3	BJ655697	BJ655697 BJ655697
c 430	95	8.9	658	6	CB440019	CB440019 690022 MA
c 431	95	8.9	666	11	LBAF054B06	BX540302 Leishmani
c 432	95	8.9	773	10	CG340962	CG340962 OGXBH02TV
c 433	95	8.9	784	6	CB966536	CB966536 NL39_A11
434	95	8.9	799	7	CK771600	CK771600 959946 MA
c 435	95	8.9	810	10	BX976767	BX976767 Reverse s
436	95	8.9	851	10	CG260771	CG260771 OG2BU37TV
437	95	8.9	853	8	CV761344	CV761344 FGAS05573
438	95	8.9	948	3	BM469249	BM469249 AGENCOURT
439	95	8.9	1048	3	BM461613	BM461613 AGENCOURT
440	95	8.9	1131	10	CL471728	CL471728 SAIL_165_
441	95	8.9	1194	8	DR137339	DR137339 49192860
442	95	8.9	1340	8	DN717529	DN717529 CNB119-A1
443	95	8.9	1761	10	AY401901	AY401901 Homo sapi
444	95	8.9	2529	10	AY421056	AY421056 Homo sapi
c 445	95	8.9	3780	4	HSM802822	AL442089 Homo sapi
446	94.5	8.8	479	10	CZ269551	CZ269551 UCDRGT788
447	94.5	8.8	568	1	AM038861	AM038861 AM038861
c 448	94.5	8.8	621	7	CF897282	CF897282 A0222H11-
c 449	94.5	8.8	633	7	CF898767	CF898767 A0244C02-
c 450	94.5	8.8	655	2	BI088570	BI088570 602853110
451	94.5	8.8	700	6	CD876252	CD876252 AZO3.109B
c 452	94.5	8.8	742	10	CW229960	CW229960 104_671_1
453	94.5	8.8	747	2	BG773033	BG773033 602721318
c 454	94.5	8.8	749	8	DN441197	DN441197 LIB5338-1
455	94.5	8.8	758	5	BX604402	BX604402 BX604402
456	94.5	8.8	796	5	BX397476	BX397476 BX397476
c 457	94.5	8.8	799	2	BE746898	BE746898 601580807
458	94.5	8.8	813	11	CNS06YEJ	AL420929 T7 end of
459	94.5	8.8	839	8	DR967569	DR967569 ZM_BFb008
c 460	94.5	8.8	856	5	BX435681	BX435681 BX435681
c 461	94.5	8.8	873	7	CV225806	CV225806 WS0162.B2
c 462	94.5	8.8	898	5	BQ682907	BQ682907 AGENCOURT
c 463	94.5	8.8	918	2	BG365772	BG365772 HVSMEi000
464	94.5	8.8	956	5	BU857245	BU857245 AGENCOURT
465	94.5	8.8	1024	2	BF163490	BF163490 601771666
466	94.5	8.8	1152	2	BF340451	BF340451 602037072
c 467	94.5	8.8	1242	9	CC282283	CC282283 CH261-98E
468	94.5	8.8	1316	3	BM811295	BM811295 AGENCOURT
469	94.5	8.8	1360	4	CR593456	CR593456 full-leng
c 470	94.5	8.8	1626	2	BF183397	BF183397 601809535
471	94.5	8.8	2023	2	BF098856	BF098856 601751127
c 472	94.5	8.8	5276	4	HSM803131	AL831818 Homo sapi
473	94	8.8	418	7	CV658359	CV658359 Mdlv2_402
c 474	94	8.8	524	1	AU190833	AU190833 AU190833
c 475	94	8.8	541	1	AU190913	AU190913 AU190913
c 476	94	8.8	561	1	AJ638222	AJ638222 AJ638222
477	94	8.8	570	6	CB516337	CB516337 ssalrgb51
478	94	8.8	585	9	BZ293781	BZ293781 CG0517.r1
479	94	8.8	588	3	BP284725	BP284725 BP284725
480	94	8.8	593	9	BZ322918	BZ322918 ia71g05.g
481	94	8.8	612	2	BF127516	BF127516 601810147
482	94	8.8	625	10	BX905500	BX905500 Leishmani
c 483	94	8.8	648	5	BY731485	BY731485 BY731485
484	94	8.8	657	2	BG423778	BG423778 602450709
485	94	8.8	658	6	CB866405	CB866405 HC07E04w
486	94	8.8	667	2	BG909370	BG909370 TaLr1101H
c 487	94	8.8	670	6	CD351214	CD351214 UI-M-FY0-
488	94	8.8	678	6	CA279040	CA279040 SCBFRT309
489	94	8.8	696	8	DR599839	DR599839 EST989967
490	94	8.8	713	8	DN266040	DN266040 LIB30320_
c 491	94	8.8	743	5	BU708602	BU708602 UI-M-FI0-
492	94	8.8	748	7	CN203148	CN203148 Tor3389 G
c 493	94	8.8	757	6	CA316632	CA316632 UI-M-FW0-
c 494	94	8.8	770	7	CO395986	CO395986 AGENCOURT
495	94	8.8	773	3	BP464618	BP464618 BP464618
496	94	8.8	806	2	BG248957	BG248957 602361907
497	94	8.8	813	7	CK308666	CK308666 SB02047A2
498	94	8.8	833	5	BU745997	BU745997 CH3#001_C
499	94	8.8	885	7	CK126144	CK126144 AGENCOURT
500	94	8.8	905	5	BX417002	BX417002 BX417002
c 501	94	8.8	905	7	CT002210	CT002210 CT002210
502	94	8.8	925	8	DR668343	DR668343 EST105846
503	94	8.8	927	8	DR675091	DR675091 EST106520
504	94	8.8	934	8	DR824420	DR824420 ZM_BFb006
505	94	8.8	936	8	DR676042	DR676042 EST106615
c 506	94	8.8	943	10	CZ373587	CZ373587 ZMMBF0130
507	94	8.8	946	2	BI144556	BI144556 602909416
c 508	94	8.8	952	11	CNS04367	AL272392 Tetraodon
509	94	8.8	976	5	BQ649013	BQ649013 AGENCOURT
c 510	94	8.8	1146	2	BF685181	BF685181 602142385
c 511	94	8.8	1278	5	BQ877601	BQ877601 AGENCOURT
c 512	94	8.8	1291	7	CK415831	CK415831 AUF_IpPit
c 513	94	8.8	1331	10	AJ862225	AJ862225 Brassica
514	94	8.8	1344	3	BM906876	BM906876 AGENCOURT
c 515	94	8.8	1701	10	AY408608	AY408608 Mus muscu
516	94	8.8	1856	2	BG252728	BG252728 602366377
c 517	94	8.8	2160	4	AK016870	AK016870 Mus muscu
518	94	8.8	2641	4	BC086862	BC086862 Homo sapi

	519	94	8.8	3001	10	AY419577 AY419577 Homo sapi
	520	93.5	8.7	390	6	CD036624 CD036624 mgsu010xL
	521	93.5	8.7	489	7	CO964148 CO964148 BeE30N14D
c	522	93.5	8.7	503	1	AV386854 AV386854
	523	93.5	8.7	512	9	AQ894696 AQ894696 HS_3193_A
	524	93.5	8.7	522	2	BG908018 BG908018 TaLr1164E
c	525	93.5	8.7	554	2	BG367682 BG367682 HVSMEi001
c	526	93.5	8.7	583	6	CB336891 CB336891 Tc024C04R
c	527	93.5	8.7	648	1	AJ456374 AJ456374 AJ456374
	528	93.5	8.7	652	3	BM625720 BM625720 170006874
	529	93.5	8.7	656	1	AJ733938 AJ733938 AJ733938
	530	93.5	8.7	698	3	BI726459 BI726459 1031085D0
	531	93.5	8.7	704	2	BG856069 BG856069 1024044E1
c	532	93.5	8.7	707	7	CN131887 CN131887 OX1_2_G11
	533	93.5	8.7	739	8	DN261507 DN261507 Meso05561
c	534	93.5	8.7	745	7	CO885965 CO885965 BovGen_14
	535	93.5	8.7	752	5	BX768729 BX768729 BX768729
	536	93.5	8.7	754	5	BX350959 BX350959 BX350959
	537	93.5	8.7	770	11	CR959257 CR959257 Homo sapi
	538	93.5	8.7	776	7	CO894094 CO894094 BovGen_22
c	539	93.5	8.7	783	7	CK138702 CK138702 AGENCOURT
c	540	93.5	8.7	783	7	CK138998 CK138998 AGENCOURT
	541	93.5	8.7	785	9	CC342983 CC342983 OGMBI38TV
	542	93.5	8.7	792	2	BG284209 BG284209 602408261
c	543	93.5	8.7	803	7	CK147272 CK147272 AGENCOURT
	544	93.5	8.7	807	10	CNS01MSX AL151346 Anopheles
c	545	93.5	8.7	808	7	CK145520 CK145520 AGENCOURT
	546	93.5	8.7	810	8	DR965192 DR965192 ZM_BFb008
c	547	93.5	8.7	810	10	CG412006 CG412006 ZMMBBb026
c	548	93.5	8.7	835	5	BX091289 BX091289 BX091289
c	549	93.5	8.7	841	2	BF216143 BF216143 601883627
c	550	93.5	8.7	847	7	CK193286 CK193286 FGAS00170
	551	93.5	8.7	847	10	CG276025 CG276025 OGWAT80TV
	552	93.5	8.7	869	4	CR616665 CR616665 full-leng
	553	93.5	8.7	881	2	BG495436 BG495436 602539747
c	554	93.5	8.7	893	2	BF301300 BF301300 602029744
c	555	93.5	8.7	895	7	CN837710 CN837710 AGENCOURT
	556	93.5	8.7	901	2	BE535688 BE535688 601060347
	557	93.5	8.7	903	2	BF316500 BF316500 601903005
	558	93.5	8.7	908	10	CG190357 CG190357 PUFRV82TB
c	559	93.5	8.7	913	10	CZ314332 CZ314332 ZMMBF0013
c	560	93.5	8.7	924	5	BQ947041 BQ947041 AGENCOURT
	561	93.5	8.7	926	5	BQ931569 BQ931569 AGENCOURT
	562	93.5	8.7	949	4	CR600796 CR600796 full-leng
	563	93.5	8.7	981	5	BQ678034 BQ678034 AGENCOURT
	564	93.5	8.7	989	4	CR616464 CR616464 full-leng
	565	93.5	8.7	992	4	CR590083 CR590083 full-leng
	566	93.5	8.7	1006	3	BM923842 BM923842 AGENCOURT
	567	93.5	8.7	1018	4	CR599331 CR599331 full-leng
	568	93.5	8.7	1035	4	CR622720 CR622720 full-leng
	569	93.5	8.7	1042	4	CR608280 CR608280 full-leng
	570	93.5	8.7	1046	4	CR597229 CR597229 full-leng
	571	93.5	8.7	1050	5	BX338315 BX338315 BX338315
	572	93.5	8.7	1057	4	CR592409 CR592409 full-leng
	573	93.5	8.7	1057	4	CR599309 CR599309 full-leng
	574	93.5	8.7	1062	4	CR601237 CR601237 full-leng
	575	93.5	8.7	1071	4	CR592150 CR592150 full-leng
c	576	93.5	8.7	1091	5	BX376207 BX376207 BX376207
c	577	93.5	8.7	1125	5	BU341031 BU341031 603518023
c	578	93.5	8.7	1227	8	DN730765 DN730765 CNB54-G05
	579	93.5	8.7	1289	3	BM007606 BM007606 603617014
	580	93.5	8.7	1360	4	CR858972 CR858972 Pongo pyg
	581	93.5	8.7	1426	2	BE870390 BE870390 601447574
	582	93.5	8.7	2119	11	DQ030170 DQ030170 Homo sapi
c	583	93	8.7	457	8	H24187 H24187 ym55f08.r1
c	584	93	8.7	479	1	AU196125 AU196125 AU196125
c	585	93	8.7	483	5	BQ444909 BQ444909 UI-M-ER0-
c	586	93	8.7	523	1	AU197133 AU197133 AU197133
c	587	93	8.7	527	1	AU195875 AU195875 AU195875
c	588	93	8.7	529	1	AU187366 AU187366 AU187366
c	589	93	8.7	544	1	AU196755 AU196755 AU196755
c	590	93	8.7	551	1	AU190569 AU190569 AU190569
	591	93	8.7	552	1	AA402260 AA402260 zu47g10.r
c	592	93	8.7	553	2	BF813148 BF813148 PM4-CI008
c	593	93	8.7	554	1	AU196348 AU196348 AU196348
c	594	93	8.7	562	6	CD217439 CD217439 TgESTzyi2
	595	93	8.7	575	9	AQ493006 AQ493006 HS_5222_B
	596	93	8.7	620	2	BE740506 BE740506 601595576
	597	93	8.7	660	2	BE394962 BE394962 601308246
	598	93	8.7	663	3	BP149942 BP149942 BP149942
c	599	93	8.7	672	5	BU442071 BU442071 603210636
c	600	93	8.7	680	8	DR031408 DR031408 bda020240
c	601	93	8.7	682	6	CA345381 CA345381 676010 NC
c	602	93	8.7	708	1	AI300083 AI300083 qn59f01.x
c	603	93	8.7	729	7	CR584907 CR584907 CR584907
c	604	93	8.7	743	9	CE121718 CE121718 tigr-gss-
	605	93	8.7	758	10	CL162855 CL162855 104_355_1
c	606	93	8.7	803	3	BI526630 BI526630 602925360
	607	93	8.7	809	9	AQ324545 AQ324545 mgxb0019C
c	608	93	8.7	828	9	BZ559272 BZ559272 pacs2-164
	609	93	8.7	837	5	BU595290 BU595290 AGENCOURT
c	610	93	8.7	846	8	CV763009 CV763009 FGAS05739
c	611	93	8.7	913	7	CN322260 CN322260 AGENCOURT
	612	93	8.7	932	2	BG104943 BG104943 602311462
	613	93	8.7	937	10	CZ503152 CZ503152 GMW2-31I1
c	614	93	8.7	974	5	BQ891731 BQ891731 AGENCOURT
	615	93	8.7	1002	3	BQ056713 BQ056713 AGENCOURT
	616	93	8.7	1014	2	BG827242 BG827242 602749384
	617	93	8.7	1026	11	DQ030748 DQ030748 Homo sapi
	618	93	8.7	1054	5	BX332874 BX332874 BX332874
	619	93	8.7	1067	5	BX332210 BX332210 BX332210
	620	93	8.7	1159	4	CR619161 CR619161 full-leng
	621	93	8.7	1411	4	CR624641 CR624641 full-leng
	622	93	8.7	1456	8	DN479377 DN479377 altr015xa
c	623	92.5	8.6	246	2	BE982497 BE982497 UI-M-CG0p
	624	92.5	8.6	502	6	CA184384 CA184384 SCRLST316
	625	92.5	8.6	557	9	CC044191 CC044191 3591_1_16
c	626	92.5	8.6	576	10	CL969506 CL969506 OsIFCC018
	627	92.5	8.6	581	3	BI683310 BI683310 464646 MA
	628	92.5	8.6	613	11	CR905132 CR905132 Sus scrof
c	629	92.5	8.6	616	2	BG366080 BG366080 HVSMEi000
	630	92.5	8.6	623	3	BJ007782 BJ007782 BJ007782
	631	92.5	8.6	629	3	BM076265 BM076265 TrEST-A14
c	632	92.5	8.6	669	8	CX662762 CX662762 Sa_mx0_66
	633	92.5	8.6	687	1	AI197829 AI197829 qi50g05.x
c	634	92.5	8.6	688	2	BF343398 BF343398 602014501
c	635	92.5	8.6	734	10	CG347028 CG347028 OG0EE59TV
c	636	92.5	8.6	774	9	BZ525826 BZ525826 OGAIT19TC
c	637	92.5	8.6	778	2	BF864063 BF864063 963048G09
c	638	92.5	8.6	784	7	CO063197 CO063197 est_k_bre
c	639	92.5	8.6	790	7	CK771355 CK771355 959618 MA
c	640	92.5	8.6	791	8	DR029554 DR029554 bda010082
c	641	92.5	8.6	814	2	BE275967 BE275967 601120733
c	642	92.5	8.6	833	8	DN259290 DN259290 Meso05183
c	643	92.5	8.6	862	3	BQ227448 BQ227448 AGENCOURT
c	644	92.5	8.6	864	9	CC720959 CC720959 OGUHI23TH
	645	92.5	8.6	865	10	CZ336654 CZ336654 ZMMBF0047
	646	92.5	8.6	881	3	BI330081 BI330081 602982183
c	647	92.5	8.6	889	3	BQ222997 BQ222997 AGENCOURT
c	648	92.5	8.6	927	10	CW953085 CW953085 TcB39.1_C
c	649	92.5	8.6	934	9	CC693300 CC693300 OGUFL73TV
	650	92.5	8.6	944	5	BQ959188 BQ959188 AGENCOURT
	651	92.5	8.6	945	9	CC693293 CC693293 OGUFL73TH
	652	92.5	8.6	947	10	AY411659 AY411659 Mus muscu
c	653	92.5	8.6	965	9	CC352324 CC352324 PUHFY89TB
	654	92.5	8.6	975	9	CC720969 CC720969 OGUHI23TV
	655	92.5	8.6	978	2	BF346392 BF346392 602020047
	656	92.5	8.6	1058	3	BM923528 BM923528 AGENCOURT
	657	92.5	8.6	1065	5	BQ960054 BQ960054 AGENCOURT
	658	92.5	8.6	1088	11	CNS05KCD AL341302 Tetraodon
	659	92.5	8.6	1097	3	BM561573 BM561573 AGENCOURT
	660	92.5	8.6	1217	8	CV769661 CV769661 FGAS06405
c	661	92.5	8.6	1229	5	BQ706361 BQ706361 AGENCOURT
c	662	92.5	8.6	1242	3	BI411510 BI411510 602965577
	663	92.5	8.6	1346	8	DN667423 DN667423 CFW38-A07
	664	92.5	8.6	1427	3	BQ233363 BQ233363 AGENCOURT

	665	92.5	8.6	1505	3	BM456701 BM456701 AGENCOURT
	666	92.5	8.6	2187	4	CR609357 full-leng CR609357
c	667	92.5	8.6	5784	11	DQ053092 DQ053092 Pan trogl
c	668	92	8.6	485	1	AI370248 AI370248 qu45c09.x
	669	92	8.6	512	1	AU193247 AU193247
c	670	92	8.6	540	7	CV580023 CV580023 kc95c05.y
c	671	92	8.6	547	7	CV067550 CV067550 Le_mx0_30
	672	92	8.6	569	6	CD363390 CD363390 UI-M-GL0-
	673	92	8.6	620	3	BJ069732 BJ069732 BJ069732
c	674	92	8.6	638	7	CV068523 CV068523 Le_mx0_33
c	675	92	8.6	643	3	BM790105 BM790105 K-EST0069
	676	92	8.6	644	10	CW755513 CW755513 OG_BBa006
	677	92	8.6	659	1	AA275761 AA275761 vc14e11.r
	678	92	8.6	660	5	BX886787 BX886787 BX886787
c	679	92	8.6	661	9	BZ798142 BZ798142 PUGEV51TD
c	680	92	8.6	672	2	BB644170 BB644170 BB644170
c	681	92	8.6	672	10	CE336642 CE336642 tigr-gss-
	682	92	8.6	675	5	BU682618 BU682618 UI-CF-EC1
c	683	92	8.6	678	10	CE543066 CE543066 tigr-gss-
c	684	92	8.6	679	3	BI381356 BI381356 BFLG1_002
c	685	92	8.6	681	6	CA298987 CA298987 SCSFFL804
c	686	92	8.6	692	8	DR713286 DR713286 Le_lv0_02
	687	92	8.6	699	3	BI521634 BI521634 603081485
	688	92	8.6	699	8	CX039564 CX039564 1352737 N
	689	92	8.6	700	8	DN888544 DN888544 nag15h08.
	690	92	8.6	715	2	BG859241 BG859241 1024062C0
	691	92	8.6	720	5	BX879788 BX879788 BX879788
	692	92	8.6	748	10	AG489053 AG489053 Mus muscu
c	693	92	8.6	755	5	BU306423 BU306423 603738821
	694	92	8.6	764	10	CL804666 CL804666 OR_CBa001
c	695	92	8.6	772	9	BH274196 BH274196 CH230-83J
	696	92	8.6	782	6	CF752820 CF752820 om_B001.4
c	697	92	8.6	802	1	AL537215 AL537215 AL537215
	698	92	8.6	806	5	BX861477 BX861477 BX861477
	699	92	8.6	808	2	BF127777 BF127777 601810473
	700	92	8.6	813	10	CG240037 CG240037 OG2AL20TH
c	701	92	8.6	821	10	CG436040 CG436040 OGVHG61TV
	702	92	8.6	847	8	CX564918 CX564918 UI-M-HA0-
	703	92	8.6	849	5	BX910732 BX910732 BX910732
c	704	92	8.6	860	10	CNS029IG AL187297 Tetraodon
	705	92	8.6	870	10	CG439162 CG439162 OGVGG43TH
	706	92	8.6	874	10	CG013174 CG013174 ZUAB603TV
	707	92	8.6	881	6	CF586482 CF586482 AGENCOURT
c	708	92	8.6	881	10	CG189905 CG189905 PUKBW19TB
c	709	92	8.6	894	6	CA272633 CA272633 SCCCSD100
	710	92	8.6	911	7	CF877530 CF877530 tric015xb
c	711	92	8.6	912	5	BU846067 BU846067 AGENCOURT
c	712	92	8.6	912	10	CG442663 CG442663 OGTAW52TV
c	713	92	8.6	916	10	CG214494 CG214494 OGWGP53TV
	714	92	8.6	921	10	CG285352 CG285352 OG3CA31TV
c	715	92	8.6	948	5	BQ958852 BQ958852 AGENCOURT
c	716	92	8.6	957	10	CW919171 CW919171 EDCA936TF
c	717	92	8.6	1002	10	CG698924 CG698924 ZMMBBc011
c	718	92	8.6	1006	10	CL396128 CL396128 ZMMBBb039
	719	92	8.6	1028	2	BG297293 BG297293 602395411
c	720	92	8.6	1040	3	BM919342 BM919342 AGENCOURT
	721	92	8.6	1056	10	CW930462 CW930462 EDCC265TR
c	722	92	8.6	1096	10	CW935481 CW935481 EDCCU13TR
	723	92	8.6	1119	7	CK216809 CK216809 FGAS02881
	724	92	8.6	1128	5	BQ890277 BQ890277 AGENCOURT
c	725	92	8.6	1258	2	BE732748 BE732748 601565222
	726	92	8.6	1264	4	CR624950 CR624950 full-leng
	727	92	8.6	1292	5	BQ647420 BQ647420 AGENCOURT
c	728	92	8.6	1400	5	BQ647196 BQ647196 AGENCOURT
	729	92	8.6	1435	4	CNS0FO5K CR680668 Tetraodon
c	730	92	8.6	1545	5	BQ832737 BQ832737 E25 AFT02
c	731	92	8.6	1560	4	CR603880 CR603880 full-leng
	732	92	8.6	1563	4	CR620848 CR620848 full-leng
c	733	91.5	8.5	399	2	BE121636 BE121636 894013H02
	734	91.5	8.5	441	6	CD444427 CD444427 EL01N0439
	735	91.5	8.5	490	10	CG599539 CG599539 OST266803
c	736	91.5	8.5	569	6	CA878772 CA878772 K0969D05-
c	737	91.5	8.5	579	1	AA603187 AA603187 nn29c10.s
c	738	91.5	8.5	583	7	CK062561 CK062561 55342rsic
	739	91.5	8.5	595	1	AA392873 AA392873 LD12012.5
	740	91.5	8.5	607	3	BI529016 BI529016 1024095C0
c	741	91.5	8.5	619	6	CA166709 CA166709 SCVPRZ302
c	742	91.5	8.5	623	2	BG369082 BG369082 HVSME1002
c	743	91.5	8.5	633	2	BE840878 BE840878 MR2-SN000
c	744	91.5	8.5	664	1	AW281366 AW281366 fj55b02.y
	745	91.5	8.5	664	9	CE069602 CE069602 tigr-gss-
	746	91.5	8.5	673	3	BM645562 BM645562 170006873
	747	91.5	8.5	673	9	CE004714 CE004714 tigr-gss-
	748	91.5	8.5	691	3	BM963799 BM963799 UI-M-EQ0-
	749	91.5	8.5	726	6	CD877596 CD877596 AZO4.100K
	750	91.5	8.5	737	10	CG271166 CG271166 OGXCC70TH
	751	91.5	8.5	738	9	BZ735360 BZ735360 OGFAK94TC
c	752	91.5	8.5	745	10	CG271174 CG271174 OGXCC70TV
	753	91.5	8.5	751	6	CA327925 CA327925 UI-M-FY0-
c	754	91.5	8.5	754	6	CA085464 CA085464 SCJLAM209
	755	91.5	8.5	768	8	CV783557 CV783557 UI-M-HY0p
c	756	91.5	8.5	779	3	BM048927 BM048927 603625449
	757	91.5	8.5	782	10	CNS02LQI AL203139 Tetraodon
	758	91.5	8.5	808	7	CJ038725 CJ038725 CJ038725
	759	91.5	8.5	815	8	DR734618 DR734618 FGAS08037
	760	91.5	8.5	827	5	BU229663 BU229663 603398837
	761	91.5	8.5	828	2	BF540923 BF540923 602067659
	762	91.5	8.5	833	5	BX744635 BX744635 BX744635
	763	91.5	8.5	835	2	BI114878 BI114878 602861464
	764	91.5	8.5	853	5	BU327158 BU327158 603491753
	765	91.5	8.5	858	8	CX562041 CX562041 UI-M-FC0-
	766	91.5	8.5	865	3	BM048166 BM048166 603620133
c	767	91.5	8.5	887	2	BF570437 BF570437 602186213
c	768	91.5	8.5	890	3	BI951864 BI951864 HVSMEm000
	769	91.5	8.5	894	9	CC330140 CC330140 OGQAH50TH
	770	91.5	8.5	933	7	CK407060 CK407060 AUF_IfLvr
	771	91.5	8.5	998	10	CG424886 CG424886 ZMMBBc004
c	772	91.5	8.5	1016	1	AL570587 AL570587 AL570587
c	773	91.5	8.5	1023	11	CNS03971 AL233542 Tetraodon
	774	91.5	8.5	1034	5	BQ441562 BQ441562 AGENCOURT
	775	91.5	8.5	1066	5	BX417546 BX417546 BX417546
c	776	91.5	8.5	1076	4	CNS0F62O CR657210 Tetraodon
	777	91.5	8.5	1139	7	CK206326 CK206326 FGAS01791
	778	91.5	8.5	1143	3	BI870340 BI870340 603393868
	779	91.5	8.5	1177	7	CK210825 CK210825 FGAS02265
	780	91.5	8.5	1256	3	BM924217 BM924217 AGENCOURT
	781	91.5	8.5	1377	2	BE565722 BE565722 601338519
	782	91.5	8.5	1494	3	BQ068052 BQ068052 AGENCOURT
	783	91.5	8.5	2045	2	BF128499 BF128499 601810356
	784	91	8.5	257	10	CE329109 CE329109 tigr-gss-
c	785	91	8.5	371	5	CA003229 CA003229 HS09M21r
	786	91	8.5	418	10	CG612799 CG612799 OST299353
	787	91	8.5	484	10	CW870183 CW870183 sh2a9-80.
c	788	91	8.5	496	6	CF610030 CF610030 INFIO01_0
c	789	91	8.5	504	1	AA982972 AA982972 ua23h09.r
c	790	91	8.5	530	2	BE364191 BE364191 PI1_12_G1
	791	91	8.5	533	10	CE450883 CE450883 tigr-gss-
	792	91	8.5	566	10	CG555767 CG555767 OST170727
	793	91	8.5	572	6	CA204275 CA204275 SCSGFL107
	794	91	8.5	604	9	BH918096 BH918096 3526_1_59
c	795	91	8.5	626	10	AG155305 AG155305 Pan trogl
c	796	91	8.5	627	6	CD088923 CD088923 MC1-0055G
c	797	91	8.5	635	2	BE297252 BE297252 601177927
c	798	91	8.5	637	10	CG435742 CG435742 OGTAZ96TV
c	799	91	8.5	639	6	CD822782 CD822782 BN25.046I
	800	91	8.5	642	2	BB657524 BB657524 BB657524
c	801	91	8.5	643	10	AG829508 AG829508 Sus scrof
	802	91	8.5	650	3	BM488367 BM488367 pgm2n.pk0
c	803	91	8.5	661	5	BU418041 BU418041 603955526
	804	91	8.5	668	2	BF312845 BF312845 601896987
	805	91	8.5	675	5	BY749730 BY749730 BY749730
	806	91	8.5	678	9	BZ745086 BZ745086 OGEDD85TC
c	807	91	8.5	679	10	CL854586 CL854586 OR_CBa008
	808	91	8.5	681	3	BI765681 BI765681 603043674
c	809	91	8.5	692	10	CW132377 CW132377 104_515_1
c	810	91	8.5	699	5	BQ769756 BQ769756 UI-M-FI0-

c	811	91	8.5	702	10	CW041544 CW041544 104_275_1
	812	91	8.5	705	7	CN790300 CN790300 4124871 B
	813	91	8.5	716	6	CA378070 CA378070 656792 NC
c	814	91	8.5	731	10	CG374754 CG374754 OGZBB87TV
	815	91	8.5	732	8	CX921605 CX921605 JGI_CAAN8
	816	91	8.5	736	7	CF869318 CF869318 tric018xp
c	817	91	8.5	737	9	BZ779319 BZ779319 ih88a11.g
	818	91	8.5	741	8	DR803185 DR803185 ZM_BFb002
	819	91	8.5	742	1	BB025147 BB025147 BB025147
	820	91	8.5	744	7	CK432632 CK432632 UI-D-GC1-
	821	91	8.5	749	9	BZ704645 BZ704645 PUCDO09TD
	822	91	8.5	750	7	CK475102 CK475102 AGENCOURT
	823	91	8.5	758	10	CG359439 CG359439 OGXAP59TH
c	824	91	8.5	761	7	CO890308 CO890308 BovGen_18
	825	91	8.5	767	7	CV554536 CV554536 UI-D-GC1-
	826	91	8.5	768	2	BG685945 BG685945 602638506
	827	91	8.5	768	6	CA223352 CA223352 SCJFFL1C0
	828	91	8.5	791	6	CB899457 CB899457 tric018xp
	829	91	8.5	791	10	CG428437 CG428437 ZMMBBb024
c	830	91	8.5	796	6	CA512703 CA512703 UI-R-FJ0-
	831	91	8.5	808	8	DN933895 DN933895 AGENCOURT
	832	91	8.5	816	6	CF596996 CF596996 AGENCOURT
c	833	91	8.5	819	7	CK872749 CK872749 AGENCOURT
	834	91	8.5	819	7	CO441577 CO441577 MZCCL1003
c	835	91	8.5	820	7	CV561895 CV561895 UI-M-FC0-
c	836	91	8.5	822	10	CG109385 CG109385 PUIDI86TD
c	837	91	8.5	828	2	BG704841 BG704841 602688484
	838	91	8.5	834	7	CN509546 CN509546 AGENCOURT
	839	91	8.5	845	10	CG246816 CG246816 OGWKO59TH
	840	91	8.5	852	2	BE614767 BE614767 601281350
c	841	91	8.5	872	2	BG575914 BG575914 602598343
	842	91	8.5	877	5	BQ439232 BQ439232 AGENCOURT
	843	91	8.5	881	5	BU956390 BU956390 AGENCOURT
	844	91	8.5	886	2	BF688145 BF688145 602067380
	845	91	8.5	894	8	DN077988 DN077988 JGI_CABD1
c	846	91	8.5	897	5	BU148738 BU148738 AGENCOURT
	847	91	8.5	897	5	BX685254 BX685254 BX685254
c	848	91	8.5	898	2	BE749066 BE749066 601571988
	849	91	8.5	905	5	BU151764 BU151764 AGENCOURT
	850	91	8.5	909	2	BF629690 BF629690 HVSMEb001
c	851	91	8.5	909	10	CL959582 CL959582 OsIFCC003
	852	91	8.5	921	5	BQ711916 BQ711916 AGENCOURT
c	853	91	8.5	923	10	CZ324491 CZ324491 ZMMBF0028
c	854	91	8.5	924	9	CC629709 CC629709 OGOAP54TV
	855	91	8.5	929	10	CG164729 CG164729 PUJBF63TD
c	856	91	8.5	940	10	CZ363056 CZ363056 ZMMBF0141
c	857	91	8.5	978	10	AG069505 AG069505 Pan trogl
c	858	91	8.5	979	9	BZ570844 BZ570844 msh2_1561
	859	91	8.5	984	2	BG336713 BG336713 602405141
c	860	91	8.5	990	3	BM548859 BM548859 AGENCOURT
	861	91	8.5	999	10	AG087841 AG087841 Pan trogl
	862	91	8.5	1013	6	CD556856 CD556856 AGENCOURT
	863	91	8.5	1071	5	BU595068 BU595068 AGENCOURT
c	864	91	8.5	1109	5	BQ952609 BQ952609 AGENCOURT
	865	91	8.5	1110	5	BU509870 BU509870 AGENCOURT
	866	91	8.5	1111	3	BI416242 BI416242 602988932
	867	91	8.5	1272	3	BM559613 BM559613 AGENCOURT
c	868	91	8.5	1313	2	BF183497 BF183497 601809977
c	869	91	8.5	1593	2	BG844073 BG844073 1024005A0
	870	91	8.5	2838	10	CL945483 CL945483 OsIFSB004
	871	91	8.5	3826	4	AK089438 AK089438 Mus muscu
	872	90.5	8.4	356	10	CE412861 CE412861 tigr-gss-
	873	90.5	8.4	451	7	CO846165 CO846165 LM_GM5_00
c	874	90.5	8.4	467	5	BX111355 BX111355 BX111355
c	875	90.5	8.4	483	6	CA190678 CA190678 SCCCRT1C0
c	876	90.5	8.4	531	7	CV003324 CV003324 ltu01-15m
c	877	90.5	8.4	563	8	DN858967 DN858967 naa33c01.
c	878	90.5	8.4	580	10	CZ747261 CZ747261 OC__Ba009
c	879	90.5	8.4	591	10	CW292677 CW292677 104_772_1
	880	90.5	8.4	609	1	AL785206 AL785206 AL785206
	881	90.5	8.4	619	11	LBAF042B05 BX539031 Leishmani
	882	90.5	8.4	624	10	CL188840 CL188840 104_405_1
	883	90.5	8.4	626	5	BU176901 BU176901 AGENCOURT
	884	90.5	8.4	626	5	BX266701 BX266701 BX266701
	885	90.5	8.4	638	3	BM982458 BM982458 UI-CF-EN1
	886	90.5	8.4	655	6	CA427872 CA427872 UI-H-DF0-
c	887	90.5	8.4	662	8	DR820954 DR820954 ZM_BFb006
	888	90.5	8.4	670	5	BU732572 BU732572 UI-E-CQ1-
c	889	90.5	8.4	672	2	BG819891 BG819891 602781975
	890	90.5	8.4	678	5	BQ448238 BQ448238 UI-H-EU1-
	891	90.5	8.4	689	3	BQ017178 BQ017178 UI-H-DT1-
	892	90.5	8.4	691	3	BI387530 BI387530 BFL26_002
c	893	90.5	8.4	703	5	BU451765 BU451765 603216411
c	894	90.5	8.4	704	5	BQ818251 BQ818251 1030069E1
	895	90.5	8.4	715	6	CB853105 CB853105 UI-CF-FN0
	896	90.5	8.4	719	7	CV105390 CV105390 AGENCOURT
	897	90.5	8.4	726	5	BX909220 BX909220 BX909220
	898	90.5	8.4	732	2	BG720499 BG720499 602691627
	899	90.5	8.4	732	3	BM333983 BM333983 MEST129-G
c	900	90.5	8.4	736	9	CC984272 CC984272 ZUADQ59TV
	901	90.5	8.4	736	10	CW229959 CW229959 104_671_1
	902	90.5	8.4	748	7	CF865716 CF865716 tric002xn
	903	90.5	8.4	760	2	BE798161 BE798161 601586067
	904	90.5	8.4	762	10	CW405386 CW405386 fsbb001f0
c	905	90.5	8.4	779	2	BF864535 BF864535 963052G04
	906	90.5	8.4	783	5	BX714517 BX714517 BX714517
	907	90.5	8.4	789	9	BZ531819 BZ531819 OGALG65TC
c	908	90.5	8.4	792	10	CG227438 CG227438 OG0GK18TH
	909	90.5	8.4	795	7	CR566328 CR566328 CR566328
c	910	90.5	8.4	800	1	AW448375 AW448375 BRY_637 B
c	911	90.5	8.4	800	5	BQ609744 BQ609744 BRY_637 w
	912	90.5	8.4	804	6	CB895631 CB895631 tric002xn
	913	90.5	8.4	812	5	BX735927 BX735927 BX735927
	914	90.5	8.4	815	7	CO401999 CO401999 AGENCOURT
	915	90.5	8.4	817	7	CN179257 CN179257 AGENCOURT
	916	90.5	8.4	818	9	AQ688669 AQ688669 nbxb0078G
c	917	90.5	8.4	825	7	CV110321 CV110321 AGENCOURT
c	918	90.5	8.4	839	7	CJ028115 CJ028115 CJ028115
	919	90.5	8.4	845	2	BE545022 BE545022 601070195
	920	90.5	8.4	852	5	BQ687546 BQ687546 AGENCOURT
	921	90.5	8.4	852	8	CX836885 CX836885 JGI_CAAK7
c	922	90.5	8.4	853	9	BZ578932 BZ578932 msh2_6070
	923	90.5	8.4	856	8	CX843498 CX843498 JGI_CAAK1
c	924	90.5	8.4	857	2	BG445122 BG445122 GA__Ea002
c	925	90.5	8.4	864	6	CF224914 CF224914 AGENCOURT
c	926	90.5	8.4	897	7	CO635445 CO635445 Contig180
	927	90.5	8.4	900	4	CNS092U2 BX039750 Single re
c	928	90.5	8.4	910	6	CD795816 CD795816 EST667177
c	929	90.5	8.4	919	2	BF300937 BF300937 602028944
c	930	90.5	8.4	941	10	CL207294 CL207294 ZMMBBb057
c	931	90.5	8.4	945	3	BM012211 BM012211 603636689
	932	90.5	8.4	961	9	BZ787951 BZ787951 PUGCE67TD
	933	90.5	8.4	980	10	AG057756 AG057756 Pan trogl
	934	90.5	8.4	991	2	BG683804 BG683804 602651653
c	935	90.5	8.4	994	4	AK013159 AK013159 Mus muscu
	936	90.5	8.4	1005	2	BE903041 BE903041 601677042
c	937	90.5	8.4	1006	5	BQ678479 BQ678479 AGENCOURT
c	938	90.5	8.4	1013	10	CL259972 CL259972 ZMMBBb061
c	939	90.5	8.4	1024	5	BY712184 BY712184 BY712184
	940	90.5	8.4	1033	5	BX423907 BX423907 BX423907
	941	90.5	8.4	1061	5	BX367229 BX367229 BX367229
	942	90.5	8.4	1075	5	BU186707 BU186707 AGENCOURT
c	943	90.5	8.4	1132	9	BZ550885 BZ550885 pacs1-60_
	944	90.5	8.4	1162	10	CW926978 CW926978 EDCBJ28TF
	945	90.5	8.4	1207	10	AG137522 AG137522 Pan trogl
c	946	90.5	8.4	1257	9	BZ554552 BZ554552 pacs1-60_
c	947	90.5	8.4	1341	8	DR124903 DR124903 49141041
	948	90.5	8.4	1379	9	BZ576867 BZ576867 msh2_514.
c	949	90.5	8.4	1449	10	CL964610 CL964610 OsIFCC038
	950	90.5	8.4	1797	4	CR604385 CR604385 full-leng
	951	90.5	8.4	2036	3	BM564010 BM564010 AGENCOURT
c	952	90.5	8.4	4968	10	CL976608 CL976608 OsIFCC029
c	953	90	8.4	408	5	BY156938 BY156938 BY156938
c	954	90	8.4	447	6	CB140257 CB140257 K-EST0193
	955	90	8.4	474	2	BE780618 BE780618 601468654
c	956	90	8.4	495	1	AA567291 AA567291 GM02277.5

957	90	8.4	495	5	BX646558	BX646558 DKFZp781M
958	90	8.4	517	8	DN144141	DN144141 4817_B10_
c 959	90	8.4	520	1	AU191428	AU191428 AU191428
c 960	90	8.4	523	1	AW574847	AW574847 UI-HF-BK0
961	90	8.4	524	5	BU977484	BU977484 HA11I03r
962	90	8.4	532	5	BQ551050	BQ551050 H4007A06-
c 963	90	8.4	534	2	BE684438	BE684438 184843 MA
964	90	8.4	544	2	BE726179	BE726179 894089E10
965	90	8.4	550	6	CD861973	CD861973 AZO1.101M
966	90	8.4	553	3	BM540145	BM540145 hb18f07.g
c 967	90	8.4	579	3	BP307104	BP307104 BP307104
968	90	8.4	588	2	BE908832	BE908832 601503235
c 969	90	8.4	599	3	BP255162	BP255162 BP255162
970	90	8.4	607	10	CW119792	CW119792 104_496_1
c 971	90	8.4	619	10	CW327116	CW327116 104_822_1
c 972	90	8.4	622	3	BQ037763	BQ037763 pgn1c.pk0
c 973	90	8.4	631	10	CG169568	CG169568 PUIJB30TB
974	90	8.4	639	5	BQ466678	BQ466678 HS01D22T
c 975	90	8.4	641	2	BE264344	BE264344 601190187
976	90	8.4	648	6	CD488756	CD488756 T14_A03 T
977	90	8.4	653	3	BI532837	BI532837 1024125B1
978	90	8.4	653	6	CD915210	CD915210 G550.125G
979	90	8.4	653	9	CC551365	CC551365 CH240_436
c 980	90	8.4	655	10	CL427898	CL427898 ZMMBBb044
c 981	90	8.4	666	9	CC730404	CC730404 OGTAI40TC
c 982	90	8.4	673	2	BB631982	BB631982 BB631982
983	90	8.4	673	10	CW266010	CW266010 104_735_1
984	90	8.4	683	8	CX033787	CX033787 1346205 N
985	90	8.4	693	10	CW312102	CW312102 104_801_1
986	90	8.4	695	6	CB939580	CB939580 IpCGJx14_
987	90	8.4	697	2	BG861227	BG861227 1024076D0
c 988	90	8.4	705	8	DN266574	DN266574 LIB30320_
989	90	8.4	706	2	BG767956	BG767956 602743701
990	90	8.4	709	5	BU379031	BU379031 603589012
c 991	90	8.4	709	10	CZ162949	CZ162949 OR_ABa000
992	90	8.4	726	5	BX075558	BX075558 BX075558
c 993	90	8.4	727	10	CL164736	CL164736 104_359_1
994	90	8.4	731	5	BX075179	BX075179 BX075179
995	90	8.4	742	6	CD442871	CD442871 EL01N0418
c 996	90	8.4	746	3	BI837311	BI837311 603090645
c 997	90	8.4	746	6	CD366893	CD366893 UI-H-FT2-
998	90	8.4	751	5	BX304044	BX304044 BX304044
999	90	8.4	761	9	CC730408	CC730408 OGTAI40TM
1000	90	8.4	793	2	BI257556	BI257556 602967108
1001	90	8.4	793	10	AG829460	AG829460 Sus scrof
c1002	90	8.4	796	10	CZ348869	CZ348869 ZMMBF0124
1003	90	8.4	797	3	BI520532	BI520532 603071542
c1004	90	8.4	809	1	AL514697	AL514697 AL514697
1005	90	8.4	811	10	CG880044	CG880044 ZMMBBb050
1006	90	8.4	813	3	BI329599	BI329599 602984019
1007	90	8.4	824	7	CN824658	CN824658 Oa_splbn_
c1008	90	8.4	832	9	CC614655	CC614655 OGOAO91TV
c1009	90	8.4	844	10	CW751649	CW751649 OP__Ba007
1010	90	8.4	846	10	CG310462	CG310462 OG5DG47TC
c1011	90	8.4	851	8	DR553380	DR553380 WS03225.C
1012	90	8.4	858	8	DR130656	DR130656 49335301
1013	90	8.4	863	10	AG826151	AG826151 Sus scrof
c1014	90	8.4	864	6	CB993947	CB993947 AGENCOURT
1015	90	8.4	865	9	CC609889	CC609889 OGVFX67TH
1016	90	8.4	867	9	CC684638	CC684638 OGPAR94TV
1017	90	8.4	893	2	BG540040	BG540040 602568665
1018	90	8.4	893	5	BU539549	BU539549 AGENCOURT
c1019	90	8.4	895	10	CZ389984	CZ389984 ZMMBF0167
1020	90	8.4	917	5	BU931064	BU931064 AGENCOURT
1021	90	8.4	919	10	CG133448	CG133448 PUKBC16TD
1022	90	8.4	922	2	BG775018	BG775018 602650162
1023	90	8.4	931	7	CV210244	CV210244 EST869954
c1024	90	8.4	937	5	BU523832	BU523832 AGENCOURT
c1025	90	8.4	975	5	BU154337	BU154337 AGENCOURT
1026	90	8.4	990	10	CNS02L4H	AL202346 Tetraodon
c1027	90	8.4	991	10	CG460903	CG460903 PUIJV81TB
1028	90	8.4	992	3	BQ065498	BQ065498 AGENCOURT
c1029	90	8.4	995	10	CNS01LDO	AL149501 Anopheles
c1030	90	8.4	1011	2	BG286316	BG286316 602382479
1031	90	8.4	1028	10	CW928378	CW928378 EDCBQ96TR
1032	90	8.4	1033	2	BF164274	BF164274 601773031
c1033	90	8.4	1035	4	CNS0F1E8	CR651146 Tetraodon
1034	90	8.4	1036	5	BQ711282	BQ711282 AGENCOURT
c1035	90	8.4	1043	5	BX379868	BX379868 BX379868
c1036	90	8.4	1075	10	CW934559	CW934559 EDCCO92TF
1037	90	8.4	1116	9	CC599145	CC599145 ZMMBBc039
c1038	90	8.4	1154	5	BX342173	BX342173 BX342173
c1039	90	8.4	1167	8	DR738666	DR738666 FGAS08388
1040	90	8.4	1178	3	BM808062	BM808062 AGENCOURT
1041	90	8.4	1188	3	BM479276	BM479276 AGENCOURT
c1042	90	8.4	1237	9	BZ578197	BZ578197 msh2_5745
c1043	90	8.4	1288	3	BM047515	BM047515 603628819
1044	90	8.4	1353	8	DN723713	DN723713 CNB150-B0
c1045	90	8.4	1380	8	DN718722	DN718722 CNB125-A0
1046	90	8.4	1382	4	AY104706	AY104706 Zea mays
1047	90	8.4	1467	3	BM545516	BM545516 AGENCOURT
c1048	90	8.4	1716	10	CL507225	CL507225 SAIL_779_
c1049	90	8.4	5064	11	DQ030897	DQ030897 Homo sapi
1050	89.5	8.3	385	8	W77211	W77211 me62g08.r1
c1051	89.5	8.3	560	3	BI708840	BI708840 fp93b04.y
c1052	89.5	8.3	560	3	BI846856	BI846856 fp89d03.y
1053	89.5	8.3	565	5	BQ829617	BQ829617 LL6in1060
1054	89.5	8.3	568	5	BQ832337	BQ832337 LL6in2061
c1055	89.5	8.3	570	3	BI705888	BI705888 fp97g04.y
1056	89.5	8.3	572	7	CO863070	CO863070 LM_SM5_00
c1057	89.5	8.3	573	9	BH063780	BH063780 RPCI-24-3
1058	89.5	8.3	574	6	CB384290	CB384290 TgESTzyh5
c1059	89.5	8.3	578	3	BI706827	BI706827 fq10h04.y
c1060	89.5	8.3	580	3	BI706027	BI706027 fp99d06.y
c1061	89.5	8.3	581	3	BI706731	BI706731 fq09d07.y
c1062	89.5	8.3	582	3	BP263582	BP263582 BP263582
1063	89.5	8.3	583	2	BG085081	BG085081 H3108D07-
c1064	89.5	8.3	587	3	BI706685	BI706685 fq08h04.y
c1065	89.5	8.3	587	7	CV667482	CV667482 LCPE04EX0
c1066	89.5	8.3	590	3	BI706940	BI706940 fq12f11.y
c1067	89.5	8.3	592	3	BI706693	BI706693 fq08h12.y
c1068	89.5	8.3	592	3	BI706772	BI706772 fq09h09.y
c1069	89.5	8.3	592	8	DN896501	DN896501 nap10d07.
c1070	89.5	8.3	598	2	BG308259	BG308259 fm59b06.y
c1071	89.5	8.3	607	1	AI456426	AI456426 LD36445.5
c1072	89.5	8.3	608	2	BG304618	BG304618 fl88f03.y
1073	89.5	8.3	609	2	BE493751	BE493751 WHE1275_H
c1074	89.5	8.3	613	7	CN124282	CN124282 RHOH1_3_F
c1075	89.5	8.3	614	2	BG306800	BG306800 fm07b11.y
c1076	89.5	8.3	619	8	DN896494	DN896494 nap10c10.
c1077	89.5	8.3	626	2	BG308035	BG308035 fm56a08.y
c1078	89.5	8.3	628	2	BF938436	BF938436 fm76f09.y
1079	89.5	8.3	636	7	CV159776	CV159776 SCARABAEU
1080	89.5	8.3	640	1	AU096688	AU096688 AU096688
c1081	89.5	8.3	643	8	DN896852	DN896852 nap14e12.
1082	89.5	8.3	646	10	CL166609	CL166609 104_362_1
c1083	89.5	8.3	647	2	BG304805	BG304805 fl91w19.y
c1084	89.5	8.3	655	8	DN899412	DN899412 nap44g08.
c1085	89.5	8.3	656	5	BU651874	BU651874 1112096B0
c1086	89.5	8.3	657	3	BQ280412	BQ280412 PL T46 P.
1087	89.5	8.3	657	7	CV667041	CV667041 LCPE04EX0
c1088	89.5	8.3	665	8	DN897207	DN897207 nap18g12.
c1089	89.5	8.3	666	8	DN239003	DN239003 MUC4LH101
c1090	89.5	8.3	669	8	DN899196	DN899196 nap42d02.
1091	89.5	8.3	669	10	CW278605	CW278605 104_753_1
1092	89.5	8.3	670	11	LBAF033C02	BX543020 Leishmani
c1093	89.5	8.3	687	10	CW298977	CW298977 104_781_1
c1094	89.5	8.3	688	5	BU373257	BU373257 603587639
1095	89.5	8.3	695	1	AL043161	AL043161 DKFZp434F
1096	89.5	8.3	697	10	CW458393	CW458393 fsbb001f2
c1097	89.5	8.3	699	2	BG308265	BG308265 fm59b12.y
c1098	89.5	8.3	700	10	CW306210	CW306210 104_791_1
1099	89.5	8.3	705	7	CF883400	CF883400 tric088xh
c1100	89.5	8.3	706	8	DN898298	DN898298 nap31g08.
c1101	89.5	8.3	709	6	CA173583	CA173583 SCCCST100
c1102	89.5	8.3	717	8	CX601619	CX601619 CT02030A2

1103	89.5	8.3	728	10	CZ979173	CZ979173 192332 To
c1104	89.5	8.3	731	8	DN899079	DN899079 nap41a05.
c1105	89.5	8.3	742	8	DN899135	DN899135 nap41f06.
c1106	89.5	8.3	743	8	DN857258	DN857258 naa11f12.
c1107	89.5	8.3	747	8	DN857119	DN857119 naa10a11.
c1108	89.5	8.3	751	8	DN899170	DN899170 nap42a07.
c1109	89.5	8.3	755	8	DN858869	DN858869 naa31h03.
c1110	89.5	8.3	758	8	DN895206	DN895206 nao64c02.
c1111	89.5	8.3	759	10	CW484241	CW484241 fsbb001f2
c1112	89.5	8.3	760	8	DN894944	DN894944 nao61b09.
1113	89.5	8.3	763	6	CB909530	CB909530 tric088xh
c1114	89.5	8.3	764	2	BE259201	BE259201 601109741
1115	89.5	8.3	769	7	CO248198	CO248198 AGENCOURT
1116	89.5	8.3	776	5	BQ821426	BQ821426 1030092C0
c1117	89.5	8.3	781	9	CC400516	CC400516 PUEDV65TD
c1118	89.5	8.3	784	8	DN897171	DN897171 nap18d07.
c1119	89.5	8.3	785	10	CL906367	CL906367 OA_ABa000
1120	89.5	8.3	788	2	BE911916	BE911916 601662667
1121	89.5	8.3	826	5	BU317894	BU317894 603853924
1122	89.5	8.3	832	10	AG851091	AG851091 Oryza sat
c1123	89.5	8.3	854	3	BI452770	BI452770 603169990
c1124	89.5	8.3	859	7	CV484389	CV484389 AGENCOURT
c1125	89.5	8.3	864	10	CG351959	CG351959 OGZBG50TV
1126	89.5	8.3	867	2	BF696802	BF696802 602125336
c1127	89.5	8.3	867	7	CN318952	CN318952 AGENCOURT
c1128	89.5	8.3	871	7	CO931396	CO931396 AGENCOURT
1129	89.5	8.3	873	2	BE312857	BE312857 601146140
c1130	89.5	8.3	874	10	AG906461	AG906461 Oryza sat
c1131	89.5	8.3	876	7	CN506827	CN506827 AGENCOURT
1132	89.5	8.3	879	5	BQ685543	BQ685543 AGENCOURT
1133	89.5	8.3	891	3	BI834823	BI834823 603090272
1134	89.5	8.3	898	4	AY849615	AY849615 Magnaport
1135	89.5	8.3	900	5	BQ939437	BQ939437 AGENCOURT
1136	89.5	8.3	912	8	CV814247	CV814247 AGENCOURT
c1137	89.5	8.3	928	10	CG377714	CG377714 OGYBZ54TV
1138	89.5	8.3	935	2	BG035192	BG035192 602324895
c1139	89.5	8.3	936	10	CG357188	CG357188 OGXCZ89TV
1140	89.5	8.3	938	10	CG220119	CG220119 OG0AH63TH
c1141	89.5	8.3	972	2	BG167342	BG167342 602342263
1142	89.5	8.3	979	10	CW923743	CW923743 EDCB031TF
c1143	89.5	8.3	979	10	CW930683	CW930683 EDCC386TR
c1144	89.5	8.3	980	5	BX463988	BX463988 BX463988
1145	89.5	8.3	981	5	BY706342	BY706342 BY706342
1146	89.5	8.3	1003	2	BG519611	BG519611 602578723
1147	89.5	8.3	1065	2	BG912398	BG912398 602808480
1148	89.5	8.3	1071	5	BX345312	BX345312 BX345312
c1149	89.5	8.3	1084	10	CW934422	CW934422 EDCCO21TF
c1150	89.5	8.3	1317	10	CL978268	CL978268 OsIFCC031
1151	89.5	8.3	1377	3	BM542793	BM542793 AGENCOURT
1152	89.5	8.3	1491	11	DQ032419	DQ032419 Homo sapi
1153	89.5	8.3	1573	3	BM455108	BM455108 AGENCOURT
1154	89.5	8.3	1705	4	AK045693	AK045693 Mus muscu
c1155	89	8.3	452	11	DE040277	DE040277 Branchios
c1156	89	8.3	458	2	BF189993	BF189993 235888 MA
1157	89	8.3	491	9	AZ965094	AZ965094 2M0235J02
c1158	89	8.3	494	6	CA881510	CA881510 K0991A05-
c1159	89	8.3	496	6	CF609350	CF609350 INFIO01_0
c1160	89	8.3	498	6	CF609145	CF609145 GERMO01_0
1161	89	8.3	508	2	BF293556	BF293556 WHE2158_C
c1162	89	8.3	510	6	CF605201	CF605201 RADIC01_0
c1163	89	8.3	517	6	CA882061	CA882061 K0994H05-
1164	89	8.3	538	2	BF827209	BF827209 MR2-HN003
c1165	89	8.3	545	3	BQ307155	BQ307155 MR0-BT250
1166	89	8.3	545	6	CB047653	CB047653 NISC_gg04
1167	89	8.3	548	2	BG684609	BG684609 602636383
c1168	89	8.3	552	5	BU741330	BU741330 UI-E-EJ0-
c1169	89	8.3	563	3	BI879080	BI879080 fm04a02.y
c1170	89	8.3	574	10	CE808768	CE808768 tigr-gss-
c1171	89	8.3	578	5	BU376561	BU376561 603589420
c1172	89	8.3	579	3	BI343365	BI343365 371491 MA
1173	89	8.3	580	9	BH224726	BH224726 1006120H1
c1174	89	8.3	586	2	BE915642	BE915642 601668365
c1175	89	8.3	587	2	BG908652	BG908652 TaLr1170B
c1176	89	8.3	594	5	BX272130	BX272130 BX272130
1177	89	8.3	609	5	BU037332	BU037332 946137G10
1178	89	8.3	614	10	CL197325	CL197325 104_424_1
1179	89	8.3	615	3	BM978357	BM978357 UI-CF-EC1
c1180	89	8.3	617	3	BI561419	BI561419 603255193
1181	89	8.3	619	2	BF528115	BF528115 602042883
c1182	89	8.3	626	7	CK226680	CK226680 702479425
c1183	89	8.3	630	3	BI390540	BI390540 pgp1n.pk0
c1184	89	8.3	638	6	CD229198	CD229198 CCC1_13_G
c1185	89	8.3	645	3	BM942164	BM942164 UI-M-CG0p
1186	89	8.3	646	3	BP140423	BP140423 BP140423
c1187	89	8.3	646	6	CD225989	CD225989 CCC1_42_G
1188	89	8.3	658	8	DR006821	DR006821 TC113762
c1189	89	8.3	659	6	CD222906	CD222906 CCC1_24_C
c1190	89	8.3	671	6	CD225331	CD225331 CCC1_39_H
c1191	89	8.3	673	2	BB434045	BB434045 BB434045
c1192	89	8.3	679	1	AL524941	AL524941 AL524941
c1193	89	8.3	687	3	BM448929	BM448929 DSA029H05
1194	89	8.3	693	7	CN366830	CN366830 170004251
c1195	89	8.3	698	3	BM449161	BM449161 DSA032G08
c1196	89	8.3	698	7	CN823272	CN823272 Oa_sp1bn_
1197	89	8.3	699	2	BG159840	BG159840 de57g02.x
1198	89	8.3	701	9	BH236265	BH236265 ATZKE29TF
c1199	89	8.3	701	9	BZ712086	BZ712086 OGBAR58TM
c1200	89	8.3	704	6	CF488242	CF488242 POL1_48_D
1201	89	8.3	709	6	CD425983	CD425983 SA1_15_D0
1202	89	8.3	727	7	CO428739	CO428739 UI-M-HW0-
1203	89	8.3	728	7	CO434803	CO434803 3b5_CAS-0
1204	89	8.3	740	8	DR972522	DR972522 ZM_BFb009
c1205	89	8.3	743	6	CD370188	CD370188 UI-H-FT1-
c1206	89	8.3	746	8	DR106758	DR106758 JHU122A09
1207	89	8.3	747	10	CL509931	CL509931 SAIL_821_
c1208	89	8.3	749	5	BW896251	BW896251 BW896251
c1209	89	8.3	755	10	CW829765	CW829765 OP__Ba008
1210	89	8.3	757	9	CC692863	CC692863 OGWBY91TH
c1211	89	8.3	762	6	CA162547	CA162547 SCRFRZ305
c1212	89	8.3	763	1	AI967990	AI967990 wu11g03.x
1213	89	8.3	771	8	DR465077	DR465077 WS00934.B
1214	89	8.3	773	8	DR955053	DR955053 ZM_BFb004
c1215	89	8.3	777	2	BG369218	BG369218 HVSMEi002
1216	89	8.3	778	10	CL954093	CL954093 OsJRUA000
1217	89	8.3	784	2	BG260459	BG260459 602371592
1218	89	8.3	798	5	BX320301	BX320301 BX320301
c1219	89	8.3	804	7	CF993697	CF993697 AGENCOURT
1220	89	8.3	815	8	DR628504	DR628504 EST101863
1221	89	8.3	816	10	CG227247	CG227247 OG0FW11TV
c1222	89	8.3	817	9	CC655834	CC655834 OGUFO54TH
1223	89	8.3	817	9	CC655841	CC655841 OGUFO54TV
1224	89	8.3	823	9	CC623803	CC623803 OGKAD53TM
1225	89	8.3	823	10	CG440330	CG440330 OGVHJ81TH
c1226	89	8.3	825	7	CO200194	CO200194 GEO2_6_A1
1227	89	8.3	825	10	CG273088	CG273088 OGWIE37TH
c1228	89	8.3	828	6	CB997083	CB997083 AGENCOURT
1229	89	8.3	834	7	CK202322	CK202322 FGAS01084
1230	89	8.3	850	8	CX782162	CX782162 HESC3_12_
c1231	89	8.3	862	5	BU306132	BU306132 603741419
1232	89	8.3	864	8	DR624761	DR624761 EST101488
c1233	89	8.3	868	10	CG415895	CG415895 ZMMBBc002
1234	89	8.3	869	6	CF616318	CF616318 AGENCOURT
1235	89	8.3	870	2	BF315773	BF315773 601900848
c1236	89	8.3	874	9	BZ535760	BZ535760 OGALV93TC
c1237	89	8.3	876	10	CG360740	CG360740 OGXFN26TH
c1238	89	8.3	878	2	BG024540	BG024540 602275308
1239	89	8.3	878	9	BZ098183	BZ098183 CH230-236
c1240	89	8.3	878	9	BZ648161	BZ648161 OGCAY11TC
c1241	89	8.3	879	2	BF127991	BF127991 601810744
c1242	89	8.3	883	6	CF377860	CF377860 AGENCOURT
c1243	89	8.3	883	10	CG972123	CG972123 MBEAS18TR
c1244	89	8.3	889	9	CC608130	CC608130 OGUBN61TV
c1245	89	8.3	892	3	BI763889	BI763889 603049654
1246	89	8.3	893	2	BG164918	BG164918 602343543
1247	89	8.3	893	9	BZ647841	BZ647841 OGCCC59TM
1248	89	8.3	899	5	BU158201	BU158201 AGENCOURT

c1249	89	8.3	900	10	CG297243	CG297243 OGZBB55TH
1250	89	8.3	905	10	CG297255	CG297255 OGZBB55TV
1251	89	8.3	909	9	CC691408	CC691408 OGLBF31TH
1252	89	8.3	912	5	BU150985	BU150985 AGENCOURT
1253	89	8.3	915	2	BF307573	BF307573 601893875
1254	89	8.3	915	5	BQ953097	BQ953097 AGENCOURT
c1255	89	8.3	915	10	CG248033	CG248033 OG0DB83TV
c1256	89	8.3	916	2	BF678776	BF678776 602084669
1257	89	8.3	918	2	BF670133	BF670133 602119461
c1258	89	8.3	925	2	BG477471	BG477471 602521523
c1259	89	8.3	939	2	BE732495	BE732495 601567693
1260	89	8.3	941	10	CG360746	CG360746 OGXFN26TV
c1261	89	8.3	956	2	BG365793	BG365793 HVSMEi000
1262	89	8.3	967	5	BQ942542	BQ942542 AGENCOURT
1263	89	8.3	969	2	BF685154	BF685154 602142353
c1264	89	8.3	970	9	CC721109	CC721109 OGOAK57TH
c1265	89	8.3	978	6	CF618844	CF618844 AGENCOURT
1266	89	8.3	984	10	CZ399229	CZ399229 ZMMBF0180
c1267	89	8.3	985	2	BE896129	BE896129 601438717
1268	89	8.3	985	9	CC663598	CC663598 OGVAQ51TV
1269	89	8.3	994	5	BQ943398	BQ943398 AGENCOURT
c1270	89	8.3	1006	2	BG770218	BG770218 602744993
c1271	89	8.3	1008	5	BX416200	BX416200 BX416200
1272	89	8.3	1025	3	BQ072530	BQ072530 AGENCOURT
c1273	89	8.3	1037	3	BM555223	BM555223 AGENCOURT
1274	89	8.3	1044	2	BE915867	BE915867 601669134
c1275	89	8.3	1050	3	BM923923	BM923923 AGENCOURT
1276	89	8.3	1086	8	DR123366	DR123366 49143241
1277	89	8.3	1097	11	CNS03RFE	AL257171 Tetraodon
1278	89	8.3	1101	4	CR623119	CR623119 full-leng
1279	89	8.3	1104	5	BQ940554	BQ940554 AGENCOURT
c1280	89	8.3	1112	7	CN248792	CN248792 EST014702
1281	89	8.3	1123	8	DR739370	DR739370 FGAS08458
1282	89	8.3	1129	8	DR137175	DR137175 49296530
1283	89	8.3	1131	1	AL545633	AL545633 AL545633
1284	89	8.3	1132	11	CNS040W4	AL269437 Tetraodon
1285	89	8.3	1133	8	DR138027	DR138027 49177745
1286	89	8.3	1141	8	DR138072	DR138072 49169166
1287	89	8.3	1151	10	CW927011	CW927011 EDCBJ46TR
1288	89	8.3	1208	11	DQ047069	DQ047069 Homo sapi
1289	89	8.3	1215	10	CL972138	CL972138 OsIFCC041
1290	89	8.3	1256	5	BU155431	BU155431 AGENCOURT
1291	89	8.3	1387	10	AY419826	AY419826 Homo sapi
1292	89	8.3	1412	8	DN476181	DN476181 altr204xk
1293	89	8.3	1721	2	BG118620	BG118620 602348374
c1294	89	8.3	1756	2	BF129804	BF129804 601811263
c1295	89	8.3	1926	4	CR624366	CR624366 full-leng
c1296	89	8.3	3010	4	CR860113	CR860113 Pongo pyg
1297	88.5	8.2	416	6	CB768216	CB768216 AMGNNUC:M
c1298	88.5	8.2	445	6	CF744362	CF744362 UI-M-GV0-
c1299	88.5	8.2	473	1	AL889680	AL889680 AL889680
1300	88.5	8.2	485	8	DN607051	DN607051 EST02262
1301	88.5	8.2	520	8	DN363783	DN363783 LIB3628-0
c1302	88.5	8.2	523	9	AQ351037	AQ351037 RPCI11-11
1303	88.5	8.2	525	6	CF019660	CF019660 QBN21c02.
c1304	88.5	8.2	526	2	BG738385	BG738385 fp57h11.y
c1305	88.5	8.2	528	9	AQ769667	AQ769667 HS_3160_A
1306	88.5	8.2	532	7	CK335061	CK335061 H3137G02-
1307	88.5	8.2	541	5	BX516333	BX516333 BX516333
c1308	88.5	8.2	557	6	CD810870	CD810870 2 Lingulo
1309	88.5	8.2	560	6	CA374851	CA374851 649374 NC
1310	88.5	8.2	564	6	CF024155	CF024155 QBS1f02.x
c1311	88.5	8.2	568	9	BH173179	BH173179 0010A03 m
c1312	88.5	8.2	570	2	BG366269	BG366269 HVSMEi000
c1313	88.5	8.2	573	9	AQ938897	AQ938897 NL1-DL1R
1314	88.5	8.2	577	3	BI721030	BI721030 1031053E1
1315	88.5	8.2	582	7	CO846310	CO846310 LM_GM5_00
1316	88.5	8.2	590	1	AV871040	AV871040 AV871040
1317	88.5	8.2	595	6	CB411867	CB411867 TgESTzyh5
c1318	88.5	8.2	597	10	CW304505	CW304505 104_789_1
1319	88.5	8.2	599	1	AV879556	AV879556 AV879556
1320	88.5	8.2	605	5	BQ391333	BQ391333 NISC_mq18
c1321	88.5	8.2	609	10	CL805567	CL805567 OR_CBa001
1322	88.5	8.2	610	5	BU307472	BU307472 603735016
1323	88.5	8.2	616	3	BJ286992	BJ286992 BJ286992
1324	88.5	8.2	617	6	CA222897	CA222897 SCBGFL405
c1325	88.5	8.2	624	6	CD809928	CD809928 635 Lingu
c1326	88.5	8.2	627	8	DN896679	DN896679 nap12e02.
c1327	88.5	8.2	629	5	BU371644	BU371644 603568076
c1328	88.5	8.2	630	1	AJ447286	AJ447286 AJ447286
1329	88.5	8.2	639	7	CO846309	CO846309 LM_GM5_00
1330	88.5	8.2	643	1	AW742498	AW742498 up58a08.y
c1331	88.5	8.2	647	1	AJ641625	AJ641625 AJ641625
1332	88.5	8.2	651	8	CX033083	CX033083 1345398 N
c1333	88.5	8.2	658	5	BU874939	BU874939 Q073F03 P
c1334	88.5	8.2	660	6	CB269904	CB269904 1008811 H
c1335	88.5	8.2	669	10	CE431670	CE431670 tigr-gss-
c1336	88.5	8.2	670	3	BM043660	BM043660 603620248
1337	88.5	8.2	670	9	BZ710361	BZ710361 OGBBB57TM
c1338	88.5	8.2	671	6	CD891276	CD891276 G118.116M
1339	88.5	8.2	675	9	CC733626	CC733626 OGVEW31TV
c1340	88.5	8.2	688	6	CA128531	CA128531 SCJLLR201
c1341	88.5	8.2	690	10	CW405385	CW405385 fsbb001f0
1342	88.5	8.2	691	6	CD767136	CD767136 AGENCOURT
1343	88.5	8.2	694	10	CG327188	CG327188 OGVDS56TV
c1344	88.5	8.2	696	9	BZ710349	BZ710349 OGBBB57TC
1345	88.5	8.2	698	7	CK063097	CK063097 64277rsic
1346	88.5	8.2	698	10	CL952821	CL952821 OsIRUA003
c1347	88.5	8.2	700	10	CW234173	CW234173 104_687_1
c1348	88.5	8.2	705	3	BI838160	BI838160 603083667
1349	88.5	8.2	713	2	BG850887	BG850887 1024029F0
1350	88.5	8.2	714	5	BX311044	BX311044 BX311044
c1351	88.5	8.2	716	7	CF971886	CF971886 AUB_IfLvr
1352	88.5	8.2	724	6	CA374930	CA374930 649470 NC
c1353	88.5	8.2	724	10	CG842891	CG842891 Ynhw3505
1354	88.5	8.2	726	7	CO530678	CO530678 3530_1_20
c1355	88.5	8.2	726	10	CW242732	CW242732 104_702_1
1356	88.5	8.2	728	1	AJ729994	AJ729994 AJ729994
c1357	88.5	8.2	755	6	CA317378	CA317378 UI-M-FW0-
1358	88.5	8.2	761	6	CA359906	CA359906 633006 NC
1359	88.5	8.2	762	5	BX865870	BX865870 BX865870
1360	88.5	8.2	771	6	CA376367	CA376367 654707 NC
1361	88.5	8.2	772	10	CG450742	CG450742 OGVGE63TH
1362	88.5	8.2	775	1	AI096909	AI096909 qb58h12.x
1363	88.5	8.2	779	9	BZ985419	BZ985419 PUGIZ27TB
1364	88.5	8.2	785	7	CO978349	CO978349 BeZSPN17E
c1365	88.5	8.2	791	10	CL404707	CL404707 ZMMBBb040
1366	88.5	8.2	797	10	CG336478	CG336478 OG3BT07TH
1367	88.5	8.2	803	6	CF132289	CF132289 UI-HF-FQ0
1368	88.5	8.2	805	9	CC754035	CC754035 ZMMBBb013
1369	88.5	8.2	807	8	DN259641	DN259641 Meso03724
c1370	88.5	8.2	807	9	BZ987551	BZ987551 PUGIA38TB
1371	88.5	8.2	809	10	CG286242	CG286242 OGWMN53TH
1372	88.5	8.2	816	9	BZ987555	BZ987555 PUGIA38TD
c1373	88.5	8.2	825	3	BI413431	BI413431 602986796
c1374	88.5	8.2	839	3	BI455555	BI455555 603173994
c1375	88.5	8.2	840	5	BU161067	BU161067 AGENCOURT
c1376	88.5	8.2	841	2	BG912641	BG912641 602808089
c1377	88.5	8.2	846	7	CR527230	CR527230 CR527230
1378	88.5	8.2	848	9	BZ731339	BZ731339 OGEBR95TC
1379	88.5	8.2	852	10	CG295838	CG295838 OG0EY13TV
c1380	88.5	8.2	853	3	BI826319	BI826319 603076048
c1381	88.5	8.2	867	2	BF210195	BF210195 601873617
1382	88.5	8.2	878	9	CC675402	CC675402 OGKAT39TV
1383	88.5	8.2	879	4	CNS09QYH	BX071013 Single re
c1384	88.5	8.2	881	10	CG207354	CG207354 OGWFL23TV
c1385	88.5	8.2	886	11	CNS06U1W	AL415290 T3 end of
c1386	88.5	8.2	894	2	BE916224	BE916224 601664076
c1387	88.5	8.2	902	6	CB908056	CB908056 tric084xe
1388	88.5	8.2	909	10	CG168723	CG168723 PUIGZ28TB
1389	88.5	8.2	913	10	CG442886	CG442886 OGVHK57TV
1390	88.5	8.2	924	10	CG443545	CG443545 OGVHK58TV
c1391	88.5	8.2	950	5	BQ933367	BQ933367 AGENCOURT
c1392	88.5	8.2	950	6	CF825598	CF825598 EST702980
c1393	88.5	8.2	958	5	BY717383	BY717383 BY717383
c1394	88.5	8.2	962	2	BI113706	BI113706 602860885

1395	88.5	8.2	966	3	BI411272	BI411272 602964637
1396	88.5	8.2	970	1	AL554966	AL554966 AL554966
c1397	88.5	8.2	970	11	CNS04CPC	AL284745 Tetraodon
c1398	88.5	8.2	971	10	CL117935	CL117935 ISB1-69J1
1399	88.5	8.2	974	1	AL582968	AL582968 AL582968
1400	88.5	8.2	974	5	BX407248	BX407248 BX407248
c1401	88.5	8.2	981	3	BM006243	BM006243 603614905
1402	88.5	8.2	982	3	BM919690	BM919690 AGENCOURT
1403	88.5	8.2	985	5	BQ720193	BQ720193 AGENCOURT
c1404	88.5	8.2	1000	10	CL952381	CL952381 OsIRUA000
1405	88.5	8.2	1010	5	BQ648510	BQ648510 AGENCOURT
c1406	88.5	8.2	1027	10	CG421445	CG421445 ZMMBBc003
1407	88.5	8.2	1056	3	BI830066	BI830066 603080167
c1408	88.5	8.2	1059	3	BM556098	BM556098 AGENCOURT
1409	88.5	8.2	1078	11	CNS046UG	AL277153 Tetraodon
1410	88.5	8.2	1138	2	BE636680	BE636680 rockefell
c1411	88.5	8.2	1154	9	BZ549360	BZ549360 pacs1-60_
1412	88.5	8.2	1156	5	BQ713462	BQ713462 AGENCOURT
1413	88.5	8.2	1165	3	BM906044	BM906044 AGENCOURT
1414	88.5	8.2	1211	2	BE730394	BE730394 601563922
c1415	88.5	8.2	1215	5	BU458326	BU458326 603370170
1416	88.5	8.2	1250	5	BQ714509	BQ714509 AGENCOURT
1417	88.5	8.2	1264	5	BU152726	BU152726 AGENCOURT
1418	88.5	8.2	1319	10	AG073666	AG073666 Pan trogl
c1419	88.5	8.2	1367	2	BE779053	BE779053 601464816
c1420	88.5	8.2	1377	10	CL972889	CL972889 OsIFCC023
c1421	88.5	8.2	1461	3	BM020179	BM020179 603648755
1422	88.5	8.2	1479	5	BU119175	BU119175 603002752
c1423	88.5	8.2	1484	2	BG845828	BG845828 1024011D0
1424	88.5	8.2	1530	3	BQ055170	BQ055170 AGENCOURT
1425	88.5	8.2	1605	10	CL976010	CL976010 OsIFCC043
c1426	88.5	8.2	1678	2	BF302588	BF302588 602032435
1427	88.5	8.2	1739	2	BF965178	BF965178 602268475
c1428	88.5	8.2	1811	4	AK017604	AK017604 Mus muscu
1429	88.5	8.2	2136	10	CL965888	CL965888 OsIFCC012
1430	88.5	8.2	2432	4	BC097288	BC097288 Rattus no
1431	88.5	8.2	4212	4	CR858816	CR858816 Pongo pyg
c1432	88.5	8.2	6451	11	DQ051430	DQ051430 Homo sapi
c1433	88	8.2	310	10	CG602660	CG602660 OST276264
c1434	88	8.2	453	11	L234Y	AL354118 Leishmani
1435	88	8.2	456	9	B49269	B49269 RPCI11-5K23
1436	88	8.2	460	10	CL592158	CL592158 OB__Ba005
c1437	88	8.2	484	8	DR083356	DR083356 PMUS1-019
1438	88	8.2	485	2	BE590470	BE590470 WHE0854_D
1439	88	8.2	492	3	BQ244942	BQ244942 TaE15033C
c1440	88	8.2	512	7	CK786490	CK786490 UI-D-GC1-
c1441	88	8.2	512	8	CX206693	CX206693 MNS11023
c1442	88	8.2	514	1	AW014733	AW014733 UI-H-BI0-
c1443	88	8.2	516	1	AU194861	AU194861 AU194861
1444	88	8.2	526	10	CZ841130	CZ841130 OC__Ba022
1445	88	8.2	538	6	CF245211	CF245211 3530_1_5_
1446	88	8.2	549	2	BE637444	BE637444 WHE0859_G
1447	88	8.2	555	10	CG195360	CG195360 PUIDE25TB
c1448	88	8.2	596	7	CV161510	CV161510 CS_gil_57
c1449	88	8.2	600	8	CX237723	CX237723 NMA10987
1450	88	8.2	601	2	BE361003	BE361003 DG1_68_F1
1451	88	8.2	602	5	BW962989	BW962989 BW962989
c1452	88	8.2	603	5	BX258733	BX258733 BX258733
1453	88	8.2	605	2	BE355610	BE355610 DG1_115_F
1454	88	8.2	606	7	CK369445	CK369445 zmrws485_
1455	88	8.2	609	7	CO968029	CO968029 BeE90N15D
c1456	88	8.2	620	1	AI360253	AI360253 qy84f11.x
c1457	88	8.2	620	6	CD631338	CD631338 55147727J
c1458	88	8.2	633	2	BG304507	BG304507 fl88h03.y
c1459	88	8.2	633	10	CW811242	CW811242 rpine_766
1460	88	8.2	635	3	BJ234737	BJ234737 BJ234737
1461	88	8.2	638	10	CZ770957	CZ770957 OC__Ba012
1462	88	8.2	640	8	DR704808	DR704808 Asn_04684
1463	88	8.2	644	3	BQ245994	BQ245994 TaE15017E
c1464	88	8.2	645	7	CV026378	CV026378 4297 Full
c1465	88	8.2	652	7	CV527638	CV527638 CS_GIL_06
1466	88	8.2	655	5	BU646530	BU646530 111205IF1
c1467	88	8.2	661	6	CA306432	CA306432 UI-H-FT1-
c1468	88	8.2	661	6	CF487974	CF487974 POL1_47_B
1469	88	8.2	661	10	CZ561656	CZ561656 1_p_bW013
1470	88	8.2	662	3	BQ245369	BQ245369 TaE15025E
c1471	88	8.2	663	1	AW565577	AW565577 LG1_346_C
c1472	88	8.2	663	8	DR799956	DR799956 ZM_BFb002
1473	88	8.2	667	3	BM072986	BM072986 MEST56-H0
1474	88	8.2	667	3	BQ246705	BQ246705 TaE15006G
c1475	88	8.2	670	2	BG850404	BG850404 1024028E0
1476	88	8.2	671	2	BG856588	BG856588 1024047A1
c1477	88	8.2	671	3	BM392321	BM392321 UI-R-DO1-
c1478	88	8.2	673	10	CW229358	CW229358 104_670_1
1479	88	8.2	674	8	CX778421	CX778421 UI-EH-HG2
c1480	88	8.2	674	10	CW819496	CW819496 rpinea_59
1481	88	8.2	675	3	BM614848	BM614848 170006871
1482	88	8.2	675	10	AG827117	AG827117 Sus scrof
1483	88	8.2	678	10	CW387603	CW387603 fsbb001f0
c1484	88	8.2	682	2	BG859842	BG859842 1024065H0
1485	88	8.2	686	3	BQ246082	BQ246082 TaE15016E
1486	88	8.2	687	5	BX108492	BX108492 BX108492
c1487	88	8.2	688	2	BG850403	BG850403 1024028E0
1488	88	8.2	691	8	DR704574	DR704574 Asn_04403
1489	88	8.2	698	1	AA127623	AA127623 zk89a12.r
c1490	88	8.2	698	3	BJ590899	BJ590899 BJ590899
c1491	88	8.2	699	6	CB646703	CB646703 OSJNEb09F
1492	88	8.2	701	10	CW249435	CW249435 104_711_1
1493	88	8.2	703	2	BG962647	BG962647 602830049
c1494	88	8.2	704	10	CW748686	CW748686 OP__Ba006
c1495	88	8.2	709	6	CB646622	CB646622 OSJNEb09D
c1496	88	8.2	710	5	BU236353	BU236353 603341655
c1497	88	8.2	711	6	CB246280	CB246280 UI-M-FO0-
1498	88	8.2	714	8	CX771633	CX771633 UI-EH-HG1
c1499	88	8.2	718	8	CX007416	CX007416 io28c07.g
1500	88	8.2	719	10	CL177216	CL177216 104_384_1

ALIGNMENTS

RESULT 1
DQ030711

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LOCUS       DQ030711                588 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Homo sapiens HC464 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ030711
VERSION     DQ030711.1  GI:66881915
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 588)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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                     /chromosome="16"
     gene            <1. .>588
                     /locus_tag="HC464"
ORIGIN

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Pred. No.:              3.93e-83        Length:         588
Score:                  1063.00         Matches:        195
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            99.1%           Indels:         0
DB:                     11              Gaps:           0

US-09-854-280-3 (1-197) x DQ030711 (1-588)

Qy          3 LeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHisAspPro 22
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCC 60

Qy         23 SerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGluGluLeu 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTG 120

Qy         43 ProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeu 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTG 180

Qy         63 ProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArgPro 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCC 240

Qy         83 SerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAspThrHis 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCAC 300

Qy        103 GlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyrProGln 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAG 360

Qy        123 LysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGlu 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAG 420

Qy        143 ThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgPro 162
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Db        421 ACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCC 480

Qy        163 CysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPhe 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTC 540

Qy        183 IleHisValProValGlyCysThrCysValLeuProArgSerVal 197
              |||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 585

RESULT 2
BC069410
LOCUS       BC069410                1027 bp    mRNA    linear   HTC 11-JUL-2005
DEFINITION  Homo sapiens cDNA clone IMAGE:7262201, with apparent retained
            intron.
ACCESSION   BC069410
VERSION     BC069410.1  GI:46854343
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1027)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1027)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBR Plate: 2 Row: b Column: 3
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7262201"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_277"
                     /note="Vector: pPCR-Script Amp SK(+) with reversed insert"
ORIGIN

Alignment Scores:
Pred. No.:              1.9e-82         Length:         1027
Score:                  1059.00         Matches:        194
Percent Similarity:     99.5%           Conservative:   0
Best Local Similarity:  99.5%           Mismatches:     1
Query Match:            98.7%           Indels:         0
DB:                     4               Gaps:           0

US-09-854-280-3 (1-197) x BC069410 (1-1027)

Qy          3 LeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHisAspPro 22
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Db        390 CTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCC 449

Qy         23 SerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGluGluLeu 42
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Db        450 TCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTG 509
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Qy          43 ProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeu 62
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Db         510 CCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTG 569

Qy          63 ProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArgPro 82
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Db         570 CCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCC 629

Qy          83 SerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAspThrHis 102
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Db         630 TCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCAC 689

Qy         103 GlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyrProGln 122
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Db         690 CAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAG 749

Qy         123 LysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGlu 142
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Db         750 AAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAG 809

Qy         143 ThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgPro 162
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Db         810 ACAGCTGCGCTCAACTCCGTGCGGCTGTTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCC 869

Qy         163 CysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPhe 182
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Db         870 TGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTC 929

Qy         183 IleHisValProValGlyCysThrCysValLeuProArgSerVal 197
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Db         930 ATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 974
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RESULT 3
DQ030712
LOCUS DQ030712 586 bp DNA linear GSS 02-JUN-2005
DEFINITION Pan troglodytes HC464 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ030712
VERSION DQ030712.1 GI:66881916
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 586)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 586)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
source 1. .586
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene <1. .>586
/locus_tag="HC464"
ORIGIN

Alignment Scores:

Pred. No.:	2.87e-69	Length:	586
Score:	905.00	Matches:	169
Percent Similarity:	87.1%	Conservative:	0
Best Local Similarity:	87.1%	Mismatches:	25
Query Match:	84.3%	Indels:	0
DB:	11	Gaps:	0

US-09-854-280-3 (1-197) x DQ030712 (1-586)

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Qy           4 LeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHisAspProSer 23
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Db           2 CTCCCTGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCC 61

Qy          24 LeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGluGluLeuPro 43
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Db          62 CTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCC 121

Qy          44 LeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeuPro 63
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Db         122 CTCGGCCACGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCT 181

Qy          64 ValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArgProSer 83
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Db         182 GTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCATAGGGGGAGGCACGAGAGGCCCTCA 241

Qy          84 AlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAspThrHisGln 103
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Db         242 GCTACGACCCAGTGCCCGGTGCTGCGGCCAGAGGAGGTGTTGGAGGCAGACACCCACCAG 301

Qy         104 ArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyrProGlnLys 123
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Db         302 CGCTCCATCTCACCCTGGAGATACCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 361

Qy         124 LeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThr 143
               |||  |||||||||  ||||||  ||||||||||||||
Db         362 NTGGCCTTNNNCGAGTGCCTGTNNNNNGGCTGTATNNNTGCGCGGACGGGCCGCGANNNN 421

Qy         144 AlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgProCys 163
               ||||||  ||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         422 NCTGCGCTCNNNTCCGTGCGGCTGCTCCNNNGCCTGCTGGTGCTGCGCCGCCGGCCCTGC 481

Qy         164 SerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIle 183
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Db         482 TCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATC 541

Qy         184 HisValProValGlyCysThrCysValLeuProArgSerVal 197
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Db         542 CACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 583
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RESULT 4
BX281422
LOCUS BX281422 466 bp mRNA linear EST 04-MAR-2003
DEFINITION BX281422 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGp998H057906 ; IMAGE:3232180, mRNA sequence.
ACCESSION BX281422
VERSION BX281422.1 GI:28612698
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 466)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
TITLE Human UnigeneSet - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998H057906.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)

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            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES              Location/Qualifiers
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                      /tissue_type="carcinoid"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Lu24"
                      /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                      modified polylinker; Plasmid DNA from the normalized
                      library NCI_CGAP_Lu5 was prepared, and ss circles were
                      made in vitro. Following HAP purification, this DNA was
                      used as tracer in a subtractive hybridization reaction.
                      The driver was PCR-amplified cDNAs from a pool of 5,000
                      clones made from the same library (cloneIDs
                      1414920-1417991 and 1520904-1522439). Subtraction by Bento
                      Soares and M. Fatima Bonaldo.  "
ORIGIN

Alignment Scores:
Pred. No.:                1.22e-37        Length:         466
Score:                    543.00          Matches:        101
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              50.6%           Indels:         0
DB:                       5               Gaps:           0

US-09-854-280-3 (1-197) x BX281422 (1-466)

Qy          97 LeuGluAlaAspThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAsp 116
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 TTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGAT 60

Qy         117 GluAspArgTyrProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAsp 136
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGAT 120

Qy         137 AlaArgThrGlyArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeu 156
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTG 180

Qy         157 ValLeuArgArgArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPhe 176
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTT 240

Qy         177 AlaPheHisThrGluPheIleHisValProValGlyCysThrCysValLeuProArgSer 196
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCA 300

Qy         197 Val 197
               |||
Db         301 GTG 303

RESULT 5
AG139411/c
LOCUS       AG139411                669 bp    DNA     linear   GSS 04-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-153O06.F, genomic survey sequence.
ACCESSION   AG139411
VERSION     AG139411.1  GI:16669089
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: -21M13
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES              Location/Qualifiers
     source           1. .669
                      /organism="Pan troglodytes"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9598"
                      /clone="PTB-153O06.F"
                      /sex="male"
                      /cell_type="lymphoblast"
                      /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

Alignment Scores:
Pred. No.:                1.11e-17        Length:         669
Score:                    318.00          Matches:        70
Percent Similarity:       86.6%           Conservative:   1
Best Local Similarity:    85.4%           Mismatches:     9
Query Match:              29.6%           Indels:         3
DB:                       10              Gaps:           0

US-09-854-280-3 (1-197) x AG139411 (1-669)

Qy         118 AspArgTyr-ProGlnLysLeuAlaPheAlaGluCys-LeuCysArgGlyCysIleAspA 137
               ||||||||| ||||||   ||||||   |||   ||| ||||||||||||||||||||||
Db         515 GACCGGTATCCCACAGGATCTGGCTGTCGCCGGATGCCTTGTGCAGAGGCTGTATCGATG 456

Qy         137 laArgThrGlyArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuV 157
               ||   |||   |||||||||   ||||||||||||||||||||||||||||||||||||
Db         455 CGCTGACGNTCCGCGAGACAGGTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTAT 396

Qy         157 alLeuArgArgArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheA 177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         395 A-CTACGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTG 337

Qy         177 laPheHisThrGluPheIleHisValProValGlyCysThrCysValLeuProArgSerV 197
               ||||||||||||||||||||||||||||||||      ||||||:::||||||||||||
Db         336 CCTTCCACACCGAGTTCATCCACGTCCCCGTCGAAAGCACATGCATACTGCCCCGTTCAG 277

Qy         197 al 197
               ||
Db         276 TG 275

RESULT 6
DN989597
LOCUS       DN989597                664 bp    mRNA    linear   EST 17-MAY-2005
DEFINITION  TC108206 Human adult whole brain, large insert, pCMV expression
            library Homo sapiens cDNA clone TC108206 5' similar to Homo sapiens
            interleukin 17D (IL17D), mRNA sequence.
```

```
ACCESSION   DN989597
VERSION     DN989597.1  GI:66249428
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 664)
  AUTHORS   Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
            Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
            Zhang,X., Jay,G. and He,W.
  TITLE     High-throughput cloning of full-length human cDNAs directly from
            cDNA libraries optimized for large and rare transcripts
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Kovacs, KF
            High Throughput cDNA Cloning
            OriGene Technologies, Inc. ( www.origene.com )
            6 Taft Court, Suite 100, Rockville, MD 20850, USA
            Tel: 301 340 3188
            Fax: 301 340 8606
            Email: cDNA@origene.com
            This EST submission is part of an on-going human full-length
            cloning project at OriGene Technologies, Inc.
            Please contact OriGene for access.
            OriGene Technologies, Inc.
            6 Taft Ct. Suite 100
            Rockville, MD 20850
            Tel: (301) 340-3188
            http://www.origene.com
            Seq primer: pCMV6 5prime forward vector primer, OriGene
            Technologies Inc.
FEATURES             Location/Qualifiers
     source          1. .664
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="TC108206"
                     /tissue_type="Whole brain"
                     /clone_lib="Human adult whole brain, large insert, pCMV
                     expression library"
                     /note="Organ: Brain; Vector: pCMV6-XL5; Site_1: EcoR1;
                     Site_2: Xho1/Sal1 compatible end ligatio; Oligo-dT primed
                     reverse transcription optimized for large and GC rich mRNA
                     transcripts, cDNA size selection, optimized ligation for
                     large inserts into mammalian expression vector, random
                     clones selected for end sequence verification of
                     full-length genes"
ORIGIN

Alignment Scores:
Pred. No.:              4.04e-08        Length:         664
Score:                  209.00          Matches:        71
Percent Similarity:     36.8%           Conservative:   15
Best Local Similarity:  30.3%           Mismatches:     63
Query Match:            19.5%           Indels:         85
DB:                     8               Gaps:           9

US-09-854-280-3 (1-197) x DN989597 (1-664)

Qy         29 HisSerHisGlyThrProHisCysTyrSerAlaGluGluLeuProLeuGlyGlnAlaPro 48
              |||      |||   |||                 |||           |||:::   |||
Db          4 CATCCTCCGGGCCGCCCTCTGGCTCCGCGGGGCGAG-----------GGGAGGCGCCCG 51

Qy         49 ProHisLeuLeuAlaArgGlyAlaLysTrpGly--------------------------- 59
              |||         |||   ||||||      |||
Db         52 CCG---------GCTCCGGGCGCCGCGGGCGGGACACGGGCGCGGGGCGCAGGCGGGCTC 102

Qy         60 ------------GlnAlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHis 75
                        :::   |||   ||||||      |||   |||||||||   |||
Db        103 CTCCGGCGCGTGCGGACGCTGAGCGTGGCCTGTCCCTCAGGGCTGGAAGCTGGNAGCCGG 162

Qy         76 ----------------------------ArgGlyArgHisGlu----------ArgPr 82
                                          |||||||||   |||          |||||
Db        163 CTTCCTGCTGGCGCTGCCGCCGAGCTGGGCCGCGGGCGCCCCGAGGGCGGGCAGGCGCCC 222

Qy         82 oSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGlu---------- 98
              |:::         |||         ||||||||||||:::||||||
Db        223 CGCGCGGCCGCGGGGCTGC---GCGGACCGGCCGGAGGAGCTACTGGAGCAGCTGTACGG 279

Qy         98 ---------------------------------------------------------- 98

Db        280 GCGCCTGGCGGCCGGCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGA 339

Qy         99 ----------------------------------------AlaAsp-------------- 100
                                                      ||||||
Db        340 GCAGGCGCGCAACGCGAGCTGCCCGGCAGGGGGCAGGCCCGCCGACCGCCGCTTCCGGCC 399

Qy        101 ----ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspAr 119
                  |||:::   ||||||:::||||||||   ||||||:::      |||       ||
Db        400 GCCCACCAACCTGCGCAGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAG 459

Qy        119 gTyrProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgTh 139
              |||||||:::   |||       |||   ||||||||||||||||||:::
Db        460 GTACCCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTT 519

Qy        139 rGlyArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuAr 159
               |||  |||                |||       :::            :::||||||||
Db        520 CGGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCG 579

Qy        159 gArgArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHi 179
              ||||   |||               |||       :::   |||
Db        580 CCGCACCCCCGCCTGCGCCGGTGGCCGTTCCGTCTACACCGAGGCC-------------- 625

Qy        179 sThrGluPheIleHisValProValGlyCysThrCysVal 192
                    ::::::   :::||||||||||||||||||||
Db        626 -------TACGTCACCATCCCCGTGGGCTGCACCTGCGTN 658

RESULT 7
CV112574
LOCUS       CV112574                728 bp    mRNA    linear   EST 30-AUG-2004
DEFINITION  AGENCOURT_31524450 NIH_MGC_270 Rattus norvegicus cDNA clone
            IMAGE:7443410 5', mRNA sequence.
ACCESSION   CV112574
VERSION     CV112574.1  GI:51627541
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Josef Lazar, Dr. Howard J. Jacob, Medical
            College of Wisconsin
             cDNA Library Preparation: Open Biosystems
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15741  row: g  column: 24
            High quality sequence stop: 705.
FEATURES             Location/Qualifiers
     source          1. .728
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:7443410"
```

```
                     /tissue_type="whole placenta, 2 pooled"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_270"
                     /note="Organ: placenta; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; Tissue was collected from two pooled
                     placentas from the 21st day of pregnancy. 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer,
                     double-stranded cDNA was cloned into the Not I and EcoRV
                     sites of pExpress-1. Library was size-selected for >1.25
                     kb fragments for an average insert size of 2.15 kb.
                     Library was normalized to Cot7. A non-normalized version
                     of this library is also available (NIH_MGC_269). Library
                     was constructed by Open Biosystems (Huntsville, AL). Note:
                     this is a Mammalian Gene Collection library"
ORIGIN

Alignment Scores:
Pred. No.:                4.69e-07       Length:          728
Score:                    197.50         Matches:         55
Percent Similarity:       46.7%          Conservative:    24
Best Local Similarity:    32.5%          Mismatches:      45
Query Match:              18.4%          Indels:          45
DB:                       7              Gaps:            7

US-09-854-280-3 (1-197) x CV112574 (1-728)

Qy          42 LeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAla 61
               |||   ||||||   |||         :::::::::   ||||||        :::
Db         233 TTGATGTTGGGATTTGCC---------ATCATCAGCTCGGGAGCA------GCTCGGAGG 277

Qy          62 LeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArg 81
               |||         :::|||:::|||:::   |||   :::
Db         278 AACCCCAAAGTAGGGCTTTCTGCTCTGCAGAAAGCCGGGAAC------------------ 319

Qy          82 ProSerAlaThrThrGlnCysProValLeuArgProGluGluVal--------------- 96
                           ||||||   |||           |||
Db         320 -----------------TGCCCTCCCCTGGAGGATAACAGTGTGAGAGTTGACATTCGC 361

Qy          97 --------------------------LeuGluAlaAspThrHisGlnArgSerIleSer 107
                                        :::     |||       ||||||   |||
Db         362 ATCTTCAATCAAAACCAGGGCATTTCTGTCCCACGTGACTTCCAGAACCGCTCCAGTTCC 421

Qy         108 ProTrpArgTyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAlaPheAla 127
               ||||||   |||   :::       |||   ||||||:::|||   :::::::|||   |||
Db         422 CCATGGGATTACAATATCACCCGAGACCCCGACCGGTTCCCCTCAGAGATCGCTGAGGCC 481

Qy         128 GluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLeuAsn 147
               :::|||         |||||||||:::|||:::   |||:::|||       ::::::|||
Db         482 CAGTGCAGACACTCAGGCTGTATCAACGCCCAG---GGGCAGGAAGACGGCTCCATGAAC 538

Qy         148 SerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgPro------CysSerArg 165
               ||||||   :::   |||   :::|||||||||||||||   |||       ||||||
Db         539 TCCGTCCCCATCCAGCAAGAAATCCTGGTCCTTCGGAGGGAGCCCCAGGGCTGTTCTAAT 598

Qy         166 AspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIleHisVal 185
                                           :::|||       |||   :::   :::
Db         599 -------------------------------TCCTTCAGGTTGGAGAAGATGCTCATA 625

Qy         186 ProValGlyCysThrCysValLeuPro 194
               ||||||||||||||||   |||
Db         626 AAAGTTGGCTGCACTTGCGTCACGCCC 652

RESULT 8
AI275406
LOCUS       AI275406                441 bp    mRNA    linear   EST 29-JAN-1999
DEFINITION  ql63c10.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1877010
            3' similar to contains TAR1.b1 TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION   AI275406
VERSION     AI275406.1  GI:3897680
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 441)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1146   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 428.
FEATURES             Location/Qualifiers
     source          1. .441
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1877010"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /clone_lib="Soares_NhHMPu_S1"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
ORIGIN

Alignment Scores:
Pred. No.:                6.45e-07       Length:          441
Score:                    192.50         Matches:         51
Percent Similarity:       43.2%          Conservative:    13
Best Local Similarity:    34.5%          Mismatches:      50
Query Match:              17.9%          Indels:          34
DB:                       1              Gaps:            4

US-09-854-280-3 (1-197) x AI275406 (1-441)

Qy          48 ProProHisLeuLeuAlaArgGlyAlaLysTrpGly------GlnAlaLeuProValAla 65
               |||||||||      |||      |||      :::   ||||||
Db          59 CCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCGAGCTGCCC------ 112

Qy          66 LeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArgProSerAlaThr 85
                                           ||||||:::      ||||||
Db         113 --------------------------GGCAGGGGGCAGGCCCGCCGACCGCCG------ 139

Qy          86 ThrGlnCysProValLeuArgProGluGluValLeuGluAla-AspThrHisGlnArgSe 105
                                                 |||   |||    |||:::   |||||
Db         140 -------------------------------CTTCCGGCCGCCCACCAACCTGCGCAG 166

Qy         105 rIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAl 125
               |:::|||||||||   ||||||:::      |||      ||||||||||:::   |||
Db         167 CGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGGTACCCCAGGTACCTGCC 226

Qy         125 aPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAl 145
                  |||   ||||||||||||||||||:::            |||   |||
Db         227 TGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCGGCGAGGAGGACGTGCG 286

Qy         145 aLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgProCysSerAr 165
                     |||      :::          :::||||||||||||   |||
Db         287 CTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCGCCGCACCCCCGCCTGCGC 346

Qy         165 gAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIleHisVa 185
```

```
Db        347 CGGCGGCCGTTCCGTCTACACCGAGGCC--------------------TACGTCACCAT 385

Qy        185 lProValGlyCysThrCysVal 192
              :||||||||||||||||||||
Db        386 CCCCGTGGGCTGCACCTGCGTC 407

RESULT 9
CA526593
LOCUS       CA526593                600 bp    mRNA    linear   EST 15-NOV-2002
DEFINITION  8013-66 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
            mRNA sequence.
ACCESSION   CA526593
VERSION     CA526593.1  GI:25040631
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
            White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
  TITLE     Gene expression in the developing mouse retina by EST sequencing
            and microarray analysis
  JOURNAL   Nucleic Acids Res. 29 (24), 4983-4993 (2001)
   PUBMED   11812828
COMMENT     Contact: Klein WH
            Department of Biochemistry and Molecular Biology
            University of Texas M.D. Anderson Cancer Center
            Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
            Tel: 713 792 3646
            Fax: 713 790 0329.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="neural retina"
                     /dev_stage="embryonic day 14.5 post-fertilization"
                     /clone_lib="Mouse E14.5 retina lambda ZAP II Library"
ORIGIN

Alignment Scores:
Pred. No.:              9.86e-07        Length:         600
Score:                  192.50          Matches:        52
Percent Similarity:     44.8%           Conservative:   13
Best Local Similarity:  35.9%           Mismatches:     52
Query Match:            17.9%           Indels:         30
DB:                     6               Gaps:           4

US-09-854-280-3 (1-197) x CA526593 (1-600)

Qy         48 ProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeuProValAlaLeuVal 67
              |||||||||      ||||||   |||:::   |||   |||:::|||   |||
Db        237 CCACCACACGCTGCAGCTCGGGCCGCGCGAGCAGGCGC-GCAATGCCAGCTGCC------ 289

Qy         68 SerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArgProSerAlaThrThrGln 87
                                                    ||||||   |||
Db        290 ------------------------------------CGGCCGGGGGCAGGGCCGCCG 310

Qy         88 CysProValLeuArgProGluGluValLeuGluAlaAspThrHisGlnArgSerIleSer 107
                    ||||||                          |||:::   ||||||:::|||
Db        311 ACCGCCGC-TTCCGGCCA-----------------CCCACCAACCTGCGCAGCGTGTCG 351

Qy        108 ProTrpArgTyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAlaPheAla 127
              ||||||   ||||||:::      |||      |||:::|||:::   |||      |||
Db        352 CCCTGGGCGTACAGGATTTCCTACGACCCTGCTCGCTTTCCGAGGTACCTGCCCGAAGCC 411

Qy        128 GluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLeuAsn 147
                 ||||||||||||||||||:::            |||   |||
Db        412 TACTGCCTGTGCCGAGGCTGCCTGACCGGGCTCTACGGGGAGGAGGACTTCCGCTTTCGC 471

Qy        148 SerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgProCysSerArgAspGly 167
              |||      :::                |||||||||||                |||
Db        472 AGCACACCCGTCTTCTCTCCAGCCGNGGTGCTGCGGCGCACAGCGGCCTGCGCGGGCGGC 531

Qy        168 SerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIleHisValProVal 187
                   :::               :::|||   |||      :::|||   :::||||||
Db        532 CGCTCTGTG--------------TACGCCGANCAC------TACATCACCATCCCGGTG 570

Qy        188 GlyCysThrCysVal 192
              ||||||||||||||||
Db        571 GGCTGCACCTGCGTG 585

RESULT 10
BI561289
LOCUS       BI561289                718 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603256441F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5298706 5',
            mRNA sequence.
ACCESSION   BI561289
VERSION     BI561289.1  GI:15448603
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 718)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11756  row: a  column: 11
            High quality sequence stop: 687.
FEATURES             Location/Qualifiers
     source          1. .718
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5298706"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_97"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.2 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              3.47e-06        Length:         718
Score:                  187.50          Matches:        37
Percent Similarity:     52.2%           Conservative:   11
Best Local Similarity:  40.2%           Mismatches:     37
Query Match:            17.5%           Indels:         7
DB:                     3               Gaps:           1

US-09-854-280-3 (1-197) x BI561289 (1-718)

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
              |||:::   ||||||:::|||||||||   ||||||:::      |||      ||||||
```

```
Db         67 ACCAACCTGCGCAGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGGTAC 126

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
              |||:::   |||       |||   |||||||||||||||||:::            |||
Db        127 CCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCGGC 186

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
                |||                 |||      :::           :::||||||||||||
Db        187 GAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCGCCGC 246

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
                |||               |||      :::   |||
Db        247 ACCCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCC----------------- 288

Qy        181 GluPheIleHisValProValGlyCysThrCysVal 192
                 ::::::   :::||||||||||||||||||||
Db        289 ---TACGTCACTATCCCCGTGGGCTGCACCTGCGTC 321

RESULT 11
BI828970
LOCUS       BI828970                836 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603074846F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5166851 5',
            mRNA sequence.
ACCESSION   BI828970
VERSION     BI828970.1  GI:15940520
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 836)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11414  row: k  column: 12
            High quality sequence stop: 748.
FEATURES             Location/Qualifiers
     source          1. .836
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5166851"
                     /tissue_type="medulla"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_119"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source normal medulla from
                     anonymous male age 27.  Library  is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.3 kb, insert size range
                     0.9-3 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 013. Note:
                     this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              4.28e-06        Length:         836
Score:                  187.50          Matches:        37
Percent Similarity:     52.2%           Conservative:   11
Best Local Similarity:  40.2%           Mismatches:     37
Query Match:            17.5%           Indels:         7
DB:                     3               Gaps:           1
```

```
US-09-854-280-3 (1-197) x BI828970 (1-836)

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
              |||:::   |||||||:::|||||||||   ||||||:::      |||      ||||||
Db         35 ACCAACCTGCGCAGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGGTAC 94

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
              |||:::   |||       |||   |||||||||||||||||:::            |||
Db         95 CCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCGGC 154

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
                |||                 |||      :::           :::||||||||||||
Db        155 GAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCGCCGC 214

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
                |||               |||      :::   |||
Db        215 ACCCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCC----------------- 256

Qy        181 GluPheIleHisValProValGlyCysThrCysVal 192
                 ::::::   :::||||||||||||||||||||
Db        257 ---TACGTCACCATCCCCGTGGGCTGCACCTGCGTC 289

RESULT 12
CB418976
LOCUS       CB418976                666 bp    mRNA    linear   EST 25-MAR-2003
DEFINITION  591812 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   CB418976
VERSION     CB418976.1  GI:29183568
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8012  row: E  column: 5
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 6BOV"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including liver, lung, hypothalamus, pituitary, and
                     placenta/endometrium."
ORIGIN

Alignment Scores:
Pred. No.:              3.83e-06        Length:         666
Score:                  186.50          Matches:        55
Percent Similarity:     41.1%           Conservative:   14
Best Local Similarity:  32.7%           Mismatches:     41
Query Match:            17.4%           Indels:         58
DB:                     6               Gaps:           7
```

```
US-09-854-280-3 (1-197) x CB418976 (1-666)

Qy          28 ProHisSerHisGlyThrProHisCysTyrSerAlaGluGluLeuProLeuGlyGlnAla 47
               |||||||||   |||   |||||||||
Db         159 CCCCACTCT---GGAGGACCACATTGT------------------------------- 182

Qy          48 ProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeuProValAlaLeuVal 67

Db         182 ------------------------------------------------------------ 182

Qy          68 SerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArgProSerAlaThrThrGln 87
                                          |||   |||       |||   |||
Db         183 ------------------------GAGGGTTGACATCCGTATCCGCAGGCG--------- 209

Qy          88 CysProValLeuArgProGluGluValLeu-GluAlaAspThrHisGlnArgSerIleSe 107
                           |||         |||       :::         ||||||||||
Db         210 ------------GAACCAGGGAGTTTTCTTCTCACGCAACTTGCAGAACCGCTCCATCTC 257

Qy         107 rProTrpArgTyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAlaPheAl 127
               |||||||   |||   :::       |||   :::|||:::|||   ::::::|||   ||
Db         258 CCCTTGGGATTACAACATCACCCGGGACGCCAACCGGTTCCCCTCTGAGATCGCGGAGGC 317

Qy         127 aGluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLeuAs 147
               |:::|||         |||||||||:::|||     |||:::|||         |||||
Db         318 CCAGTGCAGACACATGGGCTGCATCAACGCGGAG---GGACAGGAAGACAGGACCCTGAA 374

Qy         147 nSerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgProCysSerArgAspGl 167
               |||||||   :::   |||       |||||||||||||||:::         ::::::||
Db         375 CTCCGTCCCCATCCAGCAGGAGTTTCTGGTCCTCCGGAGGAAG---------CAAAACGG 425

Qy         167 ySerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIleHisValProVa 187
               |                |||||         |||       |||   :::   |||   ||
Db         426 C------------TGTCCTGGC------TTGTTCCAACTGGAGAAGGTGCTGGTGACCGT 467

Qy         187 lGlyCysThrCysValLeuPro 194
               |||||||||||||||   |||
Db         468 GGGCTGCACCTGCGTCACCCCC 489

RESULT 13
DT096353
LOCUS       DT096353                 742 bp    mRNA    linear   EST 12-AUG-2005
DEFINITION  JGI_ANNN2289.fwd ANNN Pimephales promelas Whole (L) Pimephales
            promelas cDNA clone ANNN2289 5', mRNA sequence.
ACCESSION   DT096353
VERSION     DT096353.1  GI:72437711
KEYWORDS    EST.
SOURCE      Pimephales promelas
  ORGANISM  Pimephales promelas
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Pimephales.
REFERENCE   1  (bases 1 to 742)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE     DOE Joint Genome Institute Pimephales promelas EST project
  JOURNAL   Unpublished (2005)
COMMENT     Other_ESTs: JGI_ANNN2289.rev
            Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            cDNA Library Preparation: DOE Joint Genome Institute:
            http://www.jgi.doe.gov
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
            indicates a forward sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Plate: ANNN 0021  row: b  column: 22
            High quality sequence stop: 697.
FEATURES             Location/Qualifiers
     source          1. .742
                     /organism="Pimephales promelas"
                     /mol_type="mRNA"
                     /db_xref="taxon:90988"
                     /clone="ANNN2289"
                     /tissue_type="Whole"
                     /dev_stage="Adult"
                     /clone_lib="ANNN Pimephales promelas Whole (L)"
                     /note="Vector: pDONR222; The library was made from dT
                     primed cDNA and cloned into Invitrogen vector pDONR222.
                     Poly A RNA were primed with a Biotin-attB2-Oligo(dT)
                     primer (5'- GGCGGCCGCACAACTTTGTACAAGAAAGTTGGGT(T)19 -3')
                     and the first strand synthesized using Superscript II
                     (Invitrogen). The second strand was synthesized and an
                     attB1 adaptor was ligated to the 5' end (5'-
                     TCGTCGGGGACAACTTTGTACAAAAAAGTTGG -3' and 5'-
                     CCAACTTTTTTGTACAAAGTTGTCCCC -3') . cDNA was size selected
                     using 1% agarose gel electrophoresis (L ~0.5-1.2k, M
                     ~1.2-2.5k, H ~>2.5k) and then inserted into the vector
                     using site specific recombination (flanking attB sites on
                     cDNA). The work was done at DOE Joint Genome Institute."
ORIGIN

Alignment Scores:
Pred. No.:                8.15e-06        Length:          742
Score:                    183.50          Matches:         47
Percent Similarity:       49.2%           Conservative:    18
Best Local Similarity:    35.6%           Mismatches:      48
Query Match:              17.1%           Indels:          19
DB:                       8               Gaps:            5

US-09-854-280-3 (1-197) x DT096353 (1-742)

Qy          70 LeuGluAlaAlaSerHisArgGlyArgHisGluArgProSerAlaThrThr--------- 86
               |||||||||                  |||       |||       |||:::
Db         165 CTCGAAGCTTTTCTTCCACACGTCGGACACCCGCATCCGAAGGACACCAGTCATTCGGCG 224

Qy          87 ---GlnCysProValLeuArgProGluGluValLeuGluAlaAspThrHis------Gln 103
                  |||                  |||:::       ::::::   :::|||       :::
Db         225 GACTCCTGC--------------GAGAAAGCTGCTCAGTCTCTATCGCACATCAGTGAG 269

Qy         104 ArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyrProGlnLys 123
               ||||||:::||||||||||||  |||                  |||   ||||||:::
Db         270 CGCTCACTCTCCCCCTGGCGGACAAGGACTGTGCACAAGCCAGATATGTACCCCAAATCA 329

Qy         124 LeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThr 143
                  |||:::|||||||||   |||||||||                |||   |||
Db         330 TATGAGGAAGCAAAGTGTTTGTGTGAAGGATGCATC------ATTAACGGGGTTGAGAAT 383

Qy         144 AlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgProCys 163
                  |||   |||||||||   :::   :::|||:::|||   |||::::::      |||
Db         384 ATGGCCTACAACTCTGTGCCCGTGCAGAGATCTATGTTATTCCTGAAGAAGGTCTCATGC 443

Qy         164 SerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIle 183
                        |||                |||       ::::::          |||   :::
Db         444 CCGTCTGAC-----------------CCGAACAAATACTCTTTAGAGTATGAACACGTG 485

Qy         184 HisValProValGlyCysThrCysValLeuProArg 195
               |||   |||   ||||||||||||:::||||||
Db         486 CTAGTGACTGTGGCCTGTACCTGTGTGGTCCCTCGC 521

RESULT 14
BW006143/c
LOCUS       BW006143                 627 bp    mRNA    linear   EST 12-OCT-2002
DEFINITION  BW006143 Nori Satoh unpublished cDNA library, blood cells Ciona
            intestinalis cDNA clone rcibd027j08 3', mRNA sequence.
ACCESSION   BW006143
VERSION     BW006143.1  GI:23921776
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
```

```
REFERENCE   1  (bases 1 to 627)
  AUTHORS   Satou,Y., Satake,M., Azumi,K., Nonaka,M., Shin-i,T., Kohara,Y. and
            Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .627
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcibd027j08"
                     /tissue_type="blood cells"
                     /clone_lib="Nori Satoh unpublished cDNA library, blood
                     cells"
ORIGIN

Alignment Scores:
Pred. No.:                1.6e-05       Length:          627
Score:                    179.00        Matches:         49
Percent Similarity:       49.6%         Conservative:    14
Best Local Similarity:    38.6%         Mismatches:      44
Query Match:              16.7%         Indels:          20
DB:                       5             Gaps:            5

US-09-854-280-3 (1-197) x BW006143 (1-627)

Qy          75 HisArgGlyArgHisGluArgProSerAlaThrThrGlnCysProValLeuArgProGlu 94
               |||     ||||||:::|||       :::|||       ||||||||||||       |||
Db         433 CATGGCATCCGACATAAAAGGTCGCAATCAACA------TGCCCCGTTTTGTCCGACGAA 380

Qy          95 GluValLeuGluAlaAspThrHis-----------GlnArgSerIleSerProTrpArg 110
                  :::|||         ||||||           :::|||||:::||||||:::
Db         379 TATTTACTA---------ACTCACACAAGACAAGAGGAAAGAAGTTTGTCGCCATATGTG 329

Qy         111 TyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAlaPheAlaGluCysLeu 130
                   |||   |||       |||   |||       |||       |||   ||||||
Db         328 ATAGAAGATGACATTGATAGGTTAAGAATCCCTATGGTGCTTCCACGAGCAAGATGTTTA 269

Qy         131 CysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLeuAsnSerValArg 150
               |||   ||||||||||       :::   ||||||      :::       ||||||
Db         268 TGTGATGGCTGTATCGACATGTCCAGCAGACGAGAAAACTTCTCCTTTGCGTCTGTGCCT 209

Qy         151 LeuLeuGlnSerLeuLeuValLeuArgArgArgProCysSerArgAspGlySerGlyLeu 170
               |||   ||||||      |||   :::|||       :::   :::|||
Db         208 TTGAAACAATCATTCACAGTCAGGAAAAGAAAC------ACAGAAAACGGT--------- 164

Qy         171 ProThrProGlyAlaPheAlaPheHisThrGluPheIleHisValProValGlyCysThr 190
                                      |||           :::   ||||||||||||
Db         163 -----------------CCATTGGAAACTGTTACACAAACCATTACCGTTGGTTGTACT 122

Qy         191 CysValLeuProArgSerVal 197
               ||||||:::||||||   :::
Db         121 TGTGTTGTGCCTCGTAGAATT 101

RESULT 15
BW035020
LOCUS       BW035020                649 bp    mRNA    linear   EST 13-OCT-2002
DEFINITION  BW035020 Nori Satoh unpublished cDNA library, blood cells Ciona
            intestinalis cDNA clone cibd027j08 5', mRNA sequence.
ACCESSION   BW035020
VERSION     BW035020.1  GI:23950972
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
```

```
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Satou,Y., Satake,M., Azumi,K., Nonaka,M., Shin-i,T., Kohara,Y. and
            Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cibd027j08"
                     /tissue_type="blood cells"
                     /clone_lib="Nori Satoh unpublished cDNA library, blood
                     cells"
ORIGIN

Alignment Scores:
Pred. No.:                1.68e-05      Length:          649
Score:                    179.00        Matches:         49
Percent Similarity:       49.6%         Conservative:    14
Best Local Similarity:    38.6%         Mismatches:      44
Query Match:              16.7%         Indels:          20
DB:                       5             Gaps:            5

US-09-854-280-3 (1-197) x BW035020 (1-649)

Qy          75 HisArgGlyArgHisGluArgProSerAlaThrThrGlnCysProValLeuArgProGlu 94
               |||     ||||||:::|||       :::|||       ||||||||||||       |||
Db         175 CATGGCATCCGACATAAAAGGTCGCAATCAACA------TGCCCCGTTTTGTCCGACGAA 228

Qy          95 GluValLeuGluAlaAspThrHis-----------GlnArgSerIleSerProTrpArg 110
                  :::|||         ||||||           :::|||||:::||||||:::
Db         229 TATTTACTA---------ACTCACACAAGACAAGAGGAAAGAAGTTTGTCGCCATATGTG 279

Qy         111 TyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAlaPheAlaGluCysLeu 130
                   |||   |||       |||   |||       |||       |||   ||||||
Db         280 ATAGAAGATGACATTGATAGGTTAAGAATCCCTATGGTGCTTCCACGAGCAAGATGTTTA 339

Qy         131 CysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLeuAsnSerValArg 150
               |||   ||||||||||       :::   ||||||      :::       ||||||
Db         340 TGTGATGGCTGTATCGACATGTCCAGCAGACGAGAAAACTTCTCCTTTGCGTCTGTGCCT 399

Qy         151 LeuLeuGlnSerLeuLeuValLeuArgArgArgProCysSerArgAspGlySerGlyLeu 170
               |||   ||||||      |||   :::|||       :::   :::|||
Db         400 TTGAAACAATCATTCACAGTCAGGAAAAGAAAC------ACAGAAAACGGT--------- 444

Qy         171 ProThrProGlyAlaPheAlaPheHisThrGluPheIleHisValProValGlyCysThr 190
                                      |||           :::   ||||||||||||
Db         445 -----------------CCATTGGAAACTGTTACACAAACCATTACCGTTGGTTGTACT 486

Qy         191 CysValLeuProArgSerVal 197
               ||||||:::||||||   :::
Db         487 TGTGTTGTGCCTCGTAGAATT 507


Search completed: May  1, 2006, 00:55:36
Job time : 3974 secs
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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2006, 23:50:52 ; Search time 4846 Seconds
(without alignments)
2310.805 Million cell updates/sec

Title: US-09-854-280-3
Perfect score: 1073
Sequence: 1 MTLLPGLLFLTWLHTCLAHH.....FHTEFIHVPVGCTCVLPRSV 197

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US09854280/runat_27042006_101648_27674/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US09854280_@CGN_1_1_4939_@runat_27042006_101648_27674 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
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7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1073	100.0	591	6	AX427978	AX427978 Sequence
2	1073	100.0	594	6	BD218885	BD218885 Factor af
3	1073	100.0	613	8	BC069152	BC069152 Homo sapi
4	1073	100.0	1047	6	BD218877	BD218877 Factor af
5	1073	100.0	1047	6	AR338357	AR338357 Sequence
6	1073	100.0	1047	6	AX180766	AX180766 Sequence
7	1073	100.0	1047	6	AX376380	AX376380 Sequence
8	1073	100.0	1047	8	AF152099	AF152099 Homo sapi
9	1073	100.0	1047	8	AY358471	AY358471 Homo sapi
10	1073	100.0	1067	6	BD211219	BD211219 Interleuk
11	1073	100.0	1067	6	CQ847631	CQ847631 Sequence
12	1073	100.0	1107	6	BD265555	BD265555 Interleuk
13	1073	100.0	1107	6	CS135286	CS135286 Sequence
14	1073	100.0	1107	6	AR316787	AR316787 Sequence
15	1065	99.3	1078	8	AF142410	AF142410 Homo sapi
16	1063	99.1	593	6	CQ714767	CQ714767 Sequence
17	1063	99.1	1177	6	AX223949	AX223949 Sequence
c 18	969	90.3	156899	14	AC103884	AC103884 Homo sapi
c 19	969	90.3	176797	8	AC116552	AC116552 Homo sapi
20	830.5	77.4	197192	14	AC148637	AC148637 Callithri
21	788	73.4	585	9	AF458061	AF458061 Mus muscu
22	781	72.8	231193	14	AC148624	AC148624 Otolemur
23	673.5	62.8	267809	14	AC130171	AC130171 Rattus no
24	611	56.9	179454	14	AC123737	AC123737 Mus muscu
25	611	56.9	181442	9	AC114917	AC114917 Mus muscu
26	611	56.9	221647	9	AL591003	AL591003 Mouse DNA
27	459	42.8	705	6	BD211199	BD211199 Interleuk
28	459	42.8	705	6	CQ847604	CQ847604 Sequence
29	446	41.6	521	6	BD265553	BD265553 Interleuk
30	446	41.6	521	6	BD265554	BD265554 Interleuk
31	446	41.6	521	6	AR316785	AR316785 Sequence
32	446	41.6	521	6	AR316786	AR316786 Sequence
33	407	37.9	230	6	BD218880	BD218880 Factor af
34	403	37.6	112467	14	AC164519	AC164519 Alligator
35	391.5	36.5	122853	14	AC154080	AC154080 Dromaius
36	380	35.4	599	10	BV208612	BV208612 IL17C_185
37	261.5	24.4	332	6	BD211220	BD211220 Interleuk
38	261.5	24.4	332	6	CQ847633	CQ847633 Sequence
39	218.5	20.4	2361	6	BD229893	BD229893 Mammalian
40	218.5	20.4	2361	6	AX648021	AX648021 Sequence
41	202	18.8	1379	8	AF458062	AF458062 Homo sapi
42	202	18.8	1385	6	BD265547	BD265547 Interleuk
43	202	18.8	1385	6	AR316779	AR316779 Sequence
44	201.5	18.8	609	8	AF479775	AF479775 Homo sapi
45	201.5	18.8	609	11	AY890522	AY890522 Synthetic
46	201.5	18.8	609	11	AY892988	AY892988 Synthetic
47	201.5	18.8	1754	6	CQ970522	CQ970522 Sequence
48	201.5	18.8	1754	6	AR338359	AR338359 Sequence
49	201.5	18.8	1754	6	AX180770	AX180770 Sequence
50	201.5	18.8	1754	6	AX358834	AX358834 Sequence
51	201.5	18.8	1754	6	AX362327	AX362327 Sequence
52	201.5	18.8	1754	8	AY359113	AY359113 Homo sapi
53	201.5	18.8	1819	6	BD229887	BD229887 Mammalian
54	201.5	18.8	1819	6	AX648016	AX648016 Sequence
55	201.5	18.8	1873	8	AY078238	AY078238 Homo sapi
56	201.5	18.8	1878	8	BC036243	BC036243 Homo sapi
57	197.5	18.4	1308	9	BC091568	BC091568 Rattus no
58	194.5	18.1	1496	6	AX365250	AX365250 Sequence
59	193	18.0	985	6	BD265552	BD265552 Interleuk
60	193	18.0	985	6	AR316784	AR316784 Sequence
61	193	18.0	985	6	AR451797	AR451797 Sequence
62	193	18.0	985	6	AX299775	AX299775 Sequence
63	193	18.0	985	9	AF458060	AF458060 Mus muscu
64	193	18.0	1013	6	AX365244	AX365244 Sequence
65	192.5	17.9	498	6	CQ724626	CQ724626 Sequence
66	192.5	17.9	522	6	BD211221	BD211221 Interleuk
67	192.5	17.9	522	6	CQ847634	CQ847634 Sequence
68	192.5	17.9	1143	6	BD265549	BD265549 Interleuk
69	192.5	17.9	1143	6	AR316781	AR316781 Sequence
70	192.5	17.9	1143	9	AF458063	AF458063 Mus muscu
71	192.5	17.9	1221	6	BD229890	BD229890 Mammalian
72	192.5	17.9	1221	6	AX648024	AX648024 Sequence
73	192.5	17.9	1641	6	CQ847606	CQ847606 Sequence
74	192.5	17.9	1642	6	BD211200	BD211200 Interleuk
75	192	17.9	454	6	BD265546	BD265546 Interleuk
76	192	17.9	454	6	AR316778	AR316778 Sequence

77	186	17.3	462	9	AY034088	AY034088 Mus muscu
78	184	17.1	462	9	AF458064	AF458064 Mus muscu
79	184	17.1	486	9	AB116259	AB116259 Mus muscu
80	184	17.1	1178	9	AY380822	AY380822 Mus muscu
81	177.5	16.5	1461	5	BC075405	BC075405 Xenopus t
82	176	16.4	644	6	AX253225	AX253225 Sequence
83	176	16.4	644	6	AX365242	AX365242 Sequence
84	176	16.4	644	8	AF461739	AF461739 Homo sapi
85	175	16.3	686	9	AF250308	AF250308 Mus muscu
86	175	16.3	813	6	AR080776	AR080776 Sequence
87	175	16.3	813	6	AR098182	AR098182 Sequence
88	175	16.3	813	6	I79597	I79597 Sequence 11
89	175	16.3	813	6	AR670463	AR670463 Sequence
90	175	16.3	835	8	BC070124	BC070124 Homo sapi
91	173	16.1	492	8	AF384857	AF384857 Homo sapi
92	173	16.1	535	6	AX092428	AX092428 Sequence
93	173	16.1	559	6	CS017392	CS017392 Sequence
94	173	16.1	559	6	AR338360	AR338360 Sequence
95	173	16.1	559	6	AX180772	AX180772 Sequence
96	173	16.1	692	6	BD133043	BD133043 Mammalian
97	173	16.1	692	6	AR285438	AR285438 Sequence
98	173	16.1	692	6	AR337881	AR337881 Sequence
99	173	16.1	692	6	AR406128	AR406128 Sequence
100	173	16.1	692	6	AX236267	AX236267 Sequence
101	173	16.1	692	9	AF184970	AF184970 Mus muscu
102	173	16.1	693	6	CQ743809	CQ743809 Sequence
103	173	16.1	693	9	AF218726	AF218726 Mus muscu
104	173	16.1	707	9	BC002271	BC002271 Mus muscu
105	173	16.1	735	6	CS035438	CS035438 Sequence
106	173	16.1	735	6	CS044390	CS044390 Sequence
107	173	16.1	947	8	AF332389	AF332389 Homo sapi
108	169.5	15.8	592	8	BC066251	BC066251 Homo sapi
109	169	15.8	486	8	AF458059	AF458059 Homo sapi
110	169	15.8	504	6	BD265550	BD265550 Interleuk
111	169	15.8	504	6	AR316782	AR316782 Sequence
112	169	15.8	504	6	AR451796	AR451796 Sequence
113	169	15.8	504	6	AX299773	AX299773 Sequence
114	169	15.8	564	6	BD058149	BD058149 Secreted
115	169	15.8	897	8	BC069565	BC069565 Homo sapi
116	169	15.8	1320	6	AR338358	AR338358 Sequence
117	169	15.8	1320	6	AX092424	AX092424 Sequence
118	169	15.8	1320	6	AX164145	AX164145 Sequence
119	169	15.8	1320	6	AX180768	AX180768 Sequence
120	169	15.8	1320	8	AY359127	AY359127 Homo sapi
121	169	15.8	1335	8	AF305200	AF305200 Homo sapi
122	168.5	15.7	543	6	BD265545	BD265545 Interleuk
123	168.5	15.7	543	6	AR316777	AR316777 Sequence
c 124	167.5	15.6	231050	14	AC108650	AC108650 Rattus no
125	167.5	15.6	254766	14	AC127117	AC127117 Rattus no
126	166	15.5	1202	4	AB102693	AB102693 Sus scrof
127	165	15.4	510	5	AY744450	AY744450 Gallus ga
128	165	15.4	725	5	AY920750	AY920750 Gallus ga
129	165	15.4	935	5	GGA493595	AJ493595 Gallus ga
c 130	164.5	15.3	683	5	CR352515	CR352515 Gallus ga
131	163.5	15.2	918	5	OMY580843	AJ580843 Oncorhync
132	162	15.1	669	4	AF416586	AF416586 Bos tauru
133	162	15.1	1019	4	AF412040	AF412040 Bos tauru
134	161	15.0	510	6	AR165238	AR165238 Sequence
135	161	15.0	510	6	E37764	E37764 Purified pr
136	161	15.0	510	6	AR316459	AR316459 Sequence
137	161	15.0	510	6	AR487986	AR487986 Sequence
138	161	15.0	592	8	BC066252	BC066252 Homo sapi
139	161	15.0	592	8	BC067503	BC067503 Homo sapi
140	161	15.0	592	8	BC067504	BC067504 Homo sapi
141	161	15.0	592	8	BC067505	BC067505 Homo sapi
142	161	15.0	1213	8	HSCTLA8	Z58820 H.sapiens C
143	161	15.0	1859	6	CQ718726	CQ718726 Sequence
144	161	15.0	1859	6	CS017391	CS017391 Sequence
145	161	15.0	1874	6	AR380346	AR380346 Sequence
146	161	15.0	1874	8	HSU32659	U32659 Human IL-17
147	160.5	15.0	456	6	AR165236	AR165236 Sequence
148	160.5	15.0	456	6	E37762	E37762 Purified pr
149	160.5	15.0	456	6	AR316457	AR316457 Sequence
150	160.5	15.0	459	6	AR098184	AR098184 Sequence
151	160.5	15.0	459	6	AR670465	AR670465 Sequence
152	160.5	15.0	2520	6	AR487984	AR487984 Sequence
153	160.5	15.0	2520	13	HSVIE	M60286 Herpesvirus
c 154	160.5	15.0	16325	13	HSVSPOLGBP	M31122 Herpesvirus
c 155	160.5	15.0	112930	13	HSGEND	X64346 Saimiriine
156	158.5	14.8	684	8	AF218727	AF218727 Homo sapi
157	158.5	14.8	687	6	BD218876	BD218876 Factor af
158	158.5	14.8	687	6	CQ768002	CQ768002 Sequence
159	158.5	14.8	687	6	AR338356	AR338356 Sequence
160	158.5	14.8	687	6	AX047648	AX047648 Sequence
161	158.5	14.8	687	6	AX055448	AX055448 Sequence
162	158.5	14.8	687	6	AX180764	AX180764 Sequence
163	158.5	14.8	687	6	AX464312	AX464312 Sequence
164	158.5	14.8	687	8	AF152098	AF152098 Homo sapi
165	158.5	14.8	687	8	AY358931	AY358931 Homo sapi
166	158.5	14.8	688	6	CQ726572	CQ726572 Sequence
167	158.5	14.8	688	8	AF184969	AF184969 Homo sapi
168	158.5	14.8	703	8	AF110385	AF110385 Homo sapi
169	158.5	14.8	705	6	BD073267	BD073267 Interleuk
170	158.5	14.8	705	6	AR257338	AR257338 Sequence
171	158.5	14.8	705	6	AR634313	AR634313 Sequence
172	158.5	14.8	711	8	AF212311	AF212311 Homo sapi
173	158.5	14.8	736	6	BD133035	BD133035 Mammalian
174	158.5	14.8	736	6	AR285430	AR285430 Sequence
175	158.5	14.8	736	6	AR337877	AR337877 Sequence
176	158.5	14.8	736	6	AR406120	AR406120 Sequence
177	158.5	14.8	736	6	AX236262	AX236262 Sequence
c 178	158	14.7	110000	14	AC156266_09	Continuation (10 o
179	157.5	14.7	540	9	AF218725	AF218725 Mesocrice
c 180	157.5	14.7	16552	13	HVSC488	Y13183 Herpesvirus
c 181	157.5	14.7	113027	13	SHE410493	AJ410493 Saimiriin
182	154.5	14.4	543	6	BD218884	BD218884 Factor af
183	154.5	14.4	689	6	BD275561	BD275561 MOLECULES
184	154.5	14.4	771	6	AX720706	AX720706 Sequence
185	154	14.4	592	8	BC066253	BC066253 Homo sapi
186	153.5	14.3	1667	9	AF502584	AF502584 Mus muscu
187	153.5	14.3	135110	8	AL512652	AL512652 Human DNA
c 188	153.5	14.3	140800	14	AC018392	AC018392 Homo sapi
189	151	14.1	620	6	BD265551	BD265551 Interleuk
190	151	14.1	620	6	AR316783	AR316783 Sequence
191	150.5	14.0	483	6	AX720708	AX720708 Sequence
192	150.5	14.0	498	6	AR034065	AR034065 Sequence
193	150.5	14.0	498	6	AR097655	AR097655 Sequence
194	150.5	14.0	498	6	AR097732	AR097732 Sequence
195	150.5	14.0	498	6	AR104869	AR104869 Sequence
196	150.5	14.0	498	6	AR131080	AR131080 Sequence
197	150.5	14.0	498	6	AR137602	AR137602 Sequence
198	150.5	14.0	498	6	AR453136	AR453136 Sequence
199	150.5	14.0	543	6	BD265544	BD265544 Interleuk
200	150.5	14.0	543	6	AR316776	AR316776 Sequence
201	150.5	14.0	543	6	AX720707	AX720707 Sequence
202	150.5	14.0	543	8	CR457192	CR457192 Homo sapi
203	149	13.9	1540	5	AB195258	AB195258 Danio rer
204	149	13.9	122061	5	BX950194	BX950194 Zebrafish
c 205	149	13.9	197329	5	BX323598	BX323598 Zebrafish
206	148.5	13.8	461	6	AR098183	AR098183 Sequence
207	148.5	13.8	461	6	AR670464	AR670464 Sequence
208	148.5	13.8	1080	6	AR165235	AR165235 Sequence
209	148.5	13.8	1080	6	E37761	E37761 Purified pr
210	148.5	13.8	1080	6	AR316456	AR316456 Sequence
211	148.5	13.8	1080	6	AR487983	AR487983 Sequence
212	148.5	13.8	1080	9	MUSCTLA8A	L13839 Mus musculu
213	148.5	13.8	1115	9	MMU43088	U43088 Mus Musculu
214	148.5	13.8	1134	6	AR165239	AR165239 Sequence
215	148.5	13.8	1134	6	AR487987	AR487987 Sequence
c 216	147	13.7	154606	14	AC159614	AC159614 Mus muscu
217	147	13.7	224673	9	AC156980	AC156980 Mus muscu
218	143	13.3	130904	8	HS108C2	AL034343 Human DNA
c 219	143	13.3	197452	14	AL355513	AL355513 Homo sapi
c 220	142.5	13.3	225702	14	AC121687	AC121687 Rattus no
c 221	142.5	13.3	248546	14	AC133690	AC133690 Rattus no
222	139	13.0	143666	14	CT025533	CT025533 Mus muscu

	223	138.5	12.9	723	6	AR257356 AR257356 Sequence
c	224	138.5	12.9	723	6	AR257357 AR257357 Sequence
c	225	137.5	12.8	185702	14	AC130940 AC130940 Rattus no
	226	137.5	12.8	210784	14	AC119293 AC119293 Rattus no
	227	137.5	12.8	263901	14	AC115371 AC115371 Rattus no
	228	136	12.7	258	6	CQ056602 CQ056602 Sequence
	229	136	12.7	258	6	CQ075879 CQ075879 Sequence
	230	136	12.7	258	6	CQ106856 CQ106856 Sequence
	231	136	12.7	258	6	CQ145509 CQ145509 Sequence
	232	136	12.7	258	6	CQ180956 CQ180956 Sequence
	233	136	12.7	258	6	CQ205322 CQ205322 Sequence
	234	136	12.7	258	6	CQ228711 CQ228711 Sequence
	235	136	12.7	258	6	CQ266867 CQ266867 Sequence
	236	136	12.7	258	6	CQ341148 CQ341148 Sequence
	237	135.5	12.6	497	6	BD133044 BD133044 Mammalian
	238	135.5	12.6	497	6	AR285439 AR285439 Sequence
	239	135.5	12.6	497	6	AR337882 AR337882 Sequence
	240	135.5	12.6	497	6	AR406129 AR406129 Sequence
	241	135.5	12.6	497	6	AX236269 AX236269 Sequence
c	242	133	12.4	221451	14	AC154675 AC154675 Mus muscu
	243	132	12.3	2078	5	AB195259 AB195259 Danio rer
c	244	132	12.3	125898	5	CR392366 CR392366 Zebrafish
	245	132	12.3	151862	14	BX936339 BX936339 Danio rer
c	246	131.5	12.3	110000	14	AC156266_14 Continuation (15 o
c	247	130	12.1	323	8	HUMNOTIA L23206 Human chrom
	248	129.5	12.1	333	9	AF218724 AF218724 Rattus no
c	249	127	11.8	285562	14	AC096124 AC096124 Rattus no
	250	125	11.6	237	6	AR487985 AR487985 Sequence
	251	125	11.6	239	6	E37763 E37763 Purified pr
	252	125	11.6	240	6	AR165237 AR165237 Sequence
	253	125	11.6	240	6	AR316458 AR316458 Sequence
	254	125	11.6	7422	8	AY460616 AY460616 Homo sapi
	255	125	11.6	152546	8	AL391221 AL391221 Human DNA
	256	125	11.6	197452	14	AL355513 AL355513 Homo sapi
	257	124	11.6	157910	8	CNS01DTR AL132855 Human chr
	258	124	11.6	196292	8	CNS0000B AL049829 Human chr
	259	122	11.4	514	6	BD058147 BD058147 Secreted
	260	121.5	11.3	640	5	OMY580842 AJ580842 Oncorhync
	261	120.5	11.2	2240	2	AB181457 AB181457 Ciona int
	262	120	11.2	110000	1	CP000090_18 Continuation (19 o
c	263	119	11.1	599	10	BV028804 BV028804 S212P6008
	264	119	11.1	2060	2	AB181456 AB181456 Ciona int
	265	119	11.1	2946	9	MMU35108 U35108 Mus musculu
c	266	119	11.1	128572	2	AY827840 AY827840 Ciona int
	267	119	11.1	154606	14	AC159614 AC159614 Mus muscu
c	268	119	11.1	201999	14	AC152463 AC152463 Sus scrof
	269	119	11.1	231050	14	AC108650 AC108650 Rattus no
	270	118.5	11.0	1294	5	BC085035 BC085035 Xenopus l
	271	117.5	11.0	830	6	BD218878 BD218878 Factor af
	272	116.5	10.9	1943	8	AK123964 AK123964 Homo sapi
c	273	116.5	10.9	149052	14	AC130409 AC130409 Homo sapi
c	274	116.5	10.9	151341	14	AC019297 AC019297 Homo sapi
	275	116.5	10.9	177835	8	AC012020 AC012020 Homo sapi
	276	115	10.7	2033	8	AB071099 AB071099 Macaca fa
c	277	115	10.7	39303	8	AC005595 AC005595 Homo sapi
c	278	115	10.7	181683	14	AC021618 AC021618 Homo sapi
c	279	115	10.7	198583	14	AC019114 AC019114 Homo sapi
c	280	114.5	10.7	110000	1	BA000040_36 Continuation (37 o
	281	113.5	10.6	192732	8	AC027601 AC027601 Homo sapi
c	282	113	10.5	4456	8	AK024487 AK024487 Homo sapi
	283	113	10.5	151027	14	AC019003 AC019003 Homo sapi
c	284	113	10.5	197202	14	AC153077 AC153077 Callithri
	285	112	10.4	1765	5	AB195260 AB195260 Danio rer
	286	112	10.4	4104	9	RATNMDARD1 D13213 Rattus norv
	287	112	10.4	4670	9	RATNR2DA L31611 Rattus norv
	288	112	10.4	4957	9	RNU08260 U08260 Rattus norv
	289	112	10.4	5246	9	RATNR2DB L31612 Rattus norv
	290	112	10.4	9077	8	AF386077 AF386077 Homo sapi
c	291	112	10.4	122303	8	AC008681 AC008681 Homo sapi
	292	112	10.4	125584	14	AC155415 AC155415 Zea mays
	293	112	10.4	161246	9	AC124479 AC124479 Mus muscu
c	294	112	10.4	165073	5	BX279523 BX279523 Zebrafish
	295	112	10.4	179633	8	AC131025 AC131025 Homo sapi
	296	112	10.4	254278	14	AC095693 AC095693 Rattus no
c	297	111	10.3	2553	2	AY508647 AY508647 Encephali
c	298	111	10.3	171960	9	AC153943 AC153943 Mus muscu
c	299	111	10.3	210101	9	AC153823 AC153823 Mus muscu
	300	111	10.3	219973	9	AL670227 AL670227 Mouse DNA
	301	110.5	10.3	403	6	BD265556 BD265556 Interleuk
	302	110.5	10.3	403	6	BD265557 BD265557 Interleuk
	303	110.5	10.3	403	6	AR316788 AR316788 Sequence
	304	110.5	10.3	403	6	AR316789 AR316789 Sequence
c	305	110.5	10.3	175016	9	AC115691 AC115691 Mus muscu
c	306	110.5	10.3	207265	9	AC125157 AC125157 Mus muscu
	307	110	10.3	443	6	CQ051632 CQ051632 Sequence
	308	110	10.3	443	6	CQ066689 CQ066689 Sequence
	309	110	10.3	443	6	CQ093731 CQ093731 Sequence
	310	110	10.3	443	6	CQ132506 CQ132506 Sequence
	311	110	10.3	443	6	CQ171080 CQ171080 Sequence
	312	110	10.3	443	6	CQ200218 CQ200218 Sequence
	313	110	10.3	443	6	CQ215711 CQ215711 Sequence
	314	110	10.3	443	6	CQ254303 CQ254303 Sequence
	315	110	10.3	443	6	CQ328432 CQ328432 Sequence
c	316	110	10.3	159551	14	AC156778 AC156778 Rhinoloph
	317	110	10.3	209982	2	CNS06C8G AL391737 chromosom
c	318	110	10.3	209982	2	CNS06C8G AL391737 chromosom
	319	110	10.3	238147	2	CNS07EGF AL590448 chromosom
	320	109.5	10.2	33002	8	HS349E11 AL031713 Human DNA
	321	109.5	10.2	265786	8	AE006466 AE006466 Homo sapi
	322	109	10.2	5616	2	ECU5644 AJ005644 Encephali
c	323	109	10.2	164722	14	AC129349 AC129349 Rattus no
	324	109	10.2	246805	14	AC098750 AC098750 Rattus no
c	325	108.5	10.1	110000	14	AP006487_4 Continuation (5 of
	326	108.5	10.1	232406	14	AC146898 AC146898 Pongo pyg
	327	108	10.1	110000	2	CP000081_06 Continuation (7 of
c	328	108	10.1	215960	14	AC144881 AC144881 Gorilla g
c	329	108	10.1	221135	14	AC097027 AC097027 Rattus no
	330	108	10.1	222896	14	AC119773 AC119773 Rattus no
	331	107.5	10.0	195511	14	AC013305 AC013305 Homo sapi
	332	106.5	9.9	10277	1	AE009080 AE009080 Agrobacte
	333	106.5	9.9	12230	1	AE008045 AE008045 Agrobacte
c	334	106.5	9.9	70282	8	AP001505 AP001505 Homo sapi
	335	106.5	9.9	76571	14	AC011649 AC011649 Homo sapi
	336	106.5	9.9	151163	8	HSA305P22 AL121673 Human DNA
	337	106.5	9.9	239476	14	AC165974 AC165974 Mus muscu
c	338	106.5	9.9	340000	8	HS21C101 AL163301 Homo sapi
	339	106	9.9	878	15	AK108088 AK108088 Oryza sat
c	340	106	9.9	96230	1	CR555306_42 Continuation (43 o
c	341	106	9.9	110000	1	BA000030_02 Continuation (3 of
c	342	106	9.9	110000	15	AP008214_176 Continuation (177
c	343	106	9.9	118339	15	AP003962 AP003962 Oryza sat
c	344	106	9.9	123721	14	OSJN01008 AL607100 Oryza sat
c	345	106	9.9	148947	15	AP004397 AP004397 Oryza sat
c	346	106	9.9	156842	14	AC064820 AC064820 Homo sapi
c	347	105.5	9.8	1969	9	AF188021 AF188021 Mus muscu
c	348	105.5	9.8	2061	9	AF188014 AF188014 Mus muscu
c	349	105.5	9.8	2099	9	AF188023 AF188023 Mus muscu
c	350	105.5	9.8	2112	9	AF188013 AF188013 Mus muscu
c	351	105.5	9.8	2158	9	AF188011 AF188011 Mus muscu
c	352	105.5	9.8	2344	9	AF188012 AF188012 Mus muscu
c	353	105.5	9.8	2616	9	BC099929 BC099929 Mus muscu
c	354	105.5	9.8	3075	9	AF188008 AF188008 Mus muscu
c	355	105.5	9.8	14827	9	AY480041 AY480041 Mus muscu
c	356	105.5	9.8	14853	9	AY480039 AY480039 Mus muscu
c	357	105.5	9.8	14854	9	AY480034 AY480034 Mus muscu
c	358	105.5	9.8	14906	9	AY480037 AY480037 Mus muscu
c	359	105.5	9.8	14915	9	AY480035 AY480035 Mus muscu
c	360	105.5	9.8	14919	9	AY480033 AY480033 Mus muscu
c	361	105.5	9.8	14944	9	AY480036 AY480036 Mus muscu
c	362	105.5	9.8	14944	9	AY480042 AY480042 Mus muscu
c	363	105.5	9.8	15001	9	AY480040 AY480040 Mus muscu
c	364	105.5	9.8	15001	9	AY480043 AY480043 Mus muscu
c	365	105.5	9.8	15438	9	AY480038 AY480038 Mus muscu
	366	105.5	9.8	99961	8	AL606510 AL606510 Human DNA
	367	105.5	9.8	110000	15	AP008210_180 Continuation (181
	368	105.5	9.8	131489	15	OSJN00216 AL663016 Oryza sat

c 369	105.5	9.8	143549	14	AC118287	AC118287 Oryza sat
370	105.5	9.8	174380	9	AL662805	AL662805 Mouse DNA
c 371	105.5	9.8	227448	15	BX649607	BX649607 Aspergill
c 372	105	9.8	652	10	BV629183	BV629183 S215P6126
373	105	9.8	1235	4	RABIGHAD	K00752 Oryctolagus
374	105	9.8	4622	6	AR169917	AR169917 Sequence
375	105	9.8	4622	6	AR172621	AR172621 Sequence
376	105	9.8	4622	6	AR340583	AR340583 Sequence
377	105	9.8	92537	14	AC138706	AC138706 Homo sapi
c 378	105	9.8	110000	1	CP000088_31	Continuation (32 o
c 379	105	9.8	154201	9	AC006082	AC006082 Mus muscu
380	105	9.8	158836	9	AC125114	AC125114 Mus muscu
381	105	9.8	183224	14	AC166615	AC166615 Oryctolag
382	105	9.8	188708	9	AC005817	AC005817 Mus muscu
c 383	105	9.8	204483	14	AC156259	AC156259 Oryctolag
c 384	105	9.8	211848	9	AC087064	AC087064 Mus muscu
385	105	9.8	214471	9	AC079043	AC079043 Mus muscu
c 386	105	9.8	215057	9	AC118542	AC118542 Mus muscu
c 387	105	9.8	222506	14	AC162441	AC162441 Mus muscu
388	105	9.8	226736	9	AC098881	AC098881 Mus muscu
c 389	105	9.8	292200	1	SCO939129	AL939129 Streptomy
c 390	104.5	9.7	1552	1	BSPZ95711	Z95711 Bacterial s
391	104.5	9.7	53121	14	AC136331	AC136331 Homo sapi
c 392	104.5	9.7	110000	15	AP008213_197	Continuation (198
393	104.5	9.7	131711	14	AP003954	AP003954 Oryza sat
c 394	104.5	9.7	145772	15	AP004269	AP004269 Oryza sat
395	104.5	9.7	168491	14	AC160919	AC160919 Papio ham
c 396	104.5	9.7	170959	14	AC022197	AC022197 Homo sapi
c 397	104	9.7	11236	1	AE012314	AE012314 Xanthomon
c 398	104	9.7	110000	14	CT005265_06	Continuation (7 of
c 399	104	9.7	162296	8	AL161774	AL161774 Human DNA
c 400	104	9.7	190264	14	AC161624	AC161624 Pan trogl
401	104	9.7	197714	14	AC128967	AC128967 Rattus no
402	104	9.7	199883	14	AC073736	AC073736 Mus muscu
403	104	9.7	227533	14	AC094895	AC094895 Rattus no
404	104	9.7	256455	14	AC129138	AC129138 Rattus no
405	103.5	9.6	956	8	AY363223	AY363223 Homo sapi
c 406	103.5	9.6	970	3	AY943003	AY943003 Unculture
407	103.5	9.6	5424	2	AF151371	AF151371 Toxoplasm
408	103.5	9.6	8482	2	AF151372	AF151372 Toxoplasm
409	103.5	9.6	8919	13	STLVPH969	Y07616 Simian T-ce
c 410	103.5	9.6	44335	8	AL512383	AL512383 Human DNA
411	103.5	9.6	78475	14	CR954211_5	Continuation (6 of
412	103.5	9.6	101684	15	AP005847	AP005847 Oryza sat
413	103.5	9.6	110000	15	AP008214_037	Continuation (38 o
c 414	103.5	9.6	158520	14	AC026668	AC026668 Homo sapi
415	103.5	9.6	192857	15	AP005605	AP005605 Oryza sat
416	103.5	9.6	194845	14	AC163517	AC163517 Bos tauru
417	103.5	9.6	260335	14	AC115140	AC115140 Rattus no
c 418	103	9.6	2470	2	DMNCP450R	X93090 D.melanogas
c 419	103	9.6	2721	6	CQ592419	CQ592419 Sequence
c 420	103	9.6	2734	2	AY052000	AY052000 Drosophil
421	102.5	9.6	280	4	AY014959	AY014959 Equus cab
422	102.5	9.6	1024	5	CR390256	CR390256 Gallus ga
c 423	102.5	9.6	1368	3	AY214900	AY214900 Unculture
c 424	102.5	9.6	24055	8	HSLUCA9	Z75743 Human DNA s
425	102.5	9.6	25608	1	BA000030_90	Continuation (91 o
426	102.5	9.6	69648	15	CNS08C86	AL731757 Oryza sat
427	102.5	9.6	104406	14	AC136810	AC136810 Rattus no
428	102.5	9.6	110000	1	AE016822_10	Continuation (11 o
429	102.5	9.6	110000	15	AP008218_220	Continuation (221
c 430	102.5	9.6	110000	15	AP008213_270	Continuation (271
c 431	102.5	9.6	154192	15	AP004272	AP004272 Oryza sat
c 432	102.5	9.6	161051	6	CQ870031	CQ870031 Sequence
433	102.5	9.6	222338	14	AC131610	AC131610 Rattus no
c 434	102.5	9.6	225264	14	AC106396	AC106396 Rattus no
c 435	102.5	9.6	242568	14	AC103416	AC103416 Rattus no
436	102	9.5	1256	6	CS123621	CS123621 Sequence
437	102	9.5	1256	6	CS123649	CS123649 Sequence
438	102	9.5	1349	8	BC044816	BC044816 Homo sapi
439	102	9.5	1650	6	CS123603	CS123603 Sequence
440	102	9.5	1664	6	CS123618	CS123618 Sequence
441	102	9.5	2292	6	CS123636	CS123636 Sequence
442	102	9.5	3266	6	CQ728451	CQ728451 Sequence
c 443	102	9.5	5425	6	CQ806640	CQ806640 Sequence
c 444	102	9.5	6001	6	CQ806674	CQ806674 Sequence
c 445	102	9.5	6001	6	CS124339	CS124339 Sequence
c 446	102	9.5	11012	1	AE011661	AE011661 Xanthomon
c 447	102	9.5	11445	8	AF222310	AF222310 Homo sapi
448	102	9.5	12848	6	AR204356	AR204356 Sequence
449	102	9.5	12848	6	AR637705	AR637705 Sequence
c 450	102	9.5	38522	8	AC002103	AC002103 Genomic s
c 451	102	9.5	39824	6	BD184776	BD184776 Nucleic a
452	102	9.5	45925	8	AC000401	AC000401 Genomic s
c 453	102	9.5	65189	8	AC104129	AC104129 Homo sapi
c 454	102	9.5	95091	8	AL353594	AL353594 Human DNA
c 455	102	9.5	110000	1	AE005174_12	Continuation (13 o
c 456	102	9.5	110000	1	BA000007_19	Continuation (20 o
457	102	9.5	110000	1	CP000075_11	Continuation (12 o
458	102	9.5	110000	14	CT005245_4	Continuation (5 of
459	102	9.5	113187	14	AC007732	AC007732 Homo sapi
c 460	102	9.5	119563	8	HSJ894D12	AL078605 Human DNA
c 461	102	9.5	158203	8	AC093642	AC093642 Homo sapi
c 462	102	9.5	168970	14	AC160955	AC160955 Callicebu
c 463	102	9.5	179089	14	AC084227	AC084227 Homo sapi
464	102	9.5	184349	8	AC113189	AC113189 Homo sapi
465	102	9.5	213743	14	AC145337	AC145337 Pan trogl
c 466	102	9.5	222871	14	AC108094	AC108094 Homo sapi
467	102	9.5	249736	14	AC107163	AC107163 Rattus no
c 468	101.5	9.5	1946	8	AB209710	AB209710 Homo sapi
c 469	101.5	9.5	1988	6	BD158542	BD158542 Primer fo
c 470	101.5	9.5	1988	6	AX880703	AX880703 Sequence
c 471	101.5	9.5	1988	8	AK023541	AK023541 Homo sapi
c 472	101.5	9.5	2037	6	CQ718988	CQ718988 Sequence
473	101.5	9.5	2228	2	DMBNBR	X63828 D.melanogas
c 474	101.5	9.5	2322	6	BD159575	BD159575 Primer fo
c 475	101.5	9.5	2322	6	AX882170	AX882170 Sequence
c 476	101.5	9.5	2322	8	AK027398	AK027398 Homo sapi
c 477	101.5	9.5	3118	15	AK110337	AK110337 Oryza sat
478	101.5	9.5	3382	8	BC047516	BC047516 Homo sapi
c 479	101.5	9.5	10182	6	AR619654	AR619654 Sequence
480	101.5	9.5	83450	6	AR307588	AR307588 Sequence
481	101.5	9.5	83450	6	AR475456	AR475456 Sequence
c 482	101.5	9.5	91679	14	AC107984	AC107984 Homo sapi
c 483	101.5	9.5	102926	8	AC090829	AC090829 Homo sapi
484	101.5	9.5	110000	1	CP000091_26	Continuation (27 o
485	101.5	9.5	146850	14	AC141349	AC141349 Rattus no
486	101.5	9.5	150983	8	AC012351	AC012351 Homo sapi
487	101.5	9.5	154723	14	CNS01DU2	AL133124 Homo sapi
488	101.5	9.5	156149	14	AC149468	AC149468 Bos tauru
489	101.5	9.5	182230	8	AC135050	AC135050 Homo sapi
490	101.5	9.5	195476	14	AC135044	AC135044 Homo sapi
491	101.5	9.5	221475	8	AC009562	AC009562 Homo sapi
492	101.5	9.5	280215	14	AC129648	AC129648 Rattus no
493	101	9.4	679	8	BC093716	BC093716 Homo sapi
494	101	9.4	2332	5	AB195256	AB195256 Danio rer
c 495	101	9.4	3080	1	AF166333	AF166333 Myxococcu
c 496	101	9.4	8735	9	AY032655	AY032655 Mus muscu
c 497	101	9.4	8740	9	AB055618	AB055618 Mus muscu
498	101	9.4	37237	1	AY365117	AY365117 Mycobacte
c 499	101	9.4	42685	14	AC144433	AC144433 Homo sapi
c 500	101	9.4	63365	14	AC087437	AC087437 Homo sapi
501	101	9.4	69570	14	AC067888	AC067888 Homo sapi
c 502	101	9.4	110000	1	AE014295_18	Continuation (19 o
503	101	9.4	110000	14	CT005251_1	Continuation (2 of
504	101	9.4	110000	14	LMFLCHR32_01	Continuation (2 of
505	101	9.4	110000	15	AP008209_025	Continuation (26 o
506	101	9.4	110000	15	AP008209_026	Continuation (27 o
507	101	9.4	126894	8	AL157875	AL157875 Human DNA
c 508	101	9.4	159636	15	AC090485	AC090485 Genomic S
509	101	9.4	168837	14	AC145464	AC145464 Oryctolag
510	101	9.4	188455	5	BX294375	BX294375 Zebrafish
c 511	101	9.4	202050	1	AL646065	AL646065 Ralstonia
512	101	9.4	204512	8	AL731561	AL731561 Human DNA
c 513	101	9.4	279105	14	AL732444	AL732444 Homo sapi
c 514	101	9.4	349980	6	AX491683	AX491683 Sequence

c 515	101	9.4	349980	6	AX553947	AX553947 Sequence
516	100.5	9.4	1234	8	AF038169	AF038169 Homo sapi
c 517	100.5	9.4	1327	1	UEA229205	AJ229205 Unidentif
c 518	100.5	9.4	1552	1	BSPZ95712	Z95712 Bacterial s
519	100.5	9.4	2843	6	AX195330	AX195330 Sequence
520	100.5	9.4	16951	6	AX195368	AX195368 Sequence
521	100.5	9.4	16952	8	AY044229	AY044229 Homo sapi
522	100.5	9.4	53025	8	AC118458	AC118458 Homo sapi
c 523	100.5	9.4	96066	8	AC135056	AC135056 Homo sapi
c 524	100.5	9.4	106117	8	AC103564	AC103564 Homo sapi
525	100.5	9.4	110000	1	AE017180_28	Continuation (29 o
526	100.5	9.4	110000	1	BA000045_04	Continuation (5 of
c 527	100.5	9.4	110000	14	CT005266_07	Continuation (8 of
c 528	100.5	9.4	140531	14	AC105341	AC105341 Homo sapi
c 529	100.5	9.4	144087	8	AP001621	AP001621 Homo sapi
530	100.5	9.4	161617	8	AC093724	AC093724 Homo sapi
531	100.5	9.4	178262	14	AC061974	AC061974 Homo sapi
c 532	100.5	9.4	179383	14	AC060789	AC060789 Homo sapi
533	100.5	9.4	195052	14	AC145040	AC145040 Gorilla g
c 534	100.5	9.4	202868	14	AC118777	AC118777 Rattus no
535	100.5	9.4	208615	14	AC079180	AC079180 Mus muscu
c 536	100.5	9.4	252914	14	AC097431	AC097431 Rattus no
c 537	100.5	9.4	268417	14	AC133017	AC133017 Rattus no
538	100.5	9.4	320074	14	AC162218	AC162218 Bos tauru
c 539	100.5	9.4	336578	8	AP001745	AP001745 Homo sapi
540	100.5	9.4	339221	14	AC128827	AC128827 Rattus no
541	100	9.3	1194	1	AJ633548	AJ633548 Myxococcu
542	100	9.3	1194	6	AR627709	AR627709 Sequence
c 543	100	9.3	3317	6	CS074635	CS074635 Sequence
c 544	100	9.3	3317	6	AX833961	AX833961 Sequence
c 545	100	9.3	3317	8	AK096111	AK096111 Homo sapi
546	100	9.3	4073	5	AJ851524	AJ851524 Gallus ga
547	100	9.3	8066	8	AB209851	AB209851 Homo sapi
548	100	9.3	8820	6	AR619579	AR619579 Sequence
549	100	9.3	9446	13	HCU01214	U01214 Hepatitis C
550	100	9.3	13793	8	HSBMHSP	X62515 H.sapiens m
551	100	9.3	14327	6	CS070215	CS070215 Sequence
552	100	9.3	14327	8	HUMHSPG2B	M85289 Human hepar
553	100	9.3	17799	8	AH009202S4	AF223563 Homo sapi
554	100	9.3	36538	1	DQ087286	DQ087286 Saccharop
555	100	9.3	36538	6	AX600587	AX600587 Sequence
556	100	9.3	36676	8	HSJ858B16	AL096768 Human DNA
c 557	100	9.3	110000	15	CR382128_23	Continuation (24 o
558	100	9.3	110000	15	AP008212_120	Continuation (121
559	100	9.3	114106	14	AP005150	AP005150 Oryza sat
560	100	9.3	139520	14	AC155434	AC155434 Zea mays
561	100	9.3	154252	8	AC132938	AC132938 Homo sapi
c 562	100	9.3	155399	8	AC079779	AC079779 Homo sapi
563	100	9.3	171569	8	AC132872	AC132872 Homo sapi
564	100	9.3	182153	15	AP005968	AP005968 Oryza sat
c 565	100	9.3	205549	14	AC145342	AC145342 Pan trogl
566	100	9.3	214042	9	AC127556	AC127556 Mus muscu
567	100	9.3	247489	14	AC162999	AC162999 Bos tauru
568	100	9.3	257310	1	AE017320	AE017320 Desulfovi
569	99.5	9.3	647	10	BV263679	BV263679 S235P6466
570	99.5	9.3	1429	8	BC043584	BC043584 Homo sapi
c 571	99.5	9.3	1441	3	AY330129	AY330129 Unculture
c 572	99.5	9.3	1457	3	AY289367	AY289367 Unculture
c 573	99.5	9.3	1483	3	DQ125874	DQ125874 Unculture
574	99.5	9.3	14835	1	AE010390	AE010390 Methanopy
575	99.5	9.3	33311	8	AC004235	AC004235 Homo sapi
c 576	99.5	9.3	38377	8	AC145684	AC145684 Homo sapi
577	99.5	9.3	66266	14	AP000573	AP000573 Homo sapi
578	99.5	9.3	77641	14	AP000572	AP000572 Homo sapi
c 579	99.5	9.3	110000	1	BA000045_00	BA000045 Gloeobact
580	99.5	9.3	110000	14	CT005253_1	Continuation (2 of
581	99.5	9.3	110000	15	AP008209_167	Continuation (168
582	99.5	9.3	113266	15	AC092262	AC092262 Oryza sat
583	99.5	9.3	136035	14	BX537284	BX537284 Homo sapi
c 584	99.5	9.3	143847	8	AF205589	AF205589 Homo sapi
c 585	99.5	9.3	150481	8	HSDJ614O4	AL121753 Human DNA
586	99.5	9.3	150756	14	AC130793	AC130793 Canis fam
587	99.5	9.3	154541	14	AC120212	AC120212 Canis fam
c 588	99.5	9.3	154746	6	AR607375	AR607375 Sequence
c 589	99.5	9.3	154746	13	HSV2HG52	Z86099 Herpes simp
c 590	99.5	9.3	161617	8	AC093724	AC093724 Homo sapi
c 591	99.5	9.3	163035	14	AC006405	AC006405 Homo sapi
c 592	99.5	9.3	166128	8	AP003774	AP003774 Homo sapi
c 593	99.5	9.3	166356	8	AP001453	AP001453 Homo sapi
c 594	99.5	9.3	168475	14	AC015698	AC015698 Homo sapi
595	99.5	9.3	182944	14	AC133783	AC133783 Homo sapi
c 596	99.5	9.3	212577	14	AC157132	AC157132 Bos tauru
c 597	99	9.2	779	10	BV626418	BV626418 S217P6052
598	99	9.2	785	6	CQ715562	CQ715562 Sequence
599	99	9.2	875	8	AY363222	AY363222 Homo sapi
c 600	99	9.2	1535	3	AF407697	AF407697 Unculture
601	99	9.2	1631	15	AK061866	AK061866 Oryza sat
c 602	99	9.2	5390	8	HSA314904	AJ314904 Homo sapi
c 603	99	9.2	5550	8	HSA576256	AJ576256 Homo sapi
c 604	99	9.2	9191	6	AR619523	AR619523 Sequence
605	99	9.2	70499	8	AC104411	AC104411 Homo sapi
606	99	9.2	110000	14	CT005271_15	Continuation (16 o
607	99	9.2	110000	15	AP008207_394	Continuation (395
c 608	99	9.2	110000	15	AP008208_327	Continuation (328
609	99	9.2	110000	15	AP008209_276	Continuation (277
c 610	99	9.2	116872	14	AC147279	AC147279 Pan trogl
c 611	99	9.2	127255	14	AC159162	AC159162 Carollia
612	99	9.2	130919	15	AP003380	AP003380 Oryza sat
613	99	9.2	132928	14	AC091089	AC091089 Oryza sat
c 614	99	9.2	135964	8	AL353593	AL353593 Human DNA
c 615	99	9.2	136823	15	AP004853	AP004853 Oryza sat
616	99	9.2	136982	15	AC123974	AC123974 Oryza sat
617	99	9.2	137557	8	AC009414	AC009414 Homo sapi
c 618	99	9.2	148509	8	AC068014	AC068014 Homo sapi
619	99	9.2	150841	14	AC016276	AC016276 Homo sapi
620	99	9.2	155536	15	AP006531	AP006531 Oryza sat
c 621	99	9.2	170020	8	BX072579	BX072579 Human DNA
c 622	99	9.2	170946	14	AC117933	AC117933 Papio anu
c 623	99	9.2	171201	14	CR381632	CR381632 Danio rer
c 624	99	9.2	175763	8	AC104758	AC104758 Homo sapi
c 625	99	9.2	176290	14	AC148564	AC148564 Papio anu
626	99	9.2	176598	14	AC146834	AC146834 Canis fam
627	99	9.2	176737	14	AC116439	AC116439 Pan trogl
628	99	9.2	182228	14	AC163953	AC163953 Oryctolag
629	99	9.2	182426	8	AC024952	AC024952 Homo sapi
630	99	9.2	182707	14	CR762486	CR762486 Danio rer
c 631	99	9.2	183506	14	AC122155	AC122155 Papio anu
c 632	99	9.2	184547	14	AC074373	AC074373 Homo sapi
633	99	9.2	187175	14	AC104579	AC104579 Homo sapi
634	99	9.2	195680	8	AC120498	AC120498 Homo sapi
635	99	9.2	200070	8	AC008746	AC008746 Homo sapi
636	99	9.2	200197	8	AC025594	AC025594 Homo sapi
637	99	9.2	201136	14	BX001011	BX001011 Mus muscu
638	99	9.2	205177	9	AC079276	AC079276 Mus muscu
639	99	9.2	223670	1	CR555308	CR555308 Azoarcus
c 640	99	9.2	228200	14	AC138253	AC138253 Mus muscu
641	99	9.2	245751	9	AL732461	AL732461 Mouse DNA
c 642	99	9.2	298166	14	AC087563	AC087563 Homo sapi
643	99	9.2	300052	1	AE017232	AE017232 Mycobacte
644	99	9.2	301146	1	AE017311	AE017311 Desulfovi
645	99	9.2	350000	9	AC091453	AC091453 Mus muscu
c 646	98.5	9.2	750	6	AR615613	AR615613 Sequence
c 647	98.5	9.2	750	6	AX392296	AX392296 Sequence
648	98.5	9.2	777	10	BV640392	BV640392 S216P6024
c 649	98.5	9.2	1438	3	AY330127	AY330127 Unculture
c 650	98.5	9.2	2876	8	AC002195	AC002195 Homo sapi
c 651	98.5	9.2	8617	1	AE006023	AE006023 Caulobact
c 652	98.5	9.2	10029	1	AE012456	AE012456 Xanthomon
c 653	98.5	9.2	10765	1	AE007283	AE007283 Sinorhizo
c 654	98.5	9.2	21152	9	AF532989	AF532989 Mus muscu
655	98.5	9.2	91246	14	LMFLCHR18_10	Continuation (11 o
c 656	98.5	9.2	103373	14	AC166886	AC166886 Sorex ara
657	98.5	9.2	108621	8	AC079834	AC079834 Homo sapi
c 658	98.5	9.2	108902	14	AC011430	AC011430 Homo sapi
c 659	98.5	9.2	110000	1	AE017314_2	Continuation (3 of
660	98.5	9.2	110000	1	CP000050_09	Continuation (10 o

	661	98.5	9.2	110000	14	AC113631_3 Continuation (4 of
	662	98.5	9.2	110000	14	CR954209_3 Continuation (4 of
	663	98.5	9.2	110000	14	CT005261_6 Continuation (7 of
	664	98.5	9.2	110292	14	AC150196 AC150196 Gallus ga
	665	98.5	9.2	113295	14	AC149835 AC149835 Zea mays
	666	98.5	9.2	118172	8	AC015912 AC015912 Homo sapi
	667	98.5	9.2	119191	8	AP004782 AP004782 Homo sapi
c	668	98.5	9.2	129527	14	AC166625 AC166625 Sorex ara
	669	98.5	9.2	135492	14	AC150123 AC150123 Gallus ga
	670	98.5	9.2	150292	9	AC112342 AC112342 Rattus no
	671	98.5	9.2	155473	14	AC156933 AC156933 Gallus ga
c	672	98.5	9.2	160484	8	AC106858 AC106858 Homo sapi
c	673	98.5	9.2	161355	14	AC011154 AC011154 Homo sapi
c	674	98.5	9.2	163604	4	AC092727 AC092727 Bos tauru
	675	98.5	9.2	173016	14	AC019123 AC019123 Homo sapi
	676	98.5	9.2	181971	8	AC016182 AC016182 Homo sapi
	677	98.5	9.2	182374	14	AP003968 AP003968 Homo sapi
c	678	98.5	9.2	191078	14	AC022505 AC022505 Homo sapi
c	679	98.5	9.2	204556	14	AC153750 AC153750 Callicebu
	680	98.5	9.2	207661	8	AC015884 AC015884 Homo sapi
	681	98.5	9.2	208694	14	AC130867 AC130867 Rattus no
c	682	98.5	9.2	225394	2	LMFLCHR4A AL389894 Leishmani
	683	98.5	9.2	239015	14	AC131194 AC131194 Rattus no
c	684	98.5	9.2	243290	9	AL663088 AL663088 Mouse DNA
c	685	98.5	9.2	282019	14	AC096362 AC096362 Rattus no
c	686	98.5	9.2	298450	1	SCO939107 AL939107 Streptomy
c	687	98.5	9.2	300511	1	AE016775 AE016775 Pseudomon
c	688	98.5	9.2	302998	1	AE017172 AE017172 Porphyrom
c	689	98.5	9.2	347786	1	BX640438 BX640438 Bordetell
c	690	98.5	9.2	349146	1	BX640424 BX640424 Bordetell
c	691	98	9.1	624	6	AX455985 AX455985 Sequence
c	692	98	9.1	624	6	AX456018 AX456018 Sequence
c	693	98	9.1	624	6	AX456019 AX456019 Sequence
c	694	98	9.1	1080	9	Y032691S12 AY032702 Mus muscu
c	695	98	9.1	1535	3	AF407722 AF407722 Unculture
	696	98	9.1	1953	6	AX747413 AX747413 Sequence
	697	98	9.1	1953	8	AK092217 AK092217 Homo sapi
	698	98	9.1	2154	15	MZECOPIAA M94481 Zea mays co
	699	98	9.1	2811	8	BC012325 BC012325 Homo sapi
c	700	98	9.1	3181	6	AX834654 AX834654 Sequence
c	701	98	9.1	3181	8	AK097259 AK097259 Homo sapi
	702	98	9.1	3240	6	CQ721601 CQ721601 Sequence
	703	98	9.1	3252	6	CS059038 CS059038 Sequence
	704	98	9.1	3252	6	AR533636 AR533636 Sequence
	705	98	9.1	3252	6	AX799154 AX799154 Sequence
	706	98	9.1	3252	8	AF057164 AF057164 Homo sapi
	707	98	9.1	3254	6	CQ490432 CQ490432 Sequence
	708	98	9.1	3254	6	CQ496283 CQ496283 Sequence
	709	98	9.1	3300	1	PSNOSDFY X53676 Pseudomonas
	710	98	9.1	10439	8	AB209484 AB209484 Homo sapi
	711	98	9.1	36006	8	HS357D8 AL031715 Human DNA
c	712	98	9.1	89171	8	AC008404 AC008404 Homo sapi
c	713	98	9.1	104435	8	AC016292 AC016292 Homo sapi
	714	98	9.1	110000	1	CP000090_09 Continuation (10 o
c	715	98	9.1	110000	14	AP006496_7 Continuation (8 of
c	716	98	9.1	110000	14	CT005269_14 Continuation (15 o
	717	98	9.1	139185	14	AC149258 AC149258 Papio anu
	718	98	9.1	145347	14	AC073821 AC073821 Mus muscu
c	719	98	9.1	145414	8	HSA392M18 AL121897 Human DNA
c	720	98	9.1	164127	14	AC158304 AC158304 Mus muscu
c	721	98	9.1	166506	14	AC162152 AC162152 Rhinoloph
c	722	98	9.1	170261	14	AC008542 AC008542 Homo sapi
c	723	98	9.1	170928	8	AL356740 AL356740 Human DNA
c	724	98	9.1	173391	8	AC090063 AC090063 Homo sapi
	725	98	9.1	176233	14	AC024449 AC024449 Homo sapi
	726	98	9.1	176291	14	AC023583 AC023583 Homo sapi
	727	98	9.1	182226	8	AC025263 AC025263 Homo sapi
	728	98	9.1	190102	8	AP003065 AP003065 Homo sapi
c	729	98	9.1	190635	14	AC156359 AC156359 Oryctolag
	730	98	9.1	191654	14	AC023176 AC023176 Homo sapi
c	731	98	9.1	202267	8	DJ293M10 AF111167 Homo sapi
c	732	98	9.1	217595	9	AL805959 AL805959 Mouse DNA
c	733	98	9.1	217993	14	AC109864 AC109864 Rattus no
	734	98	9.1	224373	14	AC098129 AC098129 Rattus no
	735	98	9.1	230246	14	AC162204 AC162204 Bos tauru
	736	98	9.1	233042	9	AC132144 AC132144 Mus muscu
	737	98	9.1	234452	14	AC137227 AC137227 Rattus no
c	738	98	9.1	241515	14	AC147287 AC147287 Pan trogl
c	739	98	9.1	241837	14	AC133667 AC133667 Rattus no
	740	98	9.1	245942	14	AC132792 AC132792 Rattus no
	741	98	9.1	282355	14	AC104401 AC104401 Rattus no
	742	98	9.1	347664	9	BX883043 BX883043 Rattus no
c	743	97.5	9.1	764	3	AY934450 AY934450 Unculture
c	744	97.5	9.1	1413	3	AY921837 AY921837 Unculture
c	745	97.5	9.1	4894	6	CQ582770 CQ582770 Sequence
c	746	97.5	9.1	5424	6	CQ582761 CQ582761 Sequence
c	747	97.5	9.1	12454	1	AE002019 AE002019 Deinococc
c	748	97.5	9.1	33369	8	U82670 U82670 Homo sapien
	749	97.5	9.1	50969	14	AC014793 AC014793 Drosophil
c	750	97.5	9.1	85825	14	AC149667 AC149667 Bos tauru
	751	97.5	9.1	94049	14	AC060224 AC060224 Mus muscu
c	752	97.5	9.1	104170	14	AC091510 AC091510 Leishmani
c	753	97.5	9.1	110000	1	BX571966_09 Continuation (10 o
	754	97.5	9.1	110000	2	AC125735_2 Continuation (3 of
	755	97.5	9.1	110000	14	CT005256_1 Continuation (2 of
c	756	97.5	9.1	110000	14	LMFLCHR16_08 Continuation (9 of
c	757	97.5	9.1	110000	14	LMFLCHR16_09 Continuation (10 o
	758	97.5	9.1	121981	14	AC150231 AC150231 Carollia
	759	97.5	9.1	129505	8	AL590385 AL590385 Human DNA
c	760	97.5	9.1	157101	8	AC092000 AC092000 Homo sapi
	761	97.5	9.1	160207	9	AC121889 AC121889 Mus muscu
	762	97.5	9.1	171681	14	AC091541 AC091541 Canis fam
c	763	97.5	9.1	174612	14	AC023889 AC023889 Homo sapi
	764	97.5	9.1	176715	14	AC073474 AC073474 Homo sapi
	765	97.5	9.1	189315	2	AC008319 AC008319 Drosophil
c	766	97.5	9.1	197037	9	AC161207 AC161207 Mus muscu
c	767	97.5	9.1	218799	14	AC091328 AC091328 Homo sapi
c	768	97.5	9.1	314549	2	AE003587 AE003587 Drosophil
c	769	97.5	9.1	324604	8	U82671 U82671 Homo sapien
c	770	97	9.0	633	8	HSA343038 AJ343038 Homo sapi
	771	97	9.0	653	5	AF287140 AF287140 Xenopus t
	772	97	9.0	1877	4	AF354445 AF354445 Equus cab
c	773	97	9.0	1921	8	AY726567 AY726567 Homo sapi
	774	97	9.0	2690	8	AB179022 AB179022 Macaca fa
c	775	97	9.0	2920	8	BC040323 BC040323 Homo sapi
	776	97	9.0	2926	15	AB035492 AB035492 Alternari
	777	97	9.0	3048	6	I34428 I34428 Sequence 47
	778	97	9.0	3048	6	I46826 I46826 Sequence 41
	779	97	9.0	3048	6	I55095 I55095 Sequence 47
	780	97	9.0	3048	8	HUMCA4A L34059 Homo sapien
c	781	97	9.0	4747	15	WHTGBL1A M81719 Triticum ae
c	782	97	9.0	7760	6	AR619450 AR619450 Sequence
c	783	97	9.0	11629	1	AE012222 AE012222 Xanthomon
	784	97	9.0	43834	8	AY623660 AY623660 Homo sapi
	785	97	9.0	43987	8	AC005391 AC005391 Homo sapi
	786	97	9.0	61400	14	AC101116 AC101116 Mus muscu
	787	97	9.0	80662	8	AC005606 AC005606 Homo sapi
	788	97	9.0	87387	8	AC062037 AC062037 Homo sapi
c	789	97	9.0	91435	8	AC092488 AC092488 Homo sapi
	790	97	9.0	104000	8	AP006219 AP006219 Homo sapi
	791	97	9.0	104561	1	AE017282_32 Continuation (33 o
	792	97	9.0	104771	9	AL603830 AL603830 Mouse DNA
	793	97	9.0	108457	8	HSJ800J21 AL109955 Human DNA
c	794	97	9.0	110000	1	AE013598_17 Continuation (18 o
	795	97	9.0	110000	1	AE013598_37 Continuation (38 o
	796	97	9.0	110000	1	AE013598_43 Continuation (44 o
	797	97	9.0	110000	1	CP000050_35 Continuation (36 o
	798	97	9.0	110000	1	CP000050_36 Continuation (37 o
	799	97	9.0	110000	1	CP000076_35 Continuation (36 o
c	800	97	9.0	110000	14	CT005269_09 Continuation (10 o
	801	97	9.0	139267	8	AC006435 AC006435 Homo sapi
c	802	97	9.0	162162	9	AC125101 AC125101 Mus muscu
c	803	97	9.0	166060	14	AC151937 AC151937 Dasypus n
	804	97	9.0	172794	14	AC157642 AC157642 Rhinoloph
	805	97	9.0	175694	8	AC016753 AC016753 Homo sapi
	806	97	9.0	176845	8	AL162252 AL162252 Human DNA

c	807	97	9.0	177223	8	AC009890 AC009890 Genomic S
	808	97	9.0	179786	14	AP001015 AP001015 Homo sapi
	809	97	9.0	204630	8	AC090617 AC090617 Homo sapi
c	810	97	9.0	214839	14	AC124630 AC124630 Mus muscu
c	811	97	9.0	215342	8	AC109322 AC109322 Homo sapi
c	812	97	9.0	221958	14	AC021705 AC021705 Homo sapi
	813	97	9.0	226874	14	AC160033 AC160033 Bos tauru
c	814	97	9.0	227203	14	AC011184 AC011184 Homo sapi
	815	97	9.0	234797	14	AC130921 AC130921 Rattus no
	816	97	9.0	239075	14	AC091259 AC091259 Mus muscu
	817	97	9.0	240438	14	AC152285 AC152285 Bos tauru
	818	97	9.0	245616	14	AC153298 AC153298 Bos tauru
c	819	97	9.0	254796	14	AC097920 AC097920 Rattus no
c	820	97	9.0	264908	9	AC096627 AC096627 Mus muscu
	821	97	9.0	278310	8	CR382287 CR382287 Human DNA
	822	97	9.0	298050	1	AL935260 AL935260 Lactobaci
	823	96.5	9.0	637	10	BV290298 BV290298 S232P6279
c	824	96.5	9.0	1415	3	AY921839 AY921839 Unculture
c	825	96.5	9.0	1484	3	AY326536 AY326536 Unculture
c	826	96.5	9.0	1519	3	AY382609 AY382609 Unculture
	827	96.5	9.0	1851	11	AF023672 AF023672 Synthetic
c	828	96.5	9.0	2122	15	BLYBEG1 M64372 Barley embr
	829	96.5	9.0	2152	2	AY060682 AY060682 Drosophil
	830	96.5	9.0	2282	6	CQ587868 CQ587868 Sequence
c	831	96.5	9.0	4319	6	CQ587867 CQ587867 Sequence
c	832	96.5	9.0	6132	9	CIUEF2G J03200 Hamster elo
	833	96.5	9.0	9622	14	AC012950 AC012950 Drosophil
c	834	96.5	9.0	10544	1	AE011983 Xanthomon
c	835	96.5	9.0	11377	1	AE008358 AE008358 Agrobacte
c	836	96.5	9.0	12547	1	AE004720 AE004720 Pseudomon
c	837	96.5	9.0	22384	8	AC138032 AC138032 Homo sapi
c	838	96.5	9.0	36343	8	HSY13543 Y13543 Homo sapien
c	839	96.5	9.0	37519	8	AP006324 AP006324 Homo sapi
	840	96.5	9.0	43335	8	AC138031 AC138031 Homo sapi
	841	96.5	9.0	63910	14	AC135341 AC135341 Homo sapi
	842	96.5	9.0	108964	15	AC073391 AC073391 Oryza sat
	843	96.5	9.0	110000	1	AP006840_24 Continuation (25 o
c	844	96.5	9.0	110000	1	CP000076_69 Continuation (70 o
c	845	96.5	9.0	110000	14	AP006495_1 Continuation (2 of
	846	96.5	9.0	110000	15	AP008216_154 Continuation (155
c	847	96.5	9.0	110000	15	AP008209_330 Continuation (331
c	848	96.5	9.0	110000	15	AP008211_189 Continuation (190
	849	96.5	9.0	127168	8	HS1163J1 AL031588 Human DNA
	850	96.5	9.0	130473	8	AC027559 AC027559 Homo sapi
	851	96.5	9.0	151479	15	AC093713 AC093713 Oryza sat
c	852	96.5	9.0	153649	8	AL732372 AL732372 Human DNA
c	853	96.5	9.0	154214	8	AC079753 AC079753 Homo sapi
	854	96.5	9.0	162805	14	AC020565 AC020565 Homo sapi
c	855	96.5	9.0	164709	15	AC107085 AC107085 Oryza sat
c	856	96.5	9.0	165098	2	AC018490 AC018490 Drosophil
	857	96.5	9.0	169385	2	AC012164 AC012164 Drosophil
c	858	96.5	9.0	175162	8	AL590103 AL590103 Human DNA
c	859	96.5	9.0	178531	14	AC067802 AC067802 Homo sapi
c	860	96.5	9.0	199759	8	AC009065 AC009065 Homo sapi
	861	96.5	9.0	204343	14	AL359496 AL359496 Homo sapi
	862	96.5	9.0	213660	14	AC073699 AC073699 Mus muscu
c	863	96.5	9.0	216387	8	DJ534K4 AF109907 Homo sapi
	864	96.5	9.0	229898	14	AC161564 AC161564 Bos tauru
c	865	96.5	9.0	230167	14	AC150046 AC150046 Gallus ga
	866	96.5	9.0	238357	14	AC164703 AC164703 Mus muscu
c	867	96.5	9.0	246557	14	AC106539 AC106539 Rattus no
	868	96.5	9.0	257451	14	AC098508 AC098508 Rattus no
	869	96.5	9.0	262249	14	AC109081 AC109081 Rattus no
	870	96.5	9.0	275036	14	AC150059 AC150059 Gallus ga
	871	96.5	9.0	294203	14	AC099292 AC099292 Rattus no
c	872	96.5	9.0	297236	2	AE003510 AE003510 Drosophil
	873	96.5	9.0	300029	15	AE017099 AE017099 Oryza sat
	874	96.5	9.0	309267	1	AE017235 AE017235 Mycobacte
c	875	96	8.9	562	10	BV385550 BV385550 S244P6393
	876	96	8.9	773	10	BV654904 BV654904 S216P6164
c	877	96	8.9	951	15	BT009204 BT009204 Triticum
c	878	96	8.9	970	3	AY943001 AY943001 Unculture
	879	96	8.9	1032	5	BC085515 BC085515 Danio rer
c	880	96	8.9	1348	1	AB026550 AB026550 Desulfoto
c	881	96	8.9	1419	3	AY456757 AY456757 Unculture
	882	96	8.9	1439	15	AY169227 AY169227 Prorocent
c	883	96	8.9	1476	1	AY548777 AY548777 Desulfoto
	884	96	8.9	1797	8	AF058317 AF058317 Homo sapi
	885	96	8.9	2532	15	AY826897 AY826897 Heterocap
	886	96	8.9	3617	4	RABHBZ1 J03883 Rabbit zeta
c	887	96	8.9	4779	8	AY049732 AY049732 Homo sapi
	888	96	8.9	4992	6	AR619240 AR619240 Sequence
c	889	96	8.9	5529	6	BD262969 BD262969 DNA seque
c	890	96	8.9	5529	6	AX024260 AX024260 Sequence
c	891	96	8.9	5614	8	AK160383 AK160383 Homo sapi
c	892	96	8.9	6512	15	NTITS2618 Y08427 N.tomentosi
	893	96	8.9	7539	8	AB061831 AB061831 Homo sapi
	894	96	8.9	10621	4	RABGLOBIN M74142 Rabbit zeta
	895	96	8.9	12667	1	AE004816 AE004816 Pseudomon
c	896	96	8.9	16047	6	AR619741 AR619741 Sequence
c	897	96	8.9	47713	6	BD262937 BD262937 DNA seque
c	898	96	8.9	47713	6	AX024213 AX024213 Sequence
	899	96	8.9	49999	6	AX015917 AX015917 Sequence
	900	96	8.9	50000	6	AX535264 AX535264 Sequence
c	901	96	8.9	50000	6	AX535266 AX535266 Sequence
	902	96	8.9	59816	1	AF333038 AF333038 Streptomy
	903	96	8.9	62745	14	CT010578_3 Continuation (4 of
c	904	96	8.9	83709	8	HSJ403A15 AL096711 Human DNA
	905	96	8.9	100020	8	AC092165 AC092165 Homo sapi
c	906	96	8.9	110000	1	AP006618_50 Continuation (51 o
	907	96	8.9	110000	1	BA000040_62 Continuation (63 o
c	908	96	8.9	110000	14	CT005254_3 Continuation (4 of
c	909	96	8.9	110000	14	CT005272_16 Continuation (17 o
	910	96	8.9	110000	15	AP008209_009 Continuation (10 o
c	911	96	8.9	127725	8	AC023813 AC023813 Homo sapi
c	912	96	8.9	128155	8	HSA262A13 AL096843 Human DNA
	913	96	8.9	134847	14	AC124061 AC124061 Homo sapi
c	914	96	8.9	139130	8	AC091504 AC091504 Pan trogl
c	915	96	8.9	140919	14	AC034181 AC034181 Homo sapi
c	916	96	8.9	145993	8	AC079059 AC079059 Homo sapi
	917	96	8.9	148011	15	AC134236 AC134236 Oryza sat
	918	96	8.9	153701	14	AC016437 AC016437 Homo sapi
c	919	96	8.9	158276	14	AC012033 AC012033 Homo sapi
	920	96	8.9	158520	14	AC026668 AC026668 Homo sapi
c	921	96	8.9	162336	8	AC021594 AC021594 Homo sapi
c	922	96	8.9	167646	8	BX664718 BX664718 Human DNA
	923	96	8.9	169005	8	AC034198 AC034198 Homo sapi
c	924	96	8.9	169548	14	AC158253 AC158253 Neofelis
c	925	96	8.9	172883	8	AP003967 AP003967 Homo sapi
	926	96	8.9	174409	14	AC010788 AC010788 Homo sapi
c	927	96	8.9	176584	14	AC062010 AC062010 Homo sapi
c	928	96	8.9	182990	14	AC141383 AC141383 Rattus no
	929	96	8.9	184716	8	AC018836 AC018836 Homo sapi
	930	96	8.9	185931	9	AC155257 AC155257 Mus muscu
	931	96	8.9	188833	8	HS268H5 AL008718 Human DNA
	932	96	8.9	189495	8	BX649563 BX649563 Human DNA
	933	96	8.9	190659	14	AC148961 AC148961 Callithri
c	934	96	8.9	206543	14	AC164931 AC164931 Oryctolag
c	935	96	8.9	206709	9	AL772319 AL772319 Mouse DNA
	936	96	8.9	210301	8	AF307337 AF307337 Homo sapi
	937	96	8.9	211012	8	AC018843 AC018843 Homo sapi
	938	96	8.9	227079	14	AC138431 AC138431 Homo sapi
c	939	96	8.9	228432	14	CT010573 CT010573 Mus muscu
c	940	96	8.9	232180	14	AC160740 AC160740 Bos tauru
c	941	96	8.9	242582	14	AC128397 AC128397 Rattus no
	942	96	8.9	244409	14	AC110976 AC110976 Rattus no
c	943	96	8.9	245182	14	AC145940 AC145940 Pan trogl
	944	96	8.9	245831	14	AC094430 AC094430 Rattus no
c	945	96	8.9	271451	14	AC098503 AC098503 Rattus no
	946	96	8.9	278109	14	AC109429 AC109429 Rattus no
	947	96	8.9	299991	1	AE016776 AE016776 Pseudomon
	948	95.5	8.9	694	4	AY677111 AY677111 Ornithorh
	949	95.5	8.9	740	10	BV584578 BV584578 G591P6272
c	950	95.5	8.9	764	3	AY934453 AY934453 Unculture
	951	95.5	8.9	1159	4	AHA2ABREC Y12526 Amblysomus
	952	95.5	8.9	1309	15	AK067421 AK067421 Oryza sat

953	95.5	8.9	1852	1	SACYAA	AJ223796 Stigmatel
c 954	95.5	8.9	2577	6	BD103052	BD103052 Porphorym
c 955	95.5	8.9	2583	6	BD102927	BD102927 Porphorym
c 956	95.5	8.9	2691	9	BC059023	BC059023 Mus muscu
957	95.5	8.9	4457	6	AX704759	AX704759 Sequence
958	95.5	8.9	4624	6	BD183473	BD183473 Novel gen
c 959	95.5	8.9	4680	8	BC042624	BC042624 Homo sapi
960	95.5	8.9	4832	8	AB037727	AB037727 Homo sapi
961	95.5	8.9	5761	6	CS052392	CS052392 Sequence
962	95.5	8.9	5761	8	AF451977	AF451977 Homo sapi
c 963	95.5	8.9	14756	6	AX647625	AX647625 Sequence
964	95.5	8.9	65674	8	AF158748	AF158748 Homo sapi
965	95.5	8.9	82806	8	AC007111	AC007111 Homo sapi
c 966	95.5	8.9	82806	8	AC007111	AC007111 Homo sapi
967	95.5	8.9	89881	8	AL160264	AL160264 Human DNA
968	95.5	8.9	90082	8	AF045555	AF045555 Homo sapi
c 969	95.5	8.9	94949	8	AY623115	AY623115 Homo sapi
970	95.5	8.9	100525	15	AP004079	AP004079 Oryza sat
c 971	95.5	8.9	110000	1	BA000030_18	Continuation (19 o
972	95.5	8.9	110000	1	CP000088_31	Continuation (32 o
973	95.5	8.9	110000	1	CP000088_32	Continuation (33 o
c 974	95.5	8.9	110000	14	AP006484_1	Continuation (2 of
975	95.5	8.9	110000	14	BX255276_03	Continuation (4 of
c 976	95.5	8.9	110000	14	CT005258_5	Continuation (6 of
c 977	95.5	8.9	110000	14	CT005268_00	CT005268 Leishmani
978	95.5	8.9	110000	15	AP008214_080	Continuation (81 o
c 979	95.5	8.9	110000	15	AE017341_01	Continuation (2 of
980	95.5	8.9	110000	15	AP008208_230	Continuation (231
981	95.5	8.9	126712	8	AL137077	AL137077 Human DNA
c 982	95.5	8.9	127265	4	AL773562	AL773562 Pig DNA s
c 983	95.5	8.9	132128	14	AC157320	AC157320 Zea mays
984	95.5	8.9	137914	14	AC166629	AC166629 Loxodonta
985	95.5	8.9	138615	15	AP004023	AP004023 Oryza sat
986	95.5	8.9	144836	14	AC166889	AC166889 Loxodonta
c 987	95.5	8.9	148525	14	AC016675	AC016675 Homo sapi
c 988	95.5	8.9	152224	14	AC007933	AC007933 Homo sapi
989	95.5	8.9	152331	6	BD080413	BD080413 Novel mol
c 990	95.5	8.9	155736	14	AC004229	AC004229 Homo sapi
991	95.5	8.9	157517	15	AP005603	AP005603 Oryza sat
c 992	95.5	8.9	160111	8	AC124862	AC124862 Homo sapi
993	95.5	8.9	162328	8	AP000350	AP000350 Homo sapi
c 994	95.5	8.9	167970	14	AC156766	AC156766 Rhinoloph
c 995	95.5	8.9	169391	14	AC111190	AC111190 Homo sapi
c 996	95.5	8.9	173515	14	AC073394	AC073394 Homo sapi
c 997	95.5	8.9	173883	14	AC146677	AC146677 Papio anu
998	95.5	8.9	176373	6	BD080414	BD080414 Novel mol
c 999	95.5	8.9	180290	8	AC005081	AC005081 Homo sapi
c1000	95.5	8.9	181013	4	AC149779	AC149779 Bos tauru
1001	95.5	8.9	189424	14	AC148512	AC148512 Papio anu
1002	95.5	8.9	197498	8	AC005010	AC005010 Homo sapi
c1003	95.5	8.9	198259	14	AC150810	AC150810 Callithri
1004	95.5	8.9	199759	8	AC009065	AC009065 Homo sapi
c1005	95.5	8.9	206868	9	AC151294	AC151294 Mus muscu
c1006	95.5	8.9	215705	8	AL589931	AL589931 Human DNA
1007	95.5	8.9	222086	14	AC106106	AC106106 Rattus no
c1008	95.5	8.9	223130	9	AC134913	AC134913 Mus muscu
1009	95.5	8.9	225031	9	AC132481	AC132481 Mus muscu
1010	95.5	8.9	239434	14	AC012171	AC012171 Homo sapi
c1011	95.5	8.9	239434	14	AC012171	AC012171 Homo sapi
1012	95.5	8.9	261151	8	AF181898	AF181898 Homo sapi
1013	95.5	8.9	346274	1	BX640443	BX640443 Bordetell
1014	95.5	8.9	348014	1	BX640430	BX640430 Bordetell
1015	95.5	8.9	349635	1	BX572603	BX572603 Rhodopseu
1016	95.5	8.9	349726	1	BX640421	BX640421 Bordetell
c1017	95	8.9	1244	1	AF508096	AF508096 Agrobacte
1018	95	8.9	1246	6	AX077430	AX077430 Sequence
1019	95	8.9	1246	8	AK075330	AK075330 Homo sapi
1020	95	8.9	1279	15	AK063978	AK063978 Oryza sat
1021	95	8.9	1642	6	CQ715594	CQ715594 Sequence
1022	95	8.9	1797	8	HSA269477	AJ269477 Homo sapi
1023	95	8.9	1867	8	HSA250807	AJ250807 Homo sapi
1024	95	8.9	2170	8	AF170911	AF170911 Homo sapi
1025	95	8.9	2171	8	AK092655	AK092655 Homo sapi
1026	95	8.9	2306	8	AF098277	AF098277 Homo sapi
1027	95	8.9	2360	8	BC050261	BC050261 Homo sapi
c1028	95	8.9	2724	15	AK119413	AK119413 Oryza sat
1029	95	8.9	2874	6	CQ730456	CQ730456 Sequence
1030	95	8.9	3063	6	CQ824161	CQ824161 Sequence
1031	95	8.9	3100	6	CQ841691	CQ841691 Sequence
1032	95	8.9	3100	8	AK124724	AK124724 Homo sapi
c1033	95	8.9	3118	1	MXA505753	AJ505753 Myxococcu
1034	95	8.9	3310	6	AX747020	AX747020 Sequence
1035	95	8.9	3310	8	AK091496	AK091496 Homo sapi
1036	95	8.9	3469	2	AF314212	AF314212 Trypanoso
c1037	95	8.9	6552	6	CQ597398	CQ597398 Sequence
c1038	95	8.9	6552	6	AX254563	AX254563 Sequence
1039	95	8.9	8801	8	AL831711	AL831711 Human DNA
c1040	95	8.9	9964	6	CQ729631	CQ729631 Sequence
c1041	95	8.9	9995	1	AE011763	AE011763 Xanthomon
c1042	95	8.9	11332	1	AE011848	AE011848 Xanthomon
1043	95	8.9	11778	6	AR619625	AR619625 Sequence
c1044	95	8.9	12602	2	DEU40653	U40653 Drosophila
c1045	95	8.9	14618	9	AF260753	AF260753 Cricetulu
c1046	95	8.9	17982	14	AC013097	AC013097 Drosophil
1047	95	8.9	32840	1	AB193032	AB193032 Corynebac
1048	95	8.9	79175	8	AC012516	AC012516 Homo sapi
1049	95	8.9	84518	2	AC125735_3	Continuation (4 of
1050	95	8.9	89435	14	AC142019	AC142019 Rattus no
1051	95	8.9	104972	8	AL353611	AL353611 Human DNA
1052	95	8.9	110000	1	AE017282_02	Continuation (3 of
1053	95	8.9	110000	1	AE017282_03	Continuation (4 of
1054	95	8.9	110000	1	BA000012_30	Continuation (31 o
c1055	95	8.9	110000	1	BA000012_54	Continuation (55 o
c1056	95	8.9	110000	8	HSA6345_1	Continuation (2 of
1057	95	8.9	110000	14	CT005265_04	Continuation (5 of
c1058	95	8.9	110000	14	CT005269_03	Continuation (4 of
c1059	95	8.9	110000	15	AP008216_030	Continuation (31 o
1060	95	8.9	124516	8	AP001615	AP001615 Homo sapi
1061	95	8.9	142595	14	AC129894	AC129894 Homo sapi
1062	95	8.9	145057	14	AC155196	AC155196 Pan trogl
1063	95	8.9	154169	8	AC008962	AC008962 Homo sapi
1064	95	8.9	154896	14	AC110481	AC110481 Rattus no
c1065	95	8.9	163969	14	AC121659	AC121659 Rattus no
c1066	95	8.9	166757	15	AC098565	AC098565 Oryza sat
1067	95	8.9	168763	8	AC146133	AC146133 Pan trogl
1068	95	8.9	170959	14	AC022197	AC022197 Homo sapi
1069	95	8.9	171267	14	AC154087	AC154087 Alligator
1070	95	8.9	173251	14	AC058798	AC058798 Homo sapi
c1071	95	8.9	177953	2	AC018491	AC018491 Drosophil
c1072	95	8.9	208685	14	AC147594	AC147594 Canis fam
c1073	95	8.9	211582	14	AC133740	AC133740 Rattus no
1074	95	8.9	214952	14	AC145493	AC145493 Pan trogl
c1075	95	8.9	232105	14	AC159779	AC159779 Bos tauru
1076	95	8.9	240626	14	AC105660	AC105660 Rattus no
c1077	95	8.9	241031	14	AC110658	AC110658 Rattus no
1078	95	8.9	245636	14	AC095871	AC095871 Rattus no
1079	95	8.9	247497	14	AC134073	AC134073 Rattus no
1080	95	8.9	250627	14	AC097031	AC097031 Rattus no
1081	95	8.9	253237	14	AC106474	AC106474 Rattus no
c1082	95	8.9	259356	14	AC135664	AC135664 Rattus no
c1083	95	8.9	262400	14	AC097851	AC097851 Rattus no
c1084	95	8.9	264198	14	AC156904	AC156904 Bos tauru
1085	95	8.9	276550	14	AC117926	AC117926 Rattus no
1086	95	8.9	286701	14	AC137276	AC137276 Rattus no
c1087	95	8.9	288539	14	AC164360	AC164360 Bos tauru
c1088	95	8.9	297848	2	AE002611	AE002611 Drosophil
c1089	95	8.9	300029	15	AE017057	AE017057 Oryza sat
c1090	95	8.9	300395	1	AE016785	AE016785 Pseudomon
c1091	94.5	8.8	764	3	AY934485	AY934485 Unculture
1092	94.5	8.8	969	9	AB049066	AB049066 Mus muscu
1093	94.5	8.8	1114	6	AR498701	AR498701 Sequence
1094	94.5	8.8	1114	6	AR513983	AR513983 Sequence
1095	94.5	8.8	1220	8	AF538036	AF538036 Homo sapi
1096	94.5	8.8	1325	8	BC003118	BC003118 Homo sapi
1097	94.5	8.8	1686	9	BC099762	BC099762 Rattus no
c1098	94.5	8.8	2005	6	AX746763	AX746763 Sequence

c1099	94.5	8.8	2005	8	AK091066	AK091066 Homo sapi
1100	94.5	8.8	2035	9	BC023684	BC023684 Mus muscu
1101	94.5	8.8	2070	9	AB046528	AB046528 Mus muscu
c1102	94.5	8.8	2229	15	AK120991	AK120991 Oryza sat
1103	94.5	8.8	2374	9	AB046527	AB046527 Mus muscu
1104	94.5	8.8	3294	9	AF207880	AF207880 Mus muscu
c1105	94.5	8.8	3428	15	AK121225	AK121225 Oryza sat
1106	94.5	8.8	3461	15	AK110057	AK110057 Oryza sat
c1107	94.5	8.8	3482	15	AK067491	AK067491 Oryza sat
1108	94.5	8.8	12654	1	AE012065	AE012065 Xanthomon
1109	94.5	8.8	28194	6	AR619855	AR619855 Sequence
c1110	94.5	8.8	33494	2	AC093554	AC093554 Leishmani
1111	94.5	8.8	38611	8	AC011545	AC011545 Homo sapi
c1112	94.5	8.8	53957	15	NCB2G14	BX284753 Neurospor
1113	94.5	8.8	69964	14	AC136328	AC136328 Homo sapi
1114	94.5	8.8	110000	1	AE013598_32	Continuation (33 o
c1115	94.5	8.8	110000	1	AE014295_06	Continuation (7 of
c1116	94.5	8.8	110000	1	AE017282_20	Continuation (21 o
1117	94.5	8.8	110000	1	AP006618_19	Continuation (20 o
c1118	94.5	8.8	110000	1	AY596296_0	AY596296 Haloarcul
1119	94.5	8.8	110000	1	BA000012_59	Continuation (60 o
1120	94.5	8.8	110000	1	BA000012_60	Continuation (61 o
1121	94.5	8.8	110000	1	BA000030_80	Continuation (81 o
1122	94.5	8.8	110000	1	CP000050_25	Continuation (26 o
c1123	94.5	8.8	110000	1	CP000058_02	Continuation (3 of
1124	94.5	8.8	110000	1	CP000076_57	Continuation (58 o
1125	94.5	8.8	110000	1	CP000088_26	Continuation (27 o
1126	94.5	8.8	110000	1	CP000090_19	Continuation (20 o
1127	94.5	8.8	110000	14	CT005263_6	Continuation (7 of
c1128	94.5	8.8	110000	14	CT005272_22	Continuation (23 o
c1129	94.5	8.8	110000	15	AP008217_179	Continuation (180
1130	94.5	8.8	110000	15	AP008208_344	Continuation (345
1131	94.5	8.8	110000	15	AP008213_116	Continuation (117
1132	94.5	8.8	115190	15	AP004153	AP004153 Oryza sat
c1133	94.5	8.8	127304	14	AC119051	AC119051 Gallus ga
1134	94.5	8.8	135259	8	AC004590	AC004590 Homo sapi
1135	94.5	8.8	144221	14	AC107686	AC107686 Mus muscu
1136	94.5	8.8	144792	8	AL359649	AL359649 Human DNA
1137	94.5	8.8	145064	8	AC008453	AC008453 Homo sapi
1138	94.5	8.8	145580	15	AP006344	AP006344 Oryza sat
c1139	94.5	8.8	155154	15	AC069158	AC069158 Genomic S
1140	94.5	8.8	156095	5	CR407555	CR407555 Zebrafish
1141	94.5	8.8	163267	14	AC147704	AC147704 Oryctolag
1142	94.5	8.8	171343	8	AC092045	AC092045 Homo sapi
c1143	94.5	8.8	175262	8	AC021491	AC021491 Homo sapi
1144	94.5	8.8	177145	14	AC113156	AC113156 Homo sapi
1145	94.5	8.8	180000	14	AC004578	AC004578 Homo sapi
1146	94.5	8.8	181862	5	BX255897	BX255897 Zebrafish
c1147	94.5	8.8	182828	14	AC116779	AC116779 Mus muscu
1148	94.5	8.8	183396	14	AC154112	AC154112 Pan trogl
1149	94.5	8.8	184223	8	HSA261N11	AL121827 Human DNA
c1150	94.5	8.8	187936	8	AC080003	AC080003 Homo sapi
c1151	94.5	8.8	194431	14	AC120280	AC120280 Rattus no
1152	94.5	8.8	196413	14	AC097269	AC097269 Pan trogl
c1153	94.5	8.8	197796	14	AC152610	AC152610 Bos tauru
c1154	94.5	8.8	198372	9	AC110510	AC110510 Mus muscu
1155	94.5	8.8	205496	14	AC165202	AC165202 Oryctolag
1156	94.5	8.8	206422	14	AC158521	AC158521 Mus muscu
c1157	94.5	8.8	210148	9	AC122864	AC122864 Mus muscu
c1158	94.5	8.8	214160	8	AC094021	AC094021 Homo sapi
c1159	94.5	8.8	219417	14	AC096826	AC096826 Rattus no
c1160	94.5	8.8	231954	14	AC108848	AC108848 Mus muscu
c1161	94.5	8.8	233687	14	AC159361	AC159361 Bos tauru
1162	94.5	8.8	238993	14	AC152754	AC152754 Bos tauru
1163	94.5	8.8	240294	14	AC044892	AC044892 Homo sapi
1164	94.5	8.8	241931	14	AC132528	AC132528 Rattus no
c1165	94.5	8.8	243243	14	AC156200	AC156200 Bos tauru
1166	94.5	8.8	254400	14	AC096497	AC096497 Rattus no
1167	94.5	8.8	256499	14	AC130987	AC130987 Rattus no
c1168	94.5	8.8	260041	14	AC153186	AC153186 Bos tauru
c1169	94.5	8.8	260509	14	AC162986	AC162986 Bos tauru
c1170	94.5	8.8	271043	14	AC164033	AC164033 Bos tauru
1171	94.5	8.8	300917	1	AE016919	AE016919 Chromobac
1172	94.5	8.8	302007	1	SCO939132	AL939132 Streptomy
c1173	94.5	8.8	349726	1	BX640421	BX640421 Bordetell
c1174	94.5	8.8	349980	6	AX492784	AX492784 Sequence
c1175	94.5	8.8	349980	6	AX553951	AX553951 Sequence
1176	94	8.8	783	6	AR625249	AR625249 Sequence
c1177	94	8.8	1258	3	DQ129256	DQ129256 Unculture
c1178	94	8.8	1369	1	AB114201	AB114201 Agrobacte
1179	94	8.8	1837	5	AF036319	AF036319 Sparus au
1180	94	8.8	2266	8	BC049193	BC049193 Homo sapi
1181	94	8.8	2463	8	BC004298	BC004298 Homo sapi
1182	94	8.8	2681	8	BC011891	BC011891 Homo sapi
1183	94	8.8	2740	6	CQ728972	CQ728972 Sequence
1184	94	8.8	2924	8	BC063554	BC063554 Homo sapi
c1185	94	8.8	2938	9	BC057334	BC057334 Mus muscu
1186	94	8.8	2988	8	BC073907	BC073907 Homo sapi
1187	94	8.8	3132	6	AR619121	AR619121 Sequence
1188	94	8.8	3626	6	AR338602	AR338602 Sequence
c1189	94	8.8	4057	9	BC057110	BC057110 Mus muscu
1190	94	8.8	5085	1	AF088132	AF088132 Herbaspir
1191	94	8.8	5282	8	AB011171	AB011171 Homo sapi
c1192	94	8.8	6096	9	AK220153	AK220153 Mus muscu
1193	94	8.8	26928	2	AB029444	AB029444 Leishmani
c1194	94	8.8	31713	15	AC156445	AC156445 Volvox ca
c1195	94	8.8	82098	8	AC006252	AC006252 Homo sapi
1196	94	8.8	90736	8	HS299D3	Z84468 Human DNA s
1197	94	8.8	91034	14	AC025911	AC025911 Mus muscu
c1198	94	8.8	100541	8	DQ090940	DQ090940 Homo sapi
c1199	94	8.8	101707	14	AC150157	AC150157 Gallus ga
c1200	94	8.8	110000	1	AE000516_17	Continuation (18 o
1201	94	8.8	110000	1	AE016822_05	Continuation (6 of
1202	94	8.8	110000	1	AY596297_12	Continuation (13 o
c1203	94	8.8	110000	1	BA000045_14	Continuation (15 o
c1204	94	8.8	110000	14	AC128221_1	Continuation (2 of
1205	94	8.8	110000	14	AC150790_1	Continuation (2 of
c1206	94	8.8	110000	14	AP006500_09	Continuation (10 o
1207	94	8.8	110000	14	CT005253_3	Continuation (4 of
1208	94	8.8	110000	14	CT005257_3	Continuation (4 of
c1209	94	8.8	110000	15	AP008217_108	Continuation (109
1210	94	8.8	110000	15	CR380953_05	Continuation (6 of
1211	94	8.8	110000	15	AP008210_097	Continuation (98 o
c1212	94	8.8	112077	14	AC159579	AC159579 Dasypus n
1213	94	8.8	114109	14	AC150148	AC150148 Gallus ga
c1214	94	8.8	121894	15	AC135599	AC135599 Oryza sat
1215	94	8.8	128574	15	OSJN00199	AL663002 Oryza sat
c1216	94	8.8	128769	9	AC161365	AC161365 Mus muscu
c1217	94	8.8	130263	8	HS681N20	AL031670 Human DNA
1218	94	8.8	134370	14	AC159175	AC159175 Dasypus n
1219	94	8.8	143475	14	CR925732	CR925732 Danio rer
c1220	94	8.8	145463	14	AC151507	AC151507 Dasypus n
1221	94	8.8	150501	6	CS086342	CS086342 Sequence
1222	94	8.8	158845	14	AC150171	AC150171 Gallus ga
1223	94	8.8	159393	14	AC148739	AC148739 Oryctolag
1224	94	8.8	161985	9	AL592169	AL592169 Mouse DNA
c1225	94	8.8	166080	8	AC127518	AC127518 Homo sapi
1226	94	8.8	166437	14	AC135133	AC135133 Rattus no
c1227	94	8.8	167063	14	AY914083	AY914083 Triticum
1228	94	8.8	167457	14	AC037478	AC037478 Homo sapi
1229	94	8.8	170979	14	AC026270	AC026270 Homo sapi
c1230	94	8.8	171030	8	CNS01DSF	AL121774 Human chr
c1231	94	8.8	176018	14	AC157755	AC157755 Pan trogl
1232	94	8.8	179881	9	AC121593	AC121593 Mus muscu
1233	94	8.8	181586	15	OSJN00301	BX890594 Oryza sat
1234	94	8.8	182003	8	AL355987	AL355987 Human DNA
c1235	94	8.8	186028	14	AC153265	AC153265 Bos tauru
c1236	94	8.8	195613	8	AC130371	AC130371 Homo sapi
1237	94	8.8	195891	8	CNS00007	AL049780 Human chr
1238	94	8.8	197810	9	AC116580	AC116580 Mus muscu
c1239	94	8.8	198712	14	AC160566	AC160566 Pan trogl
c1240	94	8.8	201232	9	AL845430	AL845430 Mouse DNA
c1241	94	8.8	203010	8	AC006530	AC006530 Homo sapi
c1242	94	8.8	203981	9	AC153517	AC153517 Mus muscu
1243	94	8.8	204142	8	AC010976	AC010976 Homo sapi
1244	94	8.8	209252	8	AC097637	AC097637 Homo sapi

c1245	94	8.8	212563	14	AC155675	AC155675 Bos tauru
1246	94	8.8	214160	8	AC094021	AC094021 Homo sapi
1247	94	8.8	217819	14	AC026386	AC026386 Mus muscu
1248	94	8.8	223183	14	AC131405	AC131405 Rattus no
1249	94	8.8	225253	14	AC098950	AC098950 Rattus no
1250	94	8.8	225803	9	AC149589	AC149589 Mus muscu
1251	94	8.8	226685	5	BX072537	BX072537 Zebrafish
c1252	94	8.8	227515	14	AC150065	AC150065 Gallus ga
c1253	94	8.8	227977	14	AC129157	AC129157 Rattus no
c1254	94	8.8	235201	14	AC114470	AC114470 Rattus no
c1255	94	8.8	235737	14	AC094687	AC094687 Rattus no
c1256	94	8.8	238584	14	AC156711	AC156711 Bos tauru
c1257	94	8.8	240294	14	AC044892	AC044892 Homo sapi
c1258	94	8.8	241931	14	AC132528	AC132528 Rattus no
c1259	94	8.8	242390	14	AC160982	AC160982 Mus muscu
1260	94	8.8	248921	14	AC095538	AC095538 Rattus no
c1261	94	8.8	300050	1	BX248339	BX248339 Mycobacte
c1262	94	8.8	347496	1	BX842577	BX842577 Mycobacte
1263	93.5	8.7	521	9	RNU20999	U20999 Rattus norv
c1264	93.5	8.7	764	3	AY934432	AY934432 Unculture
c1265	93.5	8.7	764	3	AY934433	AY934433 Unculture
c1266	93.5	8.7	764	3	AY934444	AY934444 Unculture
c1267	93.5	8.7	764	3	AY934452	AY934452 Unculture
1268	93.5	8.7	1077	8	BC004537	BC004537 Homo sapi
1269	93.5	8.7	1113	8	BC009290	BC009290 Homo sapi
1270	93.5	8.7	1134	8	BC007389	BC007389 Homo sapi
1271	93.5	8.7	1149	4	AF337539	AF337539 Pteropus
1272	93.5	8.7	1166	6	AX498708	AX498708 Sequence
1273	93.5	8.7	1200	1	AB178012	AB178012 Ralstonia
c1274	93.5	8.7	1233	15	AK069960	AK069960 Oryza sat
c1275	93.5	8.7	1414	3	AY921997	AY921997 Unculture
c1276	93.5	8.7	1452	3	AY289368	AY289368 Unculture
1277	93.5	8.7	1944	6	AX498702	AX498702 Sequence
1278	93.5	8.7	1944	6	AX503491	AX503491 Sequence
1279	93.5	8.7	2021	6	AX498700	AX498700 Sequence
1280	93.5	8.7	2021	6	AX503489	AX503489 Sequence
1281	93.5	8.7	2041	9	AY349615	AY349615 Mus muscu
1282	93.5	8.7	2304	6	AX498698	AX498698 Sequence
c1283	93.5	8.7	2649	8	BC021997	BC021997 Homo sapi
c1284	93.5	8.7	2655	6	AX835215	AX835215 Sequence
c1285	93.5	8.7	2655	8	AK098140	AK098140 Homo sapi
1286	93.5	8.7	2676	6	CQ734168	CQ734168 Sequence
1287	93.5	8.7	2865	6	AX498695	AX498695 Sequence
c1288	93.5	8.7	3084	1	S71770	S71770 carotenoid
1289	93.5	8.7	3296	6	AX498694	AX498694 Sequence
1290	93.5	8.7	3298	6	AX498697	AX498697 Sequence
1291	93.5	8.7	3435	6	I05008	I05008 Sequence 2
1292	93.5	8.7	3549	1	STMGALO	M18953 S.lividans
c1293	93.5	8.7	3963	6	CQ721325	CQ721325 Sequence
c1294	93.5	8.7	4375	8	BC039258	BC039258 Homo sapi
c1295	93.5	8.7	5098	6	CQ849975	CQ849975 Sequence
c1296	93.5	8.7	5098	8	AK127049	AK127049 Homo sapi
1297	93.5	8.7	6323	6	CS114267	CS114267 Sequence
c1298	93.5	8.7	6814	8	HSL219F9B	Z69924 Human DNA s
1299	93.5	8.7	10487	4	AY631942	AY631942 Equus cab
c1300	93.5	8.7	10798	1	AE004604	AE004604 Pseudomon
c1301	93.5	8.7	12797	1	AE005079	AE005079 Halobacte
1302	93.5	8.7	14974	1	AE011892	AE011892 Xanthomon
c1303	93.5	8.7	18093	9	AY052495	AY052495 Mus muscu
1304	93.5	8.7	26137	8	AC025444	AC025444 Homo sapi
1305	93.5	8.7	34667	8	HSA314905	AJ314905 Homo sapi
c1306	93.5	8.7	35356	8	AP006329	AP006329 Homo sapi
c1307	93.5	8.7	38608	8	AL731661	AL731661 Human DNA
c1308	93.5	8.7	39450	8	AC114296	AC114296 Homo sapi
c1309	93.5	8.7	40474	14	AC141235	AC141235 Homo sapi
c1310	93.5	8.7	40707	1	RSP010302	AJ010302 Rhodobact
c1311	93.5	8.7	44700	8	AC119731	AC119731 Homo sapi
c1312	93.5	8.7	47741	6	AR659744	AR659744 Sequence
1313	93.5	8.7	64027	14	AC162069	AC162069 Bos tauru
c1314	93.5	8.7	66280	1	AF195122	AF195122 Rhodobact
c1315	93.5	8.7	76727	8	HS821D11	AL021453 Human DNA
c1316	93.5	8.7	79129	8	AC011427	AC011427 Homo sapi
c1317	93.5	8.7	85781	8	AL663074	AL663074 Human DNA
1318	93.5	8.7	96891	8	AL358216	AL358216 Human DNA
1319	93.5	8.7	101043	8	AC010539	AC010539 Homo sapi
c1320	93.5	8.7	102826	2	AC136213	AC136213 Leishmani
c1321	93.5	8.7	105066	14	AP006498_8	Continuation (9 of
c1322	93.5	8.7	110000	1	AP006618_14	Continuation (15 o
1323	93.5	8.7	110000	1	AP006840_15	Continuation (16 o
1324	93.5	8.7	110000	1	BA000030_86	Continuation (87 o
1325	93.5	8.7	110000	1	BA000040_69	Continuation (70 o
1326	93.5	8.7	110000	1	CP000088_13	Continuation (14 o
1327	93.5	8.7	110000	1	CP000088_14	Continuation (15 o
c1328	93.5	8.7	110000	2	CP000078_0	CP000078 Leishmani
c1329	93.5	8.7	110000	2	CP000079_08	Continuation (9 of
1330	93.5	8.7	110000	14	AC139486_1	Continuation (2 of
1331	93.5	8.7	110000	14	AP006486_1	Continuation (2 of
1332	93.5	8.7	110000	14	CR954201_06	Continuation (7 of
1333	93.5	8.7	110000	14	CT005249_3	Continuation (4 of
c1334	93.5	8.7	110000	15	AP008210_002	Continuation (3 of
c1335	93.5	8.7	110000	15	AP008210_003	Continuation (4 of
1336	93.5	8.7	110000	15	AP008211_287	Continuation (288
1337	93.5	8.7	119725	14	AC148040	AC148040 Ovis arie
c1338	93.5	8.7	128331	15	AC134929	AC134929 Oryza sat
c1339	93.5	8.7	131535	8	AC005875	AC005875 citb_188_
c1340	93.5	8.7	133954	8	AL355493	AL355493 Human DNA
1341	93.5	8.7	135964	8	AL353593	AL353593 Human DNA
c1342	93.5	8.7	140026	8	AC005840	AC005840 Homo sapi
c1343	93.5	8.7	140053	14	AC007873	AC007873 Homo sapi
c1344	93.5	8.7	144778	15	OSJN00146	AL662935 Oryza sat
c1345	93.5	8.7	145442	8	AC004859	AC004859 Homo sapi
c1346	93.5	8.7	149006	8	AC122713	AC122713 Homo sapi
c1347	93.5	8.7	149453	9	AC084109	AC084109 Mus muscu
c1348	93.5	8.7	150434	8	AL138784	AL138784 Human DNA
c1349	93.5	8.7	151349	14	AL353647	AL353647 Homo sapi
c1350	93.5	8.7	155332	14	AL365439	AL365439 Homo sapi
1351	93.5	8.7	156073	14	AC126632	AC126632 Rattus no
c1352	93.5	8.7	157168	9	AL772232	AL772232 Mouse DNA
1353	93.5	8.7	158498	14	AC098295	AC098295 Rattus no
c1354	93.5	8.7	160149	14	AC016380	AC016380 Homo sapi
c1355	93.5	8.7	160511	14	AC022786	AC022786 Homo sapi
1356	93.5	8.7	161716	8	AC087434	AC087434 Pan trogl
c1357	93.5	8.7	162041	14	AC137797	AC137797 Homo sapi
1358	93.5	8.7	164766	14	AC026657	AC026657 Homo sapi
1359	93.5	8.7	166266	14	AP001146	AP001146 Homo sapi
1360	93.5	8.7	167972	14	AC125678	AC125678 Rattus no
1361	93.5	8.7	170976	8	AC137761	AC137761 Homo sapi
c1362	93.5	8.7	171114	8	AC136613	AC136613 Homo sapi
c1363	93.5	8.7	173621	8	AC136425	AC136425 Homo sapi
c1364	93.5	8.7	174988	14	AL928903	AL928903 Homo sapi
c1365	93.5	8.7	175691	8	AC136440	AC136440 Homo sapi
1366	93.5	8.7	177689	9	AC122441	AC122441 Mus muscu
1367	93.5	8.7	178238	4	AC092519	AC092519 Felis cat
c1368	93.5	8.7	181233	14	AC149832	AC149832 Zea mays
1369	93.5	8.7	186120	8	AL390755	AL390755 Human DNA
1370	93.5	8.7	188050	1	AL646072	AL646072 Ralstonia
c1371	93.5	8.7	188488	8	AC006057	AC006057 Homo sapi
1372	93.5	8.7	189149	14	AC046171	AC046171 Homo sapi
c1373	93.5	8.7	190998	9	AC139351	AC139351 Mus muscu
c1374	93.5	8.7	192799	8	AL583841	AL583841 Human DNA
1375	93.5	8.7	194490	8	AC140899	AC140899 Homo sapi
c1376	93.5	8.7	194508	14	AC145316	AC145316 Homo sapi
1377	93.5	8.7	195563	9	AC123708	AC123708 Mus muscu
1378	93.5	8.7	196021	8	AC138807	AC138807 Homo sapi
c1379	93.5	8.7	197273	9	AC024607	AC024607 Mus muscu
1380	93.5	8.7	201889	14	AL929415	AL929415 Mus muscu
c1381	93.5	8.7	202322	14	AC117316	AC117316 Rattus no
c1382	93.5	8.7	203690	14	AC153325	AC153325 Lemur cat
1383	93.5	8.7	204655	14	AC142537	AC142537 Homo sapi
c1384	93.5	8.7	204881	14	AL591111	AL591111 Homo sapi
1385	93.5	8.7	205191	14	AC145314	AC145314 Homo sapi
1386	93.5	8.7	213047	14	AC020557	AC020557 Homo sapi
c1387	93.5	8.7	214110	8	AC007908	AC007908 Homo sapi
1388	93.5	8.7	214332	14	AC120945	AC120945 Rattus no
c1389	93.5	8.7	215050	1	AL646057	AL646057 Ralstonia
c1390	93.5	8.7	215957	14	AC148950	AC148950 Otolemur

c1391	93.5	8.7	219325	14	AC093464	AC093464 Mus muscu
c1392	93.5	8.7	220456	9	AC124664	AC124664 Mus muscu
1393	93.5	8.7	226213	14	AC107064	AC107064 Bos tauru
1394	93.5	8.7	226637	9	AL807764	AL807764 Mouse DNA
c1395	93.5	8.7	229494	9	AL627328	AL627328 Mouse DNA
c1396	93.5	8.7	232735	14	AC115240	AC115240 Rattus no
1397	93.5	8.7	233675	14	AC112444	AC112444 Rattus no
1398	93.5	8.7	235454	14	AC132678	AC132678 Rattus no
1399	93.5	8.7	236455	1	AY316746	AY316746 Rhizobium
c1400	93.5	8.7	237432	14	AC137164	AC137164 Rattus no
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c1402	93.5	8.7	243029	14	AC115636	AC115636 Rattus no
c1403	93.5	8.7	245616	14	AC153298	AC153298 Bos tauru
1404	93.5	8.7	245651	14	AC126537	AC126537 Rattus no
1405	93.5	8.7	258742	14	AC120290	AC120290 Rattus no
1406	93.5	8.7	275140	14	AC158015	AC158015 Bos tauru
1407	93.5	8.7	283100	1	SCO939110	AL939110 Streptomy
1408	93.5	8.7	300029	1	AE016787	AE016787 Pseudomon
1409	93.5	8.7	300933	1	AE016791	AE016791 Pseudomon
1410	93.5	8.7	301589	1	AE017312	AE017312 Desulfovi
c1411	93.5	8.7	308147	1	AE016915	AE016915 Chromobac
1412	93.5	8.7	331221	14	AC136270	AC136270 Rattus no
c1413	93.5	8.7	332533	14	AC152664	AC152664 Bos tauru
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1417	93	8.7	1026	6	CQ714835	CQ714835 Sequence
c1418	93	8.7	1307	3	AM072423	AM072423 Unculture
1419	93	8.7	1393	8	BC050674	BC050674 Homo sapi
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1421	93	8.7	1669	6	AX748154	AX748154 Sequence
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1426	93	8.7	2496	15	AK120342	AK120342 Oryza sat
1427	93	8.7	2898	15	AF131736	AF131736 Chlamydom
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1430	93	8.7	4103	6	CQ850879	CQ850879 Sequence
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1474	93	8.7	135363	15	AC123517	AC123517 Oryza sat
1475	93	8.7	136377	14	AC148066	AC148066 Canis fam
1476	93	8.7	137073	14	AC163433	AC163433 Loxodonta
c1477	93	8.7	142229	9	AL954299	AL954299 Mouse DNA
1478	93	8.7	147665	8	AL138691	AL138691 Human DNA
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c1483	93	8.7	153248	14	AC112500	AC112500 Homo sapi
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c1486	93	8.7	164766	14	AC026657	AC026657 Homo sapi
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c1492	93	8.7	172716	14	AC090965	AC090965 Papio anu
c1493	93	8.7	172731	14	AC151879	AC151879 Sus scrof
c1494	93	8.7	175565	14	AC151951	AC151951 Papio anu
1495	93	8.7	175762	14	AC150666	AC150666 Bos tauru
1496	93	8.7	176562	8	AC084864	AC084864 Homo sapi
1497	93	8.7	176926	8	AC009078	AC009078 Homo sapi
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ALIGNMENTS

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RESULT 1
AX427978
LOCUS       AX427978                591 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 1 from Patent WO0233083.
ACCESSION   AX427978
VERSION     AX427978.1  GI:21538065
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Newton,C.M., Liu,L., Glasebrook,A.L. and Tetreault,J.W.
  TITLE     Methods of using a human IL-17-related polypeptide to treat disease
  JOURNAL   Patent: WO 0233083-A 1 25-APR-2002;
            LILLY CO ELI (US)
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ORIGIN
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Alignment Scores:
Pred. No.:                1.23e-59        Length:         591
Score:                    1073.00         Matches:        197
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       6               Gaps:           0

US-09-854-280-3 (1-197) x AX427978 (1-591)

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Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
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Db         61 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 120

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
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Db        121 GAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 180

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Db        181 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 240

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
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Db        241 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 300

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
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Db        301 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 360

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
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Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
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Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
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Db        541 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 591

RESULT 2
BD218885
LOCUS       BD218885                 594 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Factor affecting tumor necrosis factor receptor releasing enzyme.
ACCESSION   BD218885
VERSION     BD218885.1  GI:33028655
KEYWORDS    JP 2002514402-A/10.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Gatanaga,T. and Granger,G.A.
  TITLE     Factor affecting tumor necrosis factor receptor releasing enzyme
  JOURNAL   Patent: JP 2002514402-A 10 21-MAY-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002514402-A/10
            PD   21-MAY-2002
            PF   14-MAY-1999 JP 2000548361
            PR   14-MAY-1998 US    09/081385
            PI   TETSUYA GATANAGA,GALE A GRANGER
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12Q1/68,
            PC   G01N33/15,G01N33/50//C07K14/715,C12N15/00,C12N5/00 CC   Factor
            affecting tumor necrosis factor receptor releasing  CC
            enzyme
            FH   Key             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:                1.24e-59        Length:         594
Score:                    1073.00         Matches:        197
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              100.0%          Indels:         0
DB:                       6               Gaps:           0

US-09-854-280-3 (1-197) x BD218885 (1-594)

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Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
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Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
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Db        541 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 591

RESULT 3
BC069152
LOCUS       BC069152                 613 bp    mRNA    linear   PRI 30-JUN-2004
DEFINITION  Homo sapiens interleukin 17C, mRNA (cDNA clone MGC:95437
            IMAGE:7217012), complete cds.
ACCESSION   BC069152
VERSION     BC069152.1  GI:46575693
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KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 613)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 613)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Anup Madan, University of Iowa
cDNA Library Preparation: Anup Madan, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Neurogenomics Research Lab,
200 B EMRB, University of Iowa, Iowa City, IA-52242
anup-madan@uiowa.edu
Jessica Fahey, Tim Nelson, Jae Goon Yoon and Anup Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: Plate: Row: Column: 0.

FEATURES Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.:	1.27e-59	Length:	613
Score:	1073.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	8	Gaps:	0

US-09-854-280-3 (1-197) x BC069152 (1-613)

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Db          1 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 60

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 120

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 180

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Db        181 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 240

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 300

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 360

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 420

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 480

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 540

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
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Db        541 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 591
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RESULT 4
BD218877
LOCUS BD218877 1047 bp DNA linear PAT 17-JUL-2003
DEFINITION Factor affecting tumor necrosis factor receptor releasing enzyme.
ACCESSION BD218877
VERSION BD218877.1 GI:33028647
KEYWORDS JP 2002514402-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Gatanaga,T. and Granger,G.A.
TITLE Factor affecting tumor necrosis factor receptor releasing enzyme
JOURNAL Patent: JP 2002514402-A 2 21-MAY-2002;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

```
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002514402-A/2
            PD   21-MAY-2002
            PF   14-MAY-1999 JP 2000548361
            PR   14-MAY-1998 US    09/081385
            PI   TETSUYA GATANAGA,GALE A GRANGER
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12Q1/68,
            PC   G01N33/15,G01N33/50//C07K14/715,C12N15/00,C12N5/00 CC   Factor
            affecting tumor necrosis factor receptor releasing  CC
            enzyme
            FH   Key             Location/Qualifiers
            FT   source          1. .1047
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .1047
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ORIGIN

Alignment Scores:
Pred. No.:              2.16e-59        Length:         1047
Score:                  1073.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-09-854-280-3 (1-197) x BD218877 (1-1047)

Qy          1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
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Db         50 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 109

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
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Db        110 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 169

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
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Db        170 GAACTGCCCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 229

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Db        230 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 289

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 349

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
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Db        350 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 409

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
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Db        410 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 469

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 529

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 589

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
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Db        590 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 640

RESULT 5
AR338357
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LOCUS       AR338357                1047 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3 from patent US 6569645.
ACCESSION   AR338357
VERSION     AR338357.1  GI:33725120
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1047)
  AUTHORS   Chen,J., Filvaroff,E., Fong,S., Goddard,A., Godowski,P.,
            Grimaldi,C., Gurney,A., Li,H., Hillan,K., Tumas,D., VanLookeren,M.,
            Vandlen,R., Watanabe,C., Williams,P.M., Wood,W.I. and Yansura,D.
  TITLE     IL-17 homologous polypeptides and therapeutic uses thereof
  JOURNAL   Patent: US 6569645-A 3 27-MAY-2003;
            Genentech, Inc.; South San Francisco, CA
FEATURES             Location/Qualifiers
     source          1. .1047
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.16e-59        Length:         1047
Score:                  1073.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-09-854-280-3 (1-197) x AR338357 (1-1047)

Qy          1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         50 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 109

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 169

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 GAACTGCCCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 229

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Db        230 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 289

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 349

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 409

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 469

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 529

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 589

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 640

RESULT 6
AX180766
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LOCUS       AX180766               1047 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 3 from Patent WO0146420.
ACCESSION   AX180766
VERSION     AX180766.1  GI:15132617
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Chen,J., Filvaroff,E., Fong,S., Goddard,A., Godowski,P.J.,
            Grimaldi,C.J., Gurney,A.L., Li,H., Hillan,K.J., Tumas,D., van
            Lookeren,M., Vandlen,R.L., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Yansura,D.G.
  TITLE     Il-17 and il-17r homologous polypeptides and therapeutic uses
            thereof
  JOURNAL   Patent: WO 0146420-A 3 28-JUN-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1047
                     /organism="Homo sapiens"
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ORIGIN

Alignment Scores:
Pred. No.:              2.16e-59        Length:         1047
Score:                  1073.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-09-854-280-3 (1-197) x AX180766 (1-1047)

Qy          1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
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Db         50 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 109

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 169

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 GAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 229

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 289

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 349

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
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Db        350 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 409

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 469

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 529

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 589

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 640

RESULT 7
AX376380
LOCUS       AX376380               1047 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 447 from Patent WO0168848.
ACCESSION   AX376380
VERSION     AX376380.1  GI:19170581
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
            Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0168848-A 447 20-SEP-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1047
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              2.16e-59        Length:         1047
Score:                  1073.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-09-854-280-3 (1-197) x AX376380 (1-1047)

Qy          1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
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Db         50 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 109

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
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Db        110 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 169

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 GAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 229

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 289

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
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Db        290 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 349

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 409

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 469

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 529

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
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Db        530 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 589

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 640

RESULT 8
AF152099
LOCUS       AF152099                1047 bp    mRNA    linear   PRI 27-JAN-2000
DEFINITION  Homo sapiens interleukin 17C mRNA, complete cds.
ACCESSION   AF152099
VERSION     AF152099.1  GI:6759914
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1047)
  AUTHORS   Li,H., Chen,J., Huang,A., Stinson,J., Heldens,S., Foster,J.,
            Dowd,P., Gurney,A.L. and Wood,W.I.
  TITLE     Cloning and characterization of IL-17B and IL-17C, two new members
            of the IL-17 cytokine family
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (2), 773-778 (2000)
   PUBMED   10639155
REFERENCE   2  (bases 1 to 1047)
  AUTHORS   Li,H., Chen,J., Stinson,J. and Wood,W.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-1999) Molecular Biology, Genentech, Inc., 1 DNA
            Way, S. San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1047
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                     /chromosome="2"
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                     /clone="DNA62377"
     CDS             50. .643
                     /note="IL-17C; similar to interleukin 17"
                     /codon_start=1
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                     /protein_id="AAF28105.1"
                     /db_xref="GI:6759915"
                     /translation="MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPL
                     GQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTH
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                     RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRSV"
ORIGIN

Alignment Scores:
Pred. No.:              2.16e-59        Length:         1047
Score:                  1073.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     8               Gaps:           0

US-09-854-280-3 (1-197) x AF152099 (1-1047)

Qy          1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         50 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 109

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 169

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 GAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 229

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 289

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 349

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
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Db        350 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 409

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
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Db        410 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 469

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
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Db        470 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 529

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 589

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
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Db        590 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 640

RESULT 9
AY358471
LOCUS       AY358471                1047 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA62377 IL17C (UNQ561) mRNA, complete cds.
ACCESSION   AY358471
VERSION     AY358471.1  GI:37182064
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1047)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1047)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1047
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                     /clone="DNA62377"
     gene            1. .1047
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/db_xref="GI:37182065"
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QRSISPWRYRVDTDEDRYPQKLAFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRR
RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRSV"

ORIGIN

Alignment Scores:

Pred. No.:	2.16e-59	Length:	1047
Score:	1073.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	8	Gaps:	0

US-09-854-280-3 (1-197) x AY358471 (1-1047)

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Qy          1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
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Db         50 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 109

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 169

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 GAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 229

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 289

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 349

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 409

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 469

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 529

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 589

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 640
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RESULT 10
BD211219

LOCUS	BD211219	1067 bp	DNA	linear	PAT 17-JUL-2003

DEFINITION Interleukins-21 and 22.
ACCESSION BD211219
VERSION BD211219.1 GI:33020989
KEYWORDS JP 2002516103-A/21.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1067)
AUTHORS Ruben,S.M. and Ebner,R.
TITLE Interleukins-21 and 22
JOURNAL Patent: JP 2002516103-A 21 04-JUN-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Homo sapiens (human)
PN JP 2002516103-A/21
PD 04-JUN-2002
PF 27-MAY-1999 JP 2000551001
PR 29-MAY-1998 US 60/087340,10-SEP-1998 US 60/099805 PR
30-APR-1999 US 60/131965
PI STEVEN M RUBEN,REINHARD EBNER
PC C12N15/09,A61K38/00,A61P7/04,A61P9/00,A61P15/08,A61P25/00, PC
A61P35/04,
PC A61P43/00,A61P43/00,C07K14/54,C07K16/24,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12Q1/68,G01N33/68,C12N15/00,A61K37/02, PC
C12N5/00
CC Interleukins-21 and 22.
FH Key Location/Qualifiers
FT CDS (34). .(624).
FEATURES Location/Qualifiers
source 1. .1067
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/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.:	2.2e-59	Length:	1067
Score:	1073.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-854-280-3 (1-197) x BD211219 (1-1067)

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Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
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Db         94 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 153

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 GAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 213

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 273

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 333

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGGGTGGACACGGATGAGGACCGCTAT 393

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
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Db        394 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 453

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
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Db        454 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 513

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
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Db        514 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 573

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
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Db        574 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 624

RESULT 11
CQ847631
LOCUS       CQ847631               1067 bp    DNA     linear   PAT 19-AUG-2004
DEFINITION  Sequence 28 from Patent EP1443055.
ACCESSION   CQ847631
VERSION     CQ847631.1  GI:51469191
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ruben,S.M. and Ebner,R.
  TITLE     Interleukins-21 and 22
  JOURNAL   Patent: EP 1443055-A 28 04-AUG-2004;
            Human Genome Sciences, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             34. .627
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                     /codon_start=1
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                     /db_xref="GI:51469192"
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                     RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRSV"
ORIGIN

Alignment Scores:
Pred. No.:              2.2e-59        Length:         1067
Score:                  1073.00        Matches:        197
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     6              Gaps:           0

US-09-854-280-3 (1-197) x CQ847631 (1-1067)

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Db         34 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 93

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
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Db         94 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 153

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
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Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Db        214 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 273

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 333

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGGGTGGACACGGATGAGGACCGCTAT 393

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
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Db        394 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 453

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
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Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
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Db        514 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 573

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
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Db        574 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 624

RESULT 12
BD265555
LOCUS       BD265555               1107 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Interleukin-17-associated mammalian cytokine, polynucleotide
            encoding the same and utilization thereof.
ACCESSION   BD265555
VERSION     BD265555.1  GI:33075323
KEYWORDS    JP 2002534122-A/12.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1107)
  AUTHORS   Gorman,D.M., Bazan,F.J. and Kastelein,R.A.
  TITLE     Interleukin-17-associated mammalian cytokine, polynucleotide
            encoding the same and utilization thereof
  JOURNAL   Patent: JP 2002534122-A 12 15-OCT-2002;
            SCHERING CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534122-A/12
            PD   15-OCT-2002
            PF   10-JAN-2000 JP 2000593745
            PR   11-JAN-1999 US    09/228822
            PI   DANIEL M GORMAN,FERNANDO J BAZAN,ROBERT A KASTELEIN PC
            C12N15/09,C07K14/54,C07K16/24,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N5/10,
            PC   C12P21/02,G01N33/53//(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   C12N5/00
            CC   Interleukin-17-associated mammalian cytokine, polynucleotide
            CC           encoding the
            CC   same and utilization thereof
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            FT   mat_peptide     (166). .(705).
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ORIGIN

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Pred. No.:              2.29e-59       Length:         1107
Score:                  1073.00        Matches:        197
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     6              Gaps:           0

US-09-854-280-3 (1-197) x BD265555 (1-1107)

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Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
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Db        175 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 234

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 GAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 294

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Db        295 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 354

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
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Db        355 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 414

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
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Db        415 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 474

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
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Db        475 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 534

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 594

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 654

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
                 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 705

RESULT 13
CS135286
LOCUS       CS135286               1107 bp    DNA     linear   PAT 09-AUG-2005
DEFINITION  Sequence 23 from Patent WO2005065711.
ACCESSION   CS135286
VERSION     CS135286.1  GI:72067734
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gorman,D.M.
  TITLE     Mammalian receptor proteins; related reagents and methods
  JOURNAL   Patent: WO 2005065711-A 23 21-JUL-2005;
            Schering Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1107
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.:              2.29e-59        Length:         1107
Score:                  1073.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-09-854-280-3 (1-197) x CS135286 (1-1107)

Qy          1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
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Db        115 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 174

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 234

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 GAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 294

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 354

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 414

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
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Db        415 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 474

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 534

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
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Db        535 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 594

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
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Db        595 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 654

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
                 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 705

RESULT 14
AR316787
LOCUS       AR316787               1107 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 22 from patent US 6562578.
ACCESSION   AR316787
VERSION     AR316787.1  GI:33695749
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1107)
  AUTHORS   Gorman,D.M., Bazan,J.F. and Kastelein,R.A.
  TITLE     IL-17-like cytokine binding compounds and antibodies
  JOURNAL   Patent: US 6562578-A 22 13-MAY-2003;
            Schering Corporation; Kenilworth, NJ;
            WOX;
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              2.29e-59        Length:         1107
Score:                  1073.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     6               Gaps:           0

US-09-854-280-3 (1-197) x AR316787 (1-1107)

Qy          1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
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Db        115 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 174

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
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Db        175 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 234

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
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Db        235 GAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 294

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Db        295 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 354

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
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Db        355 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 414

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
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Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 534

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 594

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 654

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 705

RESULT 15
AF142410
LOCUS       AF142410               1078 bp    mRNA    linear   PRI 31-OCT-2000
DEFINITION  Homo sapiens cytokine CX2 precusor mRNA, complete cds.
ACCESSION   AF142410
VERSION     AF142410.1  GI:11055014
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1078)
  AUTHORS   Zhang,W., He,L., Wan,T., Yuan,Z. and Cao,X.
  TITLE     Novel human cytokine CX2 with homology to IL-17
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1078)
  AUTHORS   Zhang,W., He,L., Wan,T., Yuan,Z. and Cao,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-1999) Department of Immunology, Second Military
            Medical University & Shanghai Brilliance Biotechnology Institute,
            800 Xiangyin Road, Shanghai 200433, P.R. China
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /note="similar to IL-17"
                     /codon_start=1
                     /product="cytokine CX2 precusor"
                     /protein_id="AAG27921.1"
                     /db_xref="GI:11055015"
                     /translation="MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPL
                     GQAPPRLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTH
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ORIGIN

Alignment Scores:
Pred. No.:          7.15e-59      Length:       1078
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Best Local Similarity: 99.5%      Mismatches:   1
Query Match:        99.3%         Indels:       0
DB:                 8             Gaps:         0

US-09-854-280-3 (1-197) x AF142410 (1-1078)

Qy          1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
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Db         43 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 102

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 162

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GAACTGCCCCTCGGCCAGGCCCCCCCACGCCTGCTGGCTCGAGGTGCCAAGTGGGGGCAG 222

Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Db        223 GCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAG 282

Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 AGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGAC 342

Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 ACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTAT 402

Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 462

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 522

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 582

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
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Db        583 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 633

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Perfect score: 1073
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Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description

RESULT 1
ID AAA09153 standard; DNA; 591 BP.
DE Human interleukin-17 (IL-17) homologue coding sequence.
PN WO200020593-A1.
PD 13-APR-2000.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 2
ID AAD38083 standard; DNA; 591 BP.
DE Human LP-48 gene.
PN WO200233083-A2.
PD 25-APR-2002.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 3
ID ADV42797 standard; cDNA; 594 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 425.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 4
ID AAZ29728 standard; cDNA; 1047 BP.
DE Human Interleukin 17C, PRO1122 cDNA.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 5
ID AAA96338 standard; cDNA; 1047 BP.
DE cDNA encoding a novel polypeptide designated PRO1122.
PN WO200056889-A2.
PD 28-SEP-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 6
ID AAS46148 standard; cDNA; 1047 BP.
DE Human DNA encoding PRO polypeptide sequence #224.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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ID AAS09510 standard; cDNA; 1047 BP.
DE Human cDNA encoding Interleukin 17C ligand, IL-17C.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 8
ID ACA89598 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003036141-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 9
ID ACA73608 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 10
ID ACA05923 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 11
ID ACA66757 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO protein #224.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 12
ID ACF20332 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040063-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 13
ID ACF19718 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040064-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 14
ID ACD22006 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003027267-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 15
ID ACF13171 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036160-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 16
ID ACD28801 standard; cDNA; 1047 BP.
DE Human secreted / transmembrane polypeptide PRO1122 cDNA.
PN US2003027249-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 17
ID ACD25274 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044925-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 18
ID ACF00323 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 19
ID ACA72380 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 20
ID ACD04904 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 21
ID ACD18365 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036124-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 22
ID ACD08372 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040054-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 23
ID ACA88806 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 24
ID ACA70248 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036134-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 25
ID ACD12470 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 26
ID ACC74385 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027275-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 27
ID ACD16013 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003027324-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 28
ID ACD25581 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 29
ID ACD18058 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036123-A1.
PD 20-FEB-2003.

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 30
ID ACC88345 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036148-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 31
ID ACD21699 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040060-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 32
ID ACD18766 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044916-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 33
ID ABX98376 standard; cDNA; 1047 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 447.
PN US2003036156-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 34
ID ACD14127 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032117-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 35
ID ACD09907 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036128-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 36
ID ACC88652 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027266-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 37
ID ACD21392 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 38
ID ABX75764 standard; cDNA; 1047 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1122.
PN US2003022298-A1.
PD 30-JAN-2003.

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 39
ID ABX97967 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032102-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 40
ID ACA97443 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 41
ID ACA57906 standard; cDNA; 1047 BP.
DE Human PRO1122 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 42
ID ACD14434 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032130-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 43
ID ACC91217 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 44
ID ACC88959 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036132-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 45
ID ACA06075 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003008348-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 46
ID ACD07156 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 47
ID ACA67607 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.

PN US2003017542-A1.
PD 23-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 48
ID ACC81662 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032137-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 49
ID ACC89266 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027269-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 50
ID ACC86622 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027268-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 51
ID ACC89880 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027274-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 52
ID ACC93059 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 53
ID ACA72687 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003022295-A1.
PD 30-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 54
ID ACA89205 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003022297-A1.
PD 30-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 55
ID ACA69941 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032105-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 56
ID ACA97084 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 57
ID ACA91080 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 58
ID ACA70862 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032111-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 59
ID ACA95372 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 60
ID ACC86315 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027263-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 61
ID ACC90187 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027271-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 62
ID ACD12795 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036125-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 63
ID ACF20025 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040068-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 64
ID ABX76969 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003027280-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 65
ID ACA73301 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.

PN US2003022300-A1.
PD 30-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 66
ID ACA68844 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 67
ID ACA74688 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003036138-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 68
ID ACA70555 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032109-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 69
ID ACD14741 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003040066-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 70
ID ACA89851 standard; cDNA; 1047 BP.
DE Human cDNA (PRO1122) encoding h-IL17C.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 71
ID ACA68413 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 72
ID ABX98878 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 73
ID ACC81355 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032120-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 74
ID ACA95679 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 75
ID ACD04597 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 76
ID ACC88038 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 77
ID ACF12700 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040058-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 78
ID ACA96415 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003017540-A1.
PD 23-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 79
ID ACA65189 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032106-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 80
ID ACA73915 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032129-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 81
ID ACA74327 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 82
ID ACA96722 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032103-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 83
ID ACD10828 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.

PN US2003032107-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 84
ID ACC91524 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032139-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 85
ID ACD02859 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003022301-A1.
PD 30-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 86
ID ACC87424 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 87
ID ACC86008 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027262-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 88
ID ACA65496 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032110-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 89
ID ACA94313 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036142-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 90
ID ACA98057 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003036145-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 91
ID ACA91559 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 92
ID ACA90773 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 93
ID ACD16320 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044931-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 94
ID ACD17481 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036150-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 95
ID ACC92138 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040069-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 96
ID ACA74995 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003022293-A1.
PD 30-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 97
ID ACA91866 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032128-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 98
ID ACA71510 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032116-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 99
ID ACC90910 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032122-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 100
ID ACA65920 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO protein #224.
PN US2003036139-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 101
ID ACA64635 standard; cDNA; 1047 BP.
DE Human cDNA encoding IL-17 family member, PRO1122.
PN US2003008815-A1.

PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 102
ID ACA95065 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003017541-A1.
PD 23-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 103
ID ACD16627 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003017543-A1.
PD 23-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 104
ID ACD15706 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036152-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 105
ID ABX16809 standard; cDNA; 1047 BP.
DE Human cDNA encoding secreted/transmembrane protein #224.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 106
ID ACA97750 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032115-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 107
ID ACA99199 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 108
ID ACC91831 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 109
ID ACA67698 standard; cDNA; 1047 BP.
DE cDNA encoding human secreted polypeptide PRO122.
PN US2002192751-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 110
ID ACD11242 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 111
ID ACD15092 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044922-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 112
ID ACD11856 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032118-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 113
ID ACC95985 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036135-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 114
ID ACF16548 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 115
ID ACF02666 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 116
ID ACF02973 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 117
ID ACF21560 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 118
ID ACF10244 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068743-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 119
ID ACF78137 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 120
ID ACD46842 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 121
ID ACD49605 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 122
ID ADA76535 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036114-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 123
ID ACF28372 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 124
ID ACD89062 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 125
ID ACD84457 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 126
ID ACD99231 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 127
ID ADA78199 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 128
ID ACF48973 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104539-A1.
PD 05-JUN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 129
ID ACD09293 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036131-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 130
ID ACF12086 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040075-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 131
ID ACF41320 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 132
ID ACF15934 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044930-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 133
ID ACF16241 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 134
ID ACD32068 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 135
ID ACF18876 standard; cDNA; 1047 BP.

DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 136
ID ACF09323 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 137
ID ACF78444 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 138
ID ACF52043 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064440-A1.
PD 03-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 139
ID ADA43226 standard; cDNA; 1047 BP.
DE Human interleukin 17 related mammalian cytokine polypeptide cDNA #2.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 140
ID ACF26530 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 141
ID ACF24323 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 142
ID ACF63634 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 143
ID ACF50508 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 144
ID ACH07979 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 145
ID ACF13785 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 146
ID ACD41711 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 147
ID ACF32124 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 148
ID ACF23402 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 149
ID ACF40092 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 150
ID ACD45614 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 151
ID ACF53271 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068721-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 152
ID ACF27451 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 153
ID ACF45289 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 154
ID ACF29907 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 155
ID ACD89983 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 156
ID ACD84764 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 157
ID ACD98924 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 158
ID ACF77216 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003082717-A1.
PD 01-MAY-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 159
ID ACF76909 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 160
ID ACF49894 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104542-A1.
PD 05-JUN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 161
ID ACF50201 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104543-A1.
PD 05-JUN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 162
ID ACD09600 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036127-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 163
ID ACD08679 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040061-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 164
ID ACF12393 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036130-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 165
ID ACC94901 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 166
ID ACD22620 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 167
ID ACF15320 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044917-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 168
ID ACC97415 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044929-A1.
PD 06-MAR-2003.

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 169
ID ACC92445 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 170
ID ACF14092 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 171
ID ACF14399 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 172
ID ACF09630 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 173
ID ACD45921 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 174
ID ACD48070 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 175
ID ACD67801 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 176
ID ACF25609 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 177
ID ACF29293 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 178
ID ACD85071 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 179
ID ACD84150 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 180
ID ACD88141 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 181
ID ACF30828 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 182
ID ACF32431 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 183
ID ACH12091 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 184
ID ACH12398 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0
RESULT 185
ID ACD40790 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032134-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 186
ID ACF18262 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 187
ID ACF08709 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 188
ID ACF31510 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 189
ID ACF52350 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 190
ID ACD50219 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 191
ID ACF38922 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 192
ID ACF26837 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 193
ID ACF24937 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 194
ID ACF46517 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 195
ID ACF28065 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 196
ID ACD89369 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 197
ID ACF63941 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 198
ID ACF60581 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003087374-A1.
PD 08-MAY-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 199
ID ACH12705 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 200
ID ACH10128 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 201
ID ACD03983 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.

PN US2003040055-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 202
ID ACD10521 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036164-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 203
ID ACD12163 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040074-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 204
ID ACF42548 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 205
ID ACF18569 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 206
ID ACF02359 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 207
ID ACF21867 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 208
ID ACF10551 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073169-A1.
PD 17-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 209
ID ACF34003 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 210
ID ACF44965 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 211
ID ACD90597 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 212
ID ACD91210 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 213
ID ACF30521 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 214
ID ACD87220 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 215
ID ACF60274 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 216
ID ACF46824 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003087373-A1.
PD 08-MAY-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 217
ID ACF75681 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003096353-A1.
PD 22-MAY-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 218
ID ADA79991 standard; cDNA; 1047 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003073173-A1.
PD 17-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 219
ID ACF17341 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054458-A1.
PD 20-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 220
ID ACF23095 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 221
ID ACF08095 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 222
ID ACF08402 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 223
ID ACF40706 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 224
ID ACF53885 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 225
ID ACD47149 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 226
ID ACF48052 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 227
ID ACF47438 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 228
ID ACF46210 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 229
ID ACD86299 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 230
ID ACF52657 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003082715-A1.
PD 01-MAY-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 231
ID ACF52964 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003082716-A1.
PD 01-MAY-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 232
ID ACF64957 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 233
ID ACF76602 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 234
ID ACF61502 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0
RESULT 235
ID ACF61809 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 236
ID ACD30840 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032125-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 237
ID ACD31761 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054454-A1.
PD 20-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 238
ID ACD32682 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 239
ID ACF17648 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 240
ID ACF07481 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 241
ID ACF20639 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 242
ID ACF20946 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073172-A1.
PD 17-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 243
ID ACF21253 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073172-A1.
PD 17-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 244
ID ACD47763 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 245
ID ACF47745 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 246
ID ACF53578 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 247
ID ACD86913 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 248
ID ACH05161 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 249
ID ACF44658 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 250
ID ADA81718 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 251
ID ACD22313 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003027276-A1.
PD 06-FEB-2003.

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 252
ID ACD24660 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044920-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 253
ID ACD39863 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003027265-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 254
ID ACD40170 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 255
ID ACF13478 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 256
ID ACF03280 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 257
ID ACF78751 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 258
ID ACF11472 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073171-A1.
PD 17-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 259
ID ACF50815 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032121-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 260
ID ACF34310 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 261
ID ACD46535 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 262
ID ACD48377 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 263
ID ACF27758 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 264
ID ACF24630 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 265
ID ACD85685 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 266
ID ACD90290 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 267
ID ACD83843 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 268
ID ACF49280 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.

PN US2003104540-A1.
PD 05-JUN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 269
ID ACH07365 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 270
ID ACH07672 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 271
ID ACH08286 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 272
ID ACH11477 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 273
ID ACH11784 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 274
ID ACH10435 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 275
ID ACF01438 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040059-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 276
ID ACF41013 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 277
ID ACD24353 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044918-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 278
ID ACD31454 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032132-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 279
ID ACF17955 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 280
ID ACF32738 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 281
ID ACF40399 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 282
ID ACF48359 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064441-A1.
PD 03-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 283
ID ACF38308 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 284
ID ACF25244 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 285

ID ACF27144 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 286
ID ACF29600 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073174-A1.
PD 17-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 287
ID ACD87834 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 288
ID ACF76295 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 289
ID ACF49587 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104541-A1.
PD 05-JUN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 290
ID ACF44044 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 291
ID ACH06389 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 292
ID ACH06696 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 293
ID ADA83516 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 294
ID ACC92752 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032133-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 295
ID ACC93366 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032136-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 296
ID ACF19411 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036129-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 297
ID ACD13102 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040053-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 298
ID ACF06560 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040057-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 299
ID ACC94594 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 300
ID ACC98022 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044932-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 301
ID ACC94287 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027270-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 302
ID ACF42241 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.

PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 303
ID ACD31147 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032126-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 304
ID ACD43176 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 305
ID ACD43483 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 306
ID ACF15013 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 307
ID ACF01745 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049738-A1.
PD 13-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 308
ID ACF31817 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 309
ID ACD67494 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 310
ID ACD48684 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 311
ID ACD48991 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 312
ID ACF51429 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 313
ID ACF54192 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 314
ID ACF25916 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 315
ID ACF39229 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 316
ID ACF28986 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 317
ID ACD90903 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 318
ID ACD86606 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 319
ID ACH05468 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 320
ID ACF65264 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 321
ID ADB20559 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003082767-A1.
PD 01-MAY-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 322
ID ACF43737 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 323
ID ACH09207 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 324
ID ACH09514 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 325
ID ADA78811 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 326
ID ACF09937 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 327
ID ACF51122 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 328
ID ACF24016 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 329
ID ACD88448 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 330
ID ACH09821 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 331
ID ACH10742 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 332
ID ACD11549 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036126-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 333
ID ACC96599 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044924-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 334
ID ACD42260 standard; cDNA; 1047 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1122.
PN US2003044842-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 335
ID ACC98629 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.

PN US2003044927-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 336
ID ACF41934 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040072-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 337
ID ACF16855 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040073-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 338
ID ACD32375 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 339
ID ACD30533 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032124-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 340
ID ACD41404 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 341
ID ACF07788 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 342
ID ACF31203 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 343
ID ACF77523 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 344
ID ACF11165 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073170-A1.
PD 17-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 345
ID ACF33045 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 346
ID ACF26223 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 347
ID ACD83536 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 348
ID ACF23709 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 349
ID ACF43123 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 350
ID ACF43430 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 351
ID ACH06082 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 352

ID ACH08900 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 353
ID ACC90494 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027273-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 354
ID ACF10858 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036119-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 355
ID ACC93673 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036120-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 356
ID ACC96292 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 357
ID ACD24967 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044921-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 358
ID ACF02052 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 359
ID ACF22174 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 360
ID ACF22788 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 361
ID ACF09016 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 362
ID ACF33352 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 363
ID ACF54806 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 364
ID ADA49767 standard; cDNA; 1047 BP.
DE Human interleukin-17/interleukin-17 receptor related PRO1122 cDNA.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 365
ID ACF48666 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 366
ID ACD47456 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 367
ID ACD49298 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 368
ID ACF38001 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 369
ID ACF30214 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 370
ID ACD87527 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 371
ID ACF62116 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104538-A1.
PD 05-JUN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 372
ID ACH11049 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 373
ID ACD10214 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036158-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 374
ID ACD16939 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003036151-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 375
ID ACC99236 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040067-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 376
ID ACF00630 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054456-A1.
PD 20-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 377
ID ACD41097 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 378
ID ACF14706 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 379
ID ACF22481 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 380
ID ACF79058 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 381
ID ACF11779 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 382
ID ACF51736 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 383
ID ACF33659 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 384
ID ADA26960 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #2.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 385
ID ACD49912 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068731-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 386
ID ACF37694 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068683-A1.
PD 10-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 387
ID ACF28679 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 388
ID ACD88755 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068681-A1.
PD 10-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 389
ID ACF75374 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 390
ID ACF61195 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 391
ID ACF44351 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 392
ID ACH08593 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 393
ID ACC93980 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036122-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 394
ID ACD21085 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 395
ID ACF06867 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040065-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 396
ID ACD20778 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044919-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 397
ID ACD22927 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040077-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 398
ID ACF41627 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044928-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 399
ID ACF07174 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 400
ID ACF77830 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 401
ID ACD46228 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 402
ID ACF47131 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068757-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 403
ID ACF54499 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 404
ID ACF45903 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 405
ID ACF45596 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 406
ID ACF38615 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 407
ID ACD89676 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 408
ID ACD85378 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 409
ID ACD85992 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 410
ID ACF75988 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 411
ID ACF60888 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 412
ID ACH05775 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 413
ID ADA82882 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 414
ID ACF56034 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068680-A1.
PD 10-APR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 415
ID ACF55420 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 416
ID ADB86190 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 417
ID ACF56341 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 418
ID ACF56648 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0
RESULT 419
ID ACF55727 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 420
ID ACF55113 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 421
ID ADB66894 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #2.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 422
ID AAD59326 standard; cDNA; 1047 BP.
DE Human PRO1122 cDNA.
PN US2003049733-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 423
ID AAD59202 standard; cDNA; 1047 BP.
DE Human PRO1122 cDNA.
PN US2003049734-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 424
ID ADC29766 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003092063-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 425
ID ADD05920 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 426
ID ADC78792 standard; DNA; 1047 BP.
DE Human PRO protein coding sequence #11.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 427
ID AAD63608 standard; cDNA; 1047 BP.
DE Human IL-17C ligand (PRO1122) cDNA.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 428
ID ADG02915 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 429
ID ADG01622 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 430
ID ADF95797 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 431
ID ADG12612 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 432
ID ADG87378 standard; cDNA; 1047 BP.
DE Human PRO1122 cDNA from clone DNA62377-1381-1.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 433
ID ADH09272 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 434
ID ABX78751 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003027272-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 435
ID ACA75723 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.

PN US2003032127-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 436
ID ACA71203 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032112-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 437
ID ACC87731 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027278-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 438
ID ACC87117 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036159-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 439
ID ACD04290 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040070-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 440
ID ACA69621 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003032113-A1.
PD 13-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 441
ID ACA90466 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 442
ID ACC89573 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027264-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 443
ID ACA98364 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 444
ID ACA94006 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036149-A1.
PD 20-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 445
ID ACA06132 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003032061-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 446
ID ACD15399 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044923-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 447
ID ACD08986 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040062-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 448
ID ACC96906 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040056-A1.
PD 27-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 449
ID ACF15627 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044926-A1.
PD 06-MAR-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 450
ID ACA72994 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 451
ID ACD03166 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 452
ID ACD01981 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 453
ID ACA92173 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.

PN US2003027277-A1.
PD 06-FEB-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 454
ID ADL16674 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO1122 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 455
ID ADM30587 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 456
ID ADE74584 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003211572-A1.
PD 13-NOV-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 457
ID ADE75196 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003211574-A1.
PD 13-NOV-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 458
ID ADF09209 standard; cDNA; 1047 BP.
DE Human secreted and transmembrane protein PRO1122 cDNA.
PN US2003134327-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 459
ID ADF96409 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 460
ID ADG04680 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 461
ID ADG00840 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 462
ID ADG83096 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 463
ID ADH26377 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 464
ID ADH33346 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 465
ID ADJ55085 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 466
ID ADL16635 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO1122 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 467
ID ADL71295 standard; cDNA; 1047 BP.
DE Human IL-17C (PRO1122) encoding cDNA, DNA62377-1381-1.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 468
ID ADJ64856 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 469
ID ADM31752 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

RESULT 470
ID ADM36799 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 471
ID ADM40604 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 472
ID ADN38212 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 473
ID ADW12441 standard; cDNA; 1047 BP.
DE Human PRO1122 cDNA.
PN US2004265966-A1.
PD 30-DEC-2004.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (PANJ/) PAN J.
PA (STEW/) STEWART T A.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 474
ID ADL33051 standard; cDNA; 1048 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 475
ID ADP10630 standard; DNA; 1048 BP.
DE Reference mRNA sequences for marker probe #307.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 476
ID AAZ36836 standard; cDNA; 1067 BP.
DE Nucleotide sequence of human interleukin-21.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 477
ID AAI67878 standard; DNA; 1067 BP.
DE Human interleukin (IL)-21 nucleotide sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 478
ID ADJ61745 standard; cDNA; 1067 BP.
DE Human interleukin-21 (IL-21) cDNA #2.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 479
ID AAA59149 standard; cDNA; 1107 BP.
DE cDNA encoding a human interleukin-171 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 480
ID AAA58991 standard; cDNA; 1107 BP.
DE cDNA encoding a human interleukin (IL) 171 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 481
ID ADB32009 standard; cDNA; 1107 BP.
DE Human cDNA encoding interleukin 171, IL-171.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 482
ID ADR13812 standard; cDNA; 1107 BP.
DE Human interleukin-171 (IL-171) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 483
ID AEB55667 standard; cDNA; 1107 BP.
DE Human IL-17C cytokine receptor polypeptide encoding cDNA.
PN WO2005065711-A2.
PD 21-JUL-2005.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 484
ID AAD15291 standard; cDNA; 1177 BP.
DE Human interleukin (IL)-17 like cDNA.
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
RESULT 485

ID AAZ36834 standard; cDNA; 705 BP.
DE Partial nucleotide sequence of human interleukin-21.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 42.8% Indels: 0
RESULT 486
ID AAI67876 standard; DNA; 705 BP.
DE Human interleukin (IL)-21 partial nucleotide sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 42.8% Indels: 0
RESULT 487
ID ADJ61718 standard; cDNA; 705 BP.
DE Human interleukin-21 (IL-21) cDNA #1.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 42.8% Indels: 0
RESULT 488
ID AAA59148 standard; cDNA; 521 BP.
DE cDNA encoding a human interleukin-171 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 41.6% Indels: 0
RESULT 489
ID AAA59147 standard; cDNA; 521 BP.
DE cDNA encoding a human interleukin-171 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 41.6% Indels: 0
RESULT 490
ID AAA58989 standard; cDNA; 521 BP.
DE cDNA encoding a human interleukin (IL) 171 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 41.6% Indels: 0
RESULT 491
ID AAA58990 standard; cDNA; 521 BP.
DE cDNA encoding a human interleukin (IL) 171 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 41.6% Indels: 0
RESULT 492
ID ADB32007 standard; cDNA; 521 BP.
DE Human partial cDNA encoding interleukin 171, IL-171.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 41.6% Indels: 0
RESULT 493
ID ADR13810 standard; cDNA; 521 BP.
DE Human interleukin-171 (IL-171) partial cDNA #2.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 41.6% Indels: 0
RESULT 494
ID ADR13809 standard; cDNA; 521 BP.
DE Human interleukin-171 (IL-171) partial cDNA #1.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 41.6% Indels: 0
RESULT 495
ID AAZ29731 standard; DNA; 230 BP.
DE Virtual DNA fragment DNA49665, for isolation of human PRO1122 cDNA.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 37.9% Indels: 0
RESULT 496
ID AAZ36856 standard; DNA; 332 BP.
DE cDNA clone HTGED19RB related to human interleukin-22 CDNA sequence.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 72.7% Conservative: 2
Best Local Similarity: 70.5% Mismatches: 12
Query Match: 24.4% Indels: 12
RESULT 497
ID ADJ61747 standard; cDNA; 332 BP.
DE Interleukin-22 (IL-22) cDNA related human HTGED19RB cDNA.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 72.7% Conservative: 2
Best Local Similarity: 70.5% Mismatches: 12
Query Match: 24.4% Indels: 12
RESULT 498
ID AAZ52201 standard; cDNA; 2361 BP.
DE Human transforming growth factor beta-9, Ztgfbeta-9 variant cDNA.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 39.1% Conservative: 16
Best Local Similarity: 32.2% Mismatches: 65
Query Match: 20.4% Indels: 78
RESULT 499
ID ADE34352 standard; DNA; 2361 BP.
DE Transforming growth factor beta-9 gene #SEQ ID 33.
PN WO2003048394-A1.
PD 12-JUN-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Percent Similarity: 39.1% Conservative: 16
Best Local Similarity: 32.2% Mismatches: 65
Query Match: 20.4% Indels: 78
RESULT 500
ID AAD54507 standard; DNA; 2361 BP.
DE Human interleukin-17D (IL-17D) DNA #2.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 39.1% Conservative: 16
Best Local Similarity: 32.2% Mismatches: 65
Query Match: 20.4% Indels: 78
RESULT 501
ID ADQ92013 standard; cDNA; 2361 BP.

DE Human transforming growth factor beta-9 (Ztgfbeta-9) variant cDNA.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 39.1% Conservative: 16
Best Local Similarity: 32.2% Mismatches: 65
Query Match: 20.4% Indels: 78
RESULT 502
ID AAA59155 standard; cDNA; 1385 BP.
DE cDNA encoding a human interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 40.2% Conservative: 17
Best Local Similarity: 31.4% Mismatches: 61
Query Match: 18.8% Indels: 55
RESULT 503
ID AAA58983 standard; cDNA; 1385 BP.
DE cDNA encoding a human interleukin (IL) 173 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 40.2% Conservative: 17
Best Local Similarity: 31.4% Mismatches: 61
Query Match: 18.8% Indels: 55
RESULT 504
ID ADB31995 standard; cDNA; 1385 BP.
DE Human cDNA encoding interleukin 173, IL-173.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 40.2% Conservative: 17
Best Local Similarity: 31.4% Mismatches: 61
Query Match: 18.8% Indels: 55
RESULT 505
ID ADR13797 standard; cDNA; 1385 BP.
DE Human interleukin-173 (IL-173) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 40.2% Conservative: 17
Best Local Similarity: 31.4% Mismatches: 61
Query Match: 18.8% Indels: 55
RESULT 506
ID ADF16328 standard; DNA; 609 BP.
DE Human albumin fusion protein-related DNA sequence SeqID1420.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 507
ID ADF16330 standard; DNA; 609 BP.
DE Human albumin fusion protein-related DNA sequence SeqID1422.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 508
ID ADH21717 standard; DNA; 609 BP.
DE Human interleukin-22 fragment-encoding DNA, SEQ ID NO:514.
PN WO2003059934-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 509
ID ADH21715 standard; DNA; 609 BP.
DE Human interleukin-22 fragment-encoding DNA, SEQ ID NO:512.
PN WO2003059934-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 510
ID ADV43377 standard; cDNA; 609 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1005.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 511
ID AAS09512 standard; cDNA; 1754 BP.
DE Human cDNA encoding Interleukin 17D ligand, IL-17D.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 512
ID ABK33579 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO protein, Seq ID No 87.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 513
ID ADY31827 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN WO200193983-A1.
PD 13-DEC-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 514
ID ACA89853 standard; cDNA; 1754 BP.
DE Human cDNA (PRO21175) encoding h-IL17D.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 515
ID ACA68540 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 516
ID ACA64637 standard; cDNA; 1754 BP.
DE Human cDNA encoding IL-17 family member, PRO21175.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50

RESULT 517
ID ABT44269 standard; cDNA; 1754 BP.
DE Human PRO21175 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 518
ID ADA43230 standard; cDNA; 1754 BP.
DE Human interleukin 17 related mammalian cytokine polypeptide cDNA #4.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 519
ID ABT44552 standard; cDNA; 1754 BP.
DE Human PRO21175 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 520
ID ACD82219 standard; cDNA; 1754 BP.
DE Human secreted/transmembrane polypeptide PRO 21175 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 521
ID ADA49771 standard; cDNA; 1754 BP.
DE Human interleukin-17/interleukin-17 receptor related PRO21175 cDNA.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 522
ID ADA26964 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO polypeptide #4.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 523
ID ABT43925 standard; cDNA; 1754 BP.
DE Human membrane bound receptor/protein PRO21175 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 524
ID ADB83577 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 525
ID ADB80683 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 526
ID ADB73224 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 527
ID ADB78306 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 528
ID ADB84954 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 529
ID ADB78060 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 530
ID ADB87126 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 531
ID ADB84708 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 532
ID ADB83823 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 533
ID ADB72978 standard; cDNA; 1754 BP.

DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 534
ID ADB66898 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO polypeptide #4.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 535
ID ADC36816 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 536
ID ADC21806 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 537
ID ADC49837 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 538
ID ADC49036 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 539
ID ADC49553 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 540
ID ADC47414 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 541
ID ADC47159 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 542
ID ADC78034 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 543
ID ADD06269 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 544
ID ADC77788 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 545
ID ADD50751 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 546
ID ADD50997 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 547
ID ADD50478 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 548
ID ADD50232 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 549
ID ADD51243 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003105289-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 550
ID AAD63610 standard; cDNA; 1754 BP.
DE Human IL-17D ligand (PRO21175) cDNA.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 551
ID ADG87382 standard; cDNA; 1754 BP.
DE Human PRO21175 cDNA from clone DNA173894-2947.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 552
ID ACA66884 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO polypeptide #44.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 553
ID ACD68636 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 554
ID ADL16678 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO21175 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 555
ID ADC48790 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 556
ID ADE20961 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 557
ID ADE05805 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 558
ID ADD75034 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 559
ID ADD75780 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 560
ID ADD85012 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 561
ID ADD86838 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 562
ID ADE20715 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 563
ID ADE39012 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 564
ID ADE05559 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 565
ID ADD73544 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 566
ID ADD78384 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 567
ID ADE21207 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 568
ID ADD77322 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 569
ID ADE20469 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 570
ID ADD75534 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 571
ID ADD74050 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 572
ID ADD74296 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 573
ID ADD76026 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 574
ID ADD85518 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 575
ID ADE05067 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 576
ID ADD75280 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 577
ID ADD76824 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 578
ID ADD86592 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 579
ID ADD78060 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 580
ID ADD77568 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 581
ID ADD77814 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65

Query Match: 18.8% Indels: 50
RESULT 582
ID ADD85272 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 583
ID ADD73804 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 584
ID ADD74542 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 585
ID ADD77070 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 586
ID ADD85764 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 587
ID ADE05313 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 588
ID ADD74788 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 589
ID ADG05600 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 590
ID ADG27154 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 591
ID ADG11217 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 592
ID ADG11996 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 593
ID ADF94553 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 594
ID ADG06649 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 595
ID ADH38993 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 596
ID ADG34083 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 597
ID ADI33553 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 598

ID ADH69647 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 599
ID ADI29808 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 600
ID ADL16639 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO21175 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 601
ID ADL71299 standard; cDNA; 1754 BP.
DE Human IL-17D (PRO21175) encoding cDNA, DNA173894-2947.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 602
ID ADM27205 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 603
ID ADK66563 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 604
ID AAZ52195 standard; cDNA; 1819 BP.
DE Human transforming growth factor beta-9, Ztgfbeta-9 cDNA.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 605
ID AAD54506 standard; DNA; 1819 BP.
DE Human interleukin-17D (IL-17D) DNA #1.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 606
ID ADQ91998 standard; cDNA; 1819 BP.
DE Human transforming growth factor beta-9 (Ztgfbeta-9) cDNA.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 38.5% Conservative: 14
Best Local Similarity: 31.0% Mismatches: 65
Query Match: 18.8% Indels: 50
RESULT 607
ID AAD28773 standard; cDNA; 1496 BP.
DE Mouse non-secreted form of Interleukin-17 like (IL-17L) cDNA.
PN WO200208285-A2.
PD 31-JAN-2002.
PA (AMGE-) AMGEN INC.
Percent Similarity: 40.7% Conservative: 17
Best Local Similarity: 32.2% Mismatches: 78
Query Match: 18.1% Indels: 40
RESULT 608
ID ADE83318 standard; cDNA; 1496 BP.
DE Non secreted mouse IL-17 like cDNA.
PN US2003124092-A1.
PD 03-JUL-2003.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Percent Similarity: 40.7% Conservative: 17
Best Local Similarity: 32.2% Mismatches: 78
Query Match: 18.1% Indels: 40
RESULT 609
ID ADW64916 standard; cDNA; 1496 BP.
DE Non-secreted form of mouse IL-17 like cDNA.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Percent Similarity: 40.7% Conservative: 17
Best Local Similarity: 32.2% Mismatches: 78
Query Match: 18.1% Indels: 40
RESULT 610
ID ADZ14893 standard; cDNA; 1496 BP.
DE Non-secreted form of mouse IL-17 like cDNA, SEQ ID NO: 9.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Percent Similarity: 40.7% Conservative: 17
Best Local Similarity: 32.2% Mismatches: 78
Query Match: 18.1% Indels: 40
RESULT 611
ID AAA59160 standard; cDNA; 985 BP.
DE cDNA encoding a murine interleukin-174 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 40.1% Conservative: 17
Best Local Similarity: 31.0% Mismatches: 86
Query Match: 18.0% Indels: 26
RESULT 612
ID AAA58988 standard; cDNA; 985 BP.
DE cDNA encoding a murine interleukin (IL) 174 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.

Percent Similarity: 40.1% Conservative: 17
Best Local Similarity: 31.0% Mismatches: 86
Query Match: 18.0% Indels: 26
RESULT 613
ID ABA02394 standard; DNA; 985 BP.
DE Murine interleukin 174 (IL-174)-encoding DNA.
PN WO200179288-A2.
PD 25-OCT-2001.
PA (SCHE) SCHERING CORP.
Percent Similarity: 40.1% Conservative: 17
Best Local Similarity: 31.0% Mismatches: 86
Query Match: 18.0% Indels: 26
RESULT 614
ID ADB32005 standard; cDNA; 985 BP.
DE Mouse cDNA encoding interleukin 174, IL-174.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 40.1% Conservative: 17
Best Local Similarity: 31.0% Mismatches: 86
Query Match: 18.0% Indels: 26
RESULT 615
ID ADR13807 standard; cDNA; 985 BP.
DE Murine interleukin-174 (IL-174) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 40.1% Conservative: 17
Best Local Similarity: 31.0% Mismatches: 86
Query Match: 18.0% Indels: 26
RESULT 616
ID AAD28772 standard; cDNA; 1013 BP.
DE Mouse Interleukin-17 like (IL-17L) cDNA.
PN WO200208285-A2.
PD 31-JAN-2002.
PA (AMGE-) AMGEN INC.
Percent Similarity: 40.1% Conservative: 17
Best Local Similarity: 31.0% Mismatches: 86
Query Match: 18.0% Indels: 26
RESULT 617
ID ADE83312 standard; cDNA; 1013 BP.
DE Mouse IL-17 like cDNA.
PN US2003124092-A1.
PD 03-JUL-2003.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Percent Similarity: 40.1% Conservative: 17
Best Local Similarity: 31.0% Mismatches: 86
Query Match: 18.0% Indels: 26
RESULT 618
ID ADW64910 standard; cDNA; 1013 BP.
DE Mouse IL-17 like cDNA.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Percent Similarity: 40.1% Conservative: 17
Best Local Similarity: 31.0% Mismatches: 86
Query Match: 18.0% Indels: 26
RESULT 619
ID ADZ14887 standard; cDNA; 1013 BP.
DE Mouse IL-17 like cDNA, SEQ ID NO: 3.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Percent Similarity: 40.1% Conservative: 17
Best Local Similarity: 31.0% Mismatches: 86
Query Match: 18.0% Indels: 26
RESULT 620
ID AAZ36837 standard; cDNA; 522 BP.
DE Partial nucleotide sequence of human interleukin-22.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.2% Conservative: 13
Best Local Similarity: 34.5% Mismatches: 50
Query Match: 17.9% Indels: 34
RESULT 621
ID AAI67888 standard; DNA; 522 BP.
DE Human interleukin (IL)-22 coding sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Percent Similarity: 43.2% Conservative: 13
Best Local Similarity: 34.5% Mismatches: 50
Query Match: 17.9% Indels: 34
RESULT 622
ID ADJ61748 standard; cDNA; 522 BP.
DE Human interleukin-22 (IL-22) cDNA #2.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.2% Conservative: 13
Best Local Similarity: 34.5% Mismatches: 50
Query Match: 17.9% Indels: 34
RESULT 623
ID AAA59157 standard; cDNA; 1143 BP.
DE cDNA encoding a murine interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 45.5% Conservative: 14
Best Local Similarity: 35.9% Mismatches: 51
Query Match: 17.9% Indels: 30
RESULT 624
ID AAA58985 standard; cDNA; 1143 BP.
DE cDNA encoding a murine interleukin (IL) 173 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 45.5% Conservative: 14
Best Local Similarity: 35.9% Mismatches: 51
Query Match: 17.9% Indels: 30
RESULT 625
ID ADB31999 standard; cDNA; 1143 BP.
DE Mouse cDNA encoding interleukin 173, IL-173.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 45.5% Conservative: 14
Best Local Similarity: 35.9% Mismatches: 51
Query Match: 17.9% Indels: 30
RESULT 626
ID ADR13801 standard; cDNA; 1143 BP.
DE Murine interleukin-173 (IL-173) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 45.5% Conservative: 14
Best Local Similarity: 35.9% Mismatches: 51
Query Match: 17.9% Indels: 30
RESULT 627

ID AAZ52198 standard; cDNA; 1221 BP.
DE Murine transforming growth factor beta-9, Ztgfbeta-9 cDNA.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 45.5% Conservative: 14
Best Local Similarity: 35.9% Mismatches: 51
Query Match: 17.9% Indels: 30
RESULT 628
ID AAD54508 standard; DNA; 1221 BP.
DE Mouse interleukin-17D (IL-17D) DNA.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 45.5% Conservative: 14
Best Local Similarity: 35.9% Mismatches: 51
Query Match: 17.9% Indels: 30
RESULT 629
ID ADQ92005 standard; cDNA; 1221 BP.
DE Mouse transforming growth factor beta-9 (Ztgfbeta-9) cDNA.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 45.5% Conservative: 14
Best Local Similarity: 35.9% Mismatches: 51
Query Match: 17.9% Indels: 30
RESULT 630
ID AAD10108 standard; cDNA; 1258 BP.
DE Mouse ZCYTO7 cDNA.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 45.5% Conservative: 14
Best Local Similarity: 35.9% Mismatches: 51
Query Match: 17.9% Indels: 30
RESULT 631
ID ADJ61720 standard; cDNA; 1641 BP.
DE Human interleukin-22 (IL-22) cDNA #1.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.2% Conservative: 13
Best Local Similarity: 34.5% Mismatches: 50
Query Match: 17.9% Indels: 34
RESULT 632
ID AAZ36835 standard; cDNA; 1642 BP.
DE Partial nucleotide sequence of human interleukin-22.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.2% Conservative: 13
Best Local Similarity: 34.5% Mismatches: 50
Query Match: 17.9% Indels: 34
RESULT 633
ID AAI67877 standard; DNA; 1642 BP.
DE Human interleukin (IL)-22 nucleotide sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Percent Similarity: 43.2% Conservative: 13
Best Local Similarity: 34.5% Mismatches: 50
Query Match: 17.9% Indels: 34
RESULT 634
ID AAA59156 standard; cDNA; 454 BP.
DE cDNA encoding a rat interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 46.6% Conservative: 17
Best Local Similarity: 33.8% Mismatches: 61
Query Match: 17.9% Indels: 10
RESULT 635
ID AAA58982 standard; cDNA; 454 BP.
DE cDNA encoding a human interleukin (IL) 173 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 46.6% Conservative: 17
Best Local Similarity: 33.8% Mismatches: 61
Query Match: 17.9% Indels: 10
RESULT 636
ID ADB31993 standard; cDNA; 454 BP.
DE Human partial cDNA encoding interleukin 173, IL-173.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 46.6% Conservative: 17
Best Local Similarity: 33.8% Mismatches: 61
Query Match: 17.9% Indels: 10
RESULT 637
ID ADR13795 standard; cDNA; 454 BP.
DE Human interleukin-173 (IL-173) partial cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 46.6% Conservative: 17
Best Local Similarity: 33.8% Mismatches: 61
Query Match: 17.9% Indels: 10
RESULT 638
ID AAD28771 standard; cDNA; 644 BP.
DE Human Interleukin-17 like (IL-17L) cDNA.
PN WO200208285-A2.
PD 31-JAN-2002.
PA (AMGE-) AMGEN INC.
Percent Similarity: 42.5% Conservative: 15
Best Local Similarity: 34.3% Mismatches: 85
Query Match: 16.4% Indels: 21
RESULT 639
ID ABA03213 standard; cDNA; 644 BP.
DE Human IL-17 receptor like protein ligand, IL-17E, coding sequence.
PN WO200168705-A2.
PD 20-SEP-2001.
PA (AMGE-) AMGEN INC.
Percent Similarity: 42.5% Conservative: 15
Best Local Similarity: 34.3% Mismatches: 85
Query Match: 16.4% Indels: 21
RESULT 640
ID ADE83310 standard; cDNA; 644 BP.
DE Human IL-17 like cDNA.
PN US2003124092-A1.
PD 03-JUL-2003.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Percent Similarity: 42.5% Conservative: 15
Best Local Similarity: 34.3% Mismatches: 85
Query Match: 16.4% Indels: 21
RESULT 641
ID ADW64908 standard; cDNA; 644 BP.
DE Human IL-17 like cDNA.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Percent Similarity: 42.5% Conservative: 15
Best Local Similarity: 34.3% Mismatches: 85
Query Match: 16.4% Indels: 21
RESULT 642

ID ADZ14885 standard; cDNA; 644 BP.
DE Human IL-17 like cDNA, SEQ ID NO: 1.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Percent Similarity: 42.5% Conservative: 15
Best Local Similarity: 34.3% Mismatches: 85
Query Match: 16.4% Indels: 21
RESULT 643
ID AAT87432 standard; cDNA; 813 BP.
DE Clone B18.
PN WO9707198-A2.
PD 27-FEB-1997.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 45.5% Conservative: 28
Best Local Similarity: 30.7% Mismatches: 56
Query Match: 16.3% Indels: 47
RESULT 644
ID AAT61413 standard; cDNA; 813 BP.
DE Human CTLA-8.
PN WO9704097-A2.
PD 06-FEB-1997.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 45.5% Conservative: 28
Best Local Similarity: 30.7% Mismatches: 56
Query Match: 16.3% Indels: 47
RESULT 645
ID AAA59966 standard; cDNA; 813 BP.
DE Human cytotoxic T lymphocyte antigen-8 (CTLA-8) cDNA sequence.
PN US6074849-A.
PD 13-JUN-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 45.5% Conservative: 28
Best Local Similarity: 30.7% Mismatches: 56
Query Match: 16.3% Indels: 47
RESULT 646
ID AAA07429 standard; cDNA; 813 BP.
DE Human CTLA-8 coding sequence.
PN US6043344-A.
PD 28-MAR-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 45.5% Conservative: 28
Best Local Similarity: 30.7% Mismatches: 56
Query Match: 16.3% Indels: 47
RESULT 647
ID AEA28878 standard; cDNA; 813 BP.
DE Human CTLA-8 (IL-17F) cDNA, SEQ ID NO: 1.
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Percent Similarity: 45.5% Conservative: 28
Best Local Similarity: 30.7% Mismatches: 56
Query Match: 16.3% Indels: 47
RESULT 648
ID ABS52525 standard; cDNA; 330 BP.
DE Human ML-1 cDNA.
PN WO200264739-A2.
PD 22-AUG-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 649
ID AEA28894 standard; cDNA; 399 BP.
DE Human CTLA-8 (IL-17F) mature cDNA fragment (nucleotides 146-544).
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 650
ID AEA28893 standard; cDNA; 405 BP.
DE Human CTLA-8 (IL-17F) cDNA fragment, B18_F1 (nucleotides 140-544).
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 651
ID AEA28892 standard; cDNA; 459 BP.
DE Human CTLA-8 (IL-17F) cDNA fragment (nucleotides 86-544).
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 652
ID AEA28895 standard; cDNA; 489 BP.
DE Human CTLA-8 (IL-17F) cDNA fragment (nucleotides 56-544).
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 653
ID ADP55883 standard; cDNA; 492 BP.
DE Human PRO cDNA sequence SEQ ID NO:1859.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 654
ID ADV42799 standard; cDNA; 492 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 427.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 655
ID ADH39310 standard; cDNA; 534 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 656
ID ADH79183 standard; cDNA; 534 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 657
ID AAF92137 standard; cDNA; 535 BP.
DE Human PRO20110 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16

Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 658
ID ABS74457 standard; cDNA; 535 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO20110.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 659
ID ACA91243 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 660
ID ACD81620 standard; cDNA; 535 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO20110.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 661
ID ACA60442 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 662
ID ACA58889 standard; cDNA; 535 BP.
DE cDNA encoding human secreted polypeptide PRO20110.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 663
ID ACA64065 standard; cDNA; 535 BP.
DE cDNA encoding human PRO polypeptide #80.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 664
ID ACA91329 standard; cDNA; 535 BP.
DE cDNA encoding human PRO polypeptide #80.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 665
ID ACD45228 standard; cDNA; 535 BP.
DE Human secreted/transmembrane polypeptide PRO20110 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 666
ID ACA93776 standard; cDNA; 535 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO20110.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 667
ID ACA67350 standard; cDNA; 535 BP.
DE cDNA encoding human secreted polypeptide PRO20110.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 668
ID ACH66323 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 669
ID ACD02377 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 670
ID ACA89368 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 671
ID ACA69005 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 672
ID ACA98527 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 673
ID ACA63452 standard; cDNA; 535 BP.
DE cDNA encoding human PRO polypeptide #80.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14

RESULT 674
ID ADB17216 standard; cDNA; 535 BP.
DE Human cDNA clone (SeqID 159) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 675
ID ACH03655 standard; cDNA; 535 BP.
DE Human secreted/transmembrane polypeptide PRO 20110 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 676
ID ADA20021 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 677
ID ADB17404 standard; cDNA; 535 BP.
DE Human cDNA clone (SeqID 159) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 678
ID ADA20193 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 679
ID ACD82169 standard; cDNA; 535 BP.
DE Human secreted/transmembrane polypeptide PRO 20110 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 680
ID ADA00490 standard; cDNA; 535 BP.
DE Human secreted/transmembrane polypeptide PRO 20110 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 681
ID ADB85732 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 682
ID ADB68411 standard; cDNA; 535 BP.
DE Human PRO20110 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 683
ID ADB68218 standard; cDNA; 535 BP.
DE Human PRO20110 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 684
ID ADB91035 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 685
ID ADC07115 standard; cDNA; 535 BP.
DE Human PRO20110 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 686
ID ADC17294 standard; cDNA; 535 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 159).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 687
ID ADC14992 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 688
ID ADC52487 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 689
ID ADC78832 standard; DNA; 535 BP.
DE Human PRO protein coding sequence #31.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 690
ID ADD36163 standard; cDNA; 535 BP.

DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 691
ID ADG01164 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 692
ID ADG08717 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 693
ID ADF95338 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 694
ID ADH24191 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 695
ID ADH34217 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 696
ID ADH30050 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 697
ID ADH24021 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 698
ID ADG85425 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 699
ID ADH24701 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 700
ID ADH37557 standard; cDNA; 535 BP.
DE Human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 701
ID ADH02146 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 702
ID ADH37727 standard; cDNA; 535 BP.
DE Human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 703
ID ADG85765 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 704
ID ADH24361 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 705
ID ADH38655 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 706
ID ADG83776 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003180794-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 707
ID ADH29584 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 708
ID ADH27700 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 709
ID ADH37897 standard; cDNA; 535 BP.
DE Human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 710
ID ADH38074 standard; cDNA; 535 BP.
DE Human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 711
ID ADH57494 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 712
ID ADH53636 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 713
ID ADH53806 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 714
ID ADH52142 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 715
ID ADH49997 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 716
ID ADI25507 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 717
ID ADH90300 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 718
ID ADI25677 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 719
ID ADH97851 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 720
ID ADI03699 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 721
ID ADI12056 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 722
ID ADH90130 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 723
ID ADH98531 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 724
ID ADI11206 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 725
ID ADI11716 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 726
ID ADH98361 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 727
ID ADH98701 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 728
ID ADH98191 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 729
ID ADI05179 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 730
ID ADI03529 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 731
ID ADI04924 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 732
ID ADH78378 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 733
ID ADI19722 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 734
ID ADH90470 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 735
ID ADI03189 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 736
ID ADH78038 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 737
ID ADH98021 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 738
ID ADI01406 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31

Query Match: 16.1% Indels: 14
RESULT 739
ID ADI02101 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 740
ID ADI03359 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 741
ID ADI11546 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 742
ID ADI02448 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 743
ID ADI11886 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 744
ID ADI05523 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 745
ID ADH79595 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 746
ID ADI19552 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 747
ID ADI05353 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 748
ID ADH79765 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 749
ID ADI01591 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 750
ID ADI01761 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 751
ID ADI01931 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 752
ID ADH79935 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 753
ID ADI04753 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 754
ID ADI02889 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 755

ID ADH78208 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 756
ID ADI25847 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 757
ID ADI26017 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 758
ID ADK65529 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 759
ID ADH98871 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 760
ID ADH80112 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 761
ID ADL93842 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 762
ID ADC52297 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 763
ID ADH06729 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 764
ID ADH06559 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 765
ID ADG68980 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 766
ID ADH27870 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 767
ID ADH25211 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 768
ID ADH33843 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 769
ID ADH02486 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 770
ID ADH08093 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 771
ID ADG69490 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.

PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 772
ID ADG84051 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 773
ID ADG85595 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 774
ID ADH06389 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 775
ID ADH30219 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 776
ID ADH24531 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 777
ID ADG69660 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 778
ID ADH07923 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 779
ID ADG85935 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 780
ID ADH39481 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 781
ID ADH33673 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 782
ID ADH34013 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 783
ID ADH01223 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 784
ID ADG69830 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 785
ID ADH02316 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 786
ID ADG69320 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 787
ID ADG86105 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 788
ID ADH25041 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 789
ID ADH39658 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 790
ID ADH02656 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 791
ID ADG69150 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 792
ID ADH07753 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 793
ID ADG86275 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 794
ID ADH24871 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 795
ID ADH25919 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 796
ID ADH38485 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 797
ID ADH57324 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 798
ID ADH52311 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 799
ID ADH49677 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 800
ID ADH90640 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 801
ID ADI11376 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 802
ID ADH99041 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 803
ID ADI02271 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16

Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 804
ID ADH90810 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 805
ID ADJ98685 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 806
ID ADJ98855 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 807
ID ADH79014 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 808
ID ADJ99248 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 809
ID ADJ99418 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 810
ID ADJ99036 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 811
ID ADK01044 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 812
ID ADK14565 standard; cDNA; 535 BP.
DE Novel human secreted and transmembrane protein PRO20110 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 813
ID ADM81014 standard; cDNA; 535 BP.
DE Human PRO polynucleotide #80.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 814
ID ADY77854 standard; cDNA; 535 BP.
DE Neoplastic disease detection cDNA PRO20110.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 815
ID AAS09513 standard; cDNA; 559 BP.
DE Human cDNA encoding Interleukin 17F ligand, IL-17F.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 816
ID ACA89854 standard; cDNA; 559 BP.
DE Human cDNA (PRO20110) encoding h-IL17F.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 817
ID ACA64638 standard; cDNA; 559 BP.
DE Human cDNA encoding IL-17 family member, PRO20110.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 818
ID ADA43232 standard; cDNA; 559 BP.
DE Human interleukin 17 related mammalian cytokine polypeptide cDNA #5.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 819

ID ADA49773 standard; cDNA; 559 BP.
DE Human interleukin-17/interleukin-17 receptor related PRO20110 cDNA.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 820
ID ADA26966 standard; cDNA; 559 BP.
DE cDNA encoding human PRO polypeptide #5.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 821
ID ADB66900 standard; cDNA; 559 BP.
DE cDNA encoding human PRO polypeptide #5.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 822
ID AAD63611 standard; cDNA; 559 BP.
DE Human IL-17F ligand (PRO20110) cDNA.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 823
ID ADG87384 standard; cDNA; 559 BP.
DE Human PRO20110 cDNA from clone DNA166819.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 824
ID ADL16680 standard; cDNA; 559 BP.
DE cDNA encoding human PRO20110 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 825
ID ADL16641 standard; cDNA; 559 BP.
DE cDNA encoding human PRO20110 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 826
ID ADL71301 standard; cDNA; 559 BP.
DE Human PRO20110 encoding cDNA, DNA166819.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 827
ID ADW97143 standard; cDNA; 559 BP.
DE Human interleukin-17F cDNA.
PN WO2005010044-A2.
PD 03-FEB-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 828
ID AAV83179 standard; cDNA; 692 BP.
DE Murine Zcyto7 cDNA.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 43.8% Conservative: 28
Best Local Similarity: 29.4% Mismatches: 88
Query Match: 16.1% Indels: 21
RESULT 829
ID AAD18299 standard; cDNA; 692 BP.
DE Mouse Zcyto7 cDNA.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 43.8% Conservative: 28
Best Local Similarity: 29.4% Mismatches: 88
Query Match: 16.1% Indels: 21
RESULT 830
ID ABS57068 standard; cDNA; 692 BP.
DE Mouse cDNA encoding Zcyto7 protein.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Percent Similarity: 43.8% Conservative: 28
Best Local Similarity: 29.4% Mismatches: 88
Query Match: 16.1% Indels: 21
RESULT 831
ID ABV72469 standard; DNA; 692 BP.
DE Nucleotide sequence of murine interleukin 17B (IL-17B).
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Percent Similarity: 43.8% Conservative: 28
Best Local Similarity: 29.4% Mismatches: 88
Query Match: 16.1% Indels: 21
RESULT 832
ID ADY19138 standard; DNA; 735 BP.
DE DNA encoding a PRO polypeptide, SEQ ID NO 4944.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.0% Conservative: 16
Best Local Similarity: 39.0% Mismatches: 31
Query Match: 16.1% Indels: 14
RESULT 833
ID AAX84473 standard; DNA; 756 BP.
DE Murine EDIRF I coding sequence.
PN WO9932632-A1.
PD 01-JUL-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Percent Similarity: 43.8% Conservative: 28
Best Local Similarity: 29.4% Mismatches: 88
Query Match: 16.1% Indels: 21
RESULT 834
ID AAA59158 standard; cDNA; 504 BP.
DE cDNA encoding a human interleukin-174 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 835

ID AAA58986 standard; cDNA; 504 BP.
DE cDNA encoding a human interleukin (IL) 174 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 836
ID ABA02393 standard; DNA; 504 BP.
DE Human interleukin 174 (IL-174)-encoding DNA.
PN WO200179288-A2.
PD 25-OCT-2001.
PA (SCHE) SCHERING CORP.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 837
ID ADB32001 standard; cDNA; 504 BP.
DE Human cDNA encoding interleukin 174, IL-174.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 838
ID ADR13803 standard; cDNA; 504 BP.
DE Human interleukin-174 (IL-174) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 839
ID ADV42798 standard; cDNA; 534 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 426.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 840
ID AAV86026 standard; cDNA; 564 BP.
DE EST clone B26.
PN WO9845435-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 45.5% Conservative: 28
Best Local Similarity: 30.5% Mismatches: 55
Query Match: 15.8% Indels: 47
RESULT 841
ID ADC38643 standard; cDNA; 812 BP.
DE Human cDNA encoding a secreted protein #1.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 44.6% Conservative: 25
Best Local Similarity: 31.2% Mismatches: 56
Query Match: 15.8% Indels: 47
RESULT 842
ID AAC85969 standard; cDNA; 1320 BP.
DE Native sequence of PRO10272 cDNA, clone DNA147531-2821.
PN WO200140465-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 843
ID AAF92135 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 844
ID AAS09511 standard; cDNA; 1320 BP.
DE Human cDNA encoding Interleukin 17E ligand, IL-17E.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 845
ID ABS74455 standard; cDNA; 1320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO10272.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 846
ID ACA91241 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 847
ID ACD81618 standard; cDNA; 1320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO10272.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 848
ID ACA60440 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 849
ID ACA58887 standard; cDNA; 1320 BP.
DE cDNA encoding human secreted polypeptide PRO10272.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 850
ID ACA64063 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #78.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 851
ID ACA91327 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #78.

PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 852
ID ACD45226 standard; cDNA; 1320 BP.
DE Human secreted/transmembrane polypeptide PRO10272 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 853
ID ACA93774 standard; cDNA; 1320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO10272.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 854
ID ACA89852 standard; cDNA; 1320 BP.
DE Human cDNA (PRO102721) encoding h-IL17E.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 855
ID ACA67348 standard; cDNA; 1320 BP.
DE cDNA encoding human secreted polypeptide PRO10272.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 856
ID ACH66321 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 857
ID ACD02375 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 858
ID ACA89366 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 859
ID ACA69003 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 860
ID ACA64636 standard; cDNA; 1320 BP.
DE Human cDNA encoding IL-17 family member, PRO10272.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 861
ID ACA98525 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 862
ID ACA63450 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #78.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 863
ID ADA26943 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #9.
PN US2003087380-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 864
ID ADB17212 standard; cDNA; 1320 BP.
DE Human cDNA clone (SeqID 155) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 865
ID ADA43228 standard; cDNA; 1320 BP.
DE Human interleukin 17 related mammalian cytokine polypeptide cDNA #3.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 866
ID ACH03653 standard; cDNA; 1320 BP.
DE Human secreted/transmembrane polypeptide PRO 10272 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 867
ID ADA20017 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 868
ID ADB17400 standard; cDNA; 1320 BP.
DE Human cDNA clone (SeqID 155) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 869
ID ADA20189 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 870
ID ACD82167 standard; cDNA; 1320 BP.
DE Human secreted/transmembrane polypeptide PRO 10272 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 871
ID ADA00486 standard; cDNA; 1320 BP.
DE Human secreted/transmembrane polypeptide PRO 10272 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 872
ID ADA49769 standard; cDNA; 1320 BP.
DE Human interleukin-17/interleukin-17 receptor related PRO10272 cDNA.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 873
ID ACD27959 standard; cDNA; 1320 BP.
DE cDNA encoding novel human protein PRO10272.
PN US2003054484-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 874
ID ADA26962 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 875
ID ADB85728 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 876
ID ADB68407 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 877
ID ADB68214 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 878
ID ADB91031 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 879
ID ADB66896 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 880
ID ADC07111 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 881
ID ADC17290 standard; cDNA; 1320 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 155).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 882
ID ADC14988 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 883
ID ADC52483 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15

Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 884
ID ADD36159 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 885
ID ADE86210 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN US2003153015-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 886
ID AAD63609 standard; cDNA; 1320 BP.
DE Human IL-17E ligand (PRO10272) cDNA.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 887
ID ADG01160 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 888
ID ADG08713 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 889
ID ADF95334 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 890
ID ADH24187 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 891
ID ADG87380 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA from clone DNA147531-2821.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 892
ID ADH34213 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 893
ID ADH30046 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 894
ID ADH24017 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 895
ID ADG85421 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 896
ID ADH24697 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 897
ID ADH37553 standard; cDNA; 1320 BP.
DE Human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 898
ID ADH02142 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 899
ID ADG87368 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA from clone DNA147531-2821.
PN US2003077738-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21

RESULT 900
ID ADH37723 standard; cDNA; 1320 BP.
DE Human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 901
ID ADG85761 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 902
ID ADH24357 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 903
ID ADH38651 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 904
ID ADG88790 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN US2003077737-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 905
ID ADG83772 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 906
ID ADH29580 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 907
ID ADH27696 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 908
ID ADH37893 standard; cDNA; 1320 BP.
DE Human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 909
ID ADH38070 standard; cDNA; 1320 BP.
DE Human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 910
ID ADH57490 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 911
ID ADH53632 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 912
ID ADH53802 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 913
ID ADH52138 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 914
ID ADH49993 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 915
ID ADI25503 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 916
ID ADH90296 standard; cDNA; 1320 BP.

DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 917
ID ADI25673 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 918
ID ADH97847 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 919
ID ADI03695 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 920
ID ADI12052 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 921
ID ADH90126 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 922
ID ADH98527 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 923
ID ADI11202 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 924
ID ADI11712 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 925
ID ADH98357 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 926
ID ADH98697 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 927
ID ADH98187 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 928
ID ADI05175 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 929
ID ADI03525 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 930
ID ADI04920 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 931
ID ADH78374 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 932
ID ADI19718 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181676-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 933
ID ADH90466 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 934
ID ADI03185 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 935
ID ADH78034 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 936
ID ADH98017 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 937
ID ADI01402 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 938
ID ADI02097 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 939
ID ADI03355 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 940
ID ADI11542 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 941
ID ADI02444 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 942
ID ADI11882 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 943
ID ADI05519 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 944
ID ADH79591 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 945
ID ADI19548 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 946
ID ADI05349 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 947
ID ADH79761 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 948
ID ADI01587 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 949
ID ADI01757 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 950
ID ADI01927 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 951
ID ADH79931 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 952
ID ADI04749 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 953
ID ADI02885 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 954
ID ADH78204 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 955
ID ADI25843 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 956
ID ADI26013 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 957
ID ADK65525 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 958
ID ADL16676 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO10272 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 959
ID ADH98867 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 960
ID ADH80108 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 961
ID ADL93838 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 962
ID ADC52293 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 963
ID ADH06725 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 964
ID ADH06555 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76

Query Match: 15.8% Indels: 21
RESULT 965
ID ADG68976 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 966
ID ADH27866 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 967
ID ADH25207 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 968
ID ADH33839 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 969
ID ADH02482 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 970
ID ADH08089 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 971
ID ADG69486 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 972
ID ADH39306 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 973
ID ADG84047 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 974
ID ADG47090 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA from clone DNA1475531-2821.
PN US2003100063-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 975
ID ADG85591 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 976
ID ADH06385 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 977
ID ADH30215 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 978
ID ADH24527 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 979
ID ADG69656 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 980
ID ADH07919 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 981

ID ADG85931 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 982
ID ADH39477 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 983
ID ADH33669 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 984
ID ADH34009 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 985
ID ADH01219 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 986
ID ADG69826 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 987
ID ADH02312 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 988
ID ADG69316 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 989
ID ADG86101 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 990
ID ADH25037 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 991
ID ADH39654 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 992
ID ADH02652 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 993
ID ADG69146 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 994
ID ADH07749 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 995
ID ADG86271 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 996
ID ADH24867 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 997
ID ADH25915 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.

PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 998
ID ADH38481 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 999
ID ADH57320 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1000
ID ADH52307 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1001
ID ADH49673 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1002
ID ADH90636 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1003
ID ADI11372 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1004
ID ADH99037 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1005
ID ADI02267 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1006
ID ADH90806 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1007
ID ADJ98681 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1008
ID ADJ98851 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1009
ID ADH79010 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1010
ID ADJ99244 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1011
ID ADJ99414 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1012
ID ADJ99032 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1013
ID ADH79179 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1014
ID ADK01040 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1015
ID ADL16637 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO10272 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1016
ID ADK14561 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1017
ID ADL71297 standard; cDNA; 1320 BP.
DE Human IL-17E (PRO10272) encoding cDNA, DNA147531-2821.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1018
ID ADM81010 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1019
ID ADY77850 standard; cDNA; 1320 BP.
DE Neoplastic disease detection cDNA PRO10272.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Percent Similarity: 43.5% Conservative: 15
Best Local Similarity: 34.5% Mismatches: 76
Query Match: 15.8% Indels: 21
RESULT 1020
ID AAX89402 standard; cDNA; 540 BP.
DE Mouse interleukin-17D polynucleotide.
PN WO9935267-A1.
PD 15-JUL-1999.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 41.3% Conservative: 28
Best Local Similarity: 27.0% Mismatches: 82
Query Match: 15.7% Indels: 33
RESULT 1021
ID AAA59153 standard; cDNA; 543 BP.
DE cDNA encoding a murine interleukin-172 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 41.3% Conservative: 28
Best Local Similarity: 27.0% Mismatches: 82
Query Match: 15.7% Indels: 33
RESULT 1022
ID AAA58981 standard; cDNA; 543 BP.
DE cDNA encoding a murine interleukin (IL) 172 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 41.3% Conservative: 28
Best Local Similarity: 27.0% Mismatches: 82
Query Match: 15.7% Indels: 33
RESULT 1023
ID ADB31991 standard; cDNA; 543 BP.
DE Mouse cDNA encoding interleukin 172, IL-172.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 41.3% Conservative: 28
Best Local Similarity: 27.0% Mismatches: 82
Query Match: 15.7% Indels: 33
RESULT 1024
ID ADR13793 standard; cDNA; 543 BP.
DE Murine interleukin-172 (IL-172) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 41.3% Conservative: 28
Best Local Similarity: 27.0% Mismatches: 82
Query Match: 15.7% Indels: 33
RESULT 1025
ID AAA88789 standard; cDNA; 1107 BP.
DE Human SECX cDNA Clone 2191999.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.1% Conservative: 26
Best Local Similarity: 28.2% Mismatches: 75
Query Match: 15.7% Indels: 24
RESULT 1026
ID ADD18249 standard; DNA; 1107 BP.
DE Human molecule (MOL) protein MOL9 DNA sequence.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.1% Conservative: 26
Best Local Similarity: 28.2% Mismatches: 75
Query Match: 15.7% Indels: 24
RESULT 1027
ID ACA63324 standard; cDNA; 510 BP.
DE Human cytotoxic T-lymphocyte antigen CTLA-8 cDNA #2.
PN US2003040603-A1.
PD 27-FEB-2003.
PA (GOLS/) GOLSTEIN P.
PA (ROUV/) ROUVIER E.
PA (FOSS/) FOSSIEZ F.
PA (LEBE/) LEBECQUE S J E.
PA (DJOS/) DJOSSOU O.
PA (BANC/) BANCHEREAU J.
Percent Similarity: 43.3% Conservative: 17
Best Local Similarity: 33.7% Mismatches: 65
Query Match: 15.1% Indels: 36
RESULT 1028
ID ADV43390 standard; cDNA; 468 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1018.

PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 44.9% Conservative: 20
Best Local Similarity: 33.7% Mismatches: 62
Query Match: 15.0% Indels: 36
RESULT 1029
ID AAQ92884 standard; DNA; 510 BP.
DE Human CTLA-8 cDNA.
PN WO9518826-A2.
PD 13-JUL-1995.
PA (SCHE) SCHERING CORP.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1030
ID AAH77244 standard; cDNA; 510 BP.
DE Human cytokine-like protein CTLA-8 coding sequence.
PN US6274711-B1.
PD 14-AUG-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (SCHE) SCHERING CORP.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1031
ID ADC17322 standard; cDNA; 510 BP.
DE Human cytotoxic T lymphocyte-associated antigen (CTLA-8) cDNA.
PN US6562333-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1032
ID ADC78782 standard; DNA; 1213 BP.
DE Human PRO protein coding sequence #6.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1033
ID ADP10433 standard; DNA; 1859 BP.
DE Reference mRNA sequences for marker probe #110.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1034
ID ADW97142 standard; cDNA; 1859 BP.
DE Human interleukin-17 cDNA.
PN WO2005010044-A2.
PD 03-FEB-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1035
ID ADD25543 standard; DNA; 1874 BP.
DE Binding domain-immunoglobulin fusion protein-associated DNA #56.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENECRAFT INC.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1036
ID ADI31565 standard; cDNA; 1874 BP.
DE Human cDNA #891.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1037
ID ADL24266 standard; DNA; 1874 BP.
DE Human IL-17 coding sequence.
PN WO2004019866-A2.
PD 11-MAR-2004.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1038
ID ADP55159 standard; cDNA; 1874 BP.
DE Human PRO cDNA sequence SEQ ID NO:1135.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1039
ID ADS83632 standard; cDNA; 1874 BP.
DE Human lymph node cDNA #891.
PN US2004077003-A1.
PD 22-APR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 41.2% Conservative: 19
Best Local Similarity: 30.0% Mismatches: 64
Query Match: 15.0% Indels: 37
RESULT 1040
ID AAQ92882 standard; cDNA; 456 BP.
DE Herpesvirus ORF13.
PN WO9518826-A2.
PD 13-JUL-1995.
PA (SCHE) SCHERING CORP.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
Percent Similarity: 42.9% Conservative: 23
Best Local Similarity: 28.6% Mismatches: 57
Query Match: 15.0% Indels: 35
RESULT 1041
ID AAH77242 standard; cDNA; 456 BP.
DE Herpesvirus saimiri open reading frame ORF13.
PN US6274711-B1.
PD 14-AUG-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (SCHE) SCHERING CORP.
Percent Similarity: 42.9% Conservative: 23
Best Local Similarity: 28.6% Mismatches: 57
Query Match: 15.0% Indels: 35
RESULT 1042
ID ADC17318 standard; DNA; 456 BP.
DE Herpesvirus Saimiri ORF13 (KCLF2) DNA.
PN US6562333-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 42.9% Conservative: 23
Best Local Similarity: 28.6% Mismatches: 57
Query Match: 15.0% Indels: 35
RESULT 1043
ID AAT61415 standard; cDNA; 459 BP.
DE Herpesvirus Saimir ORF13.
PN WO9704097-A2.
PD 06-FEB-1997.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 42.9% Conservative: 23
Best Local Similarity: 28.6% Mismatches: 57
Query Match: 15.0% Indels: 35
RESULT 1044

ID AAA59968 standard; cDNA; 459 BP.
DE Herpesvirus Saimiri ORF13 (herpes CTLA-8) cDNA sequence.
PN US6074849-A.
PD 13-JUN-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 42.9% Conservative: 23
Best Local Similarity: 28.6% Mismatches: 57
Query Match: 15.0% Indels: 35
RESULT 1045
ID AAA07431 standard; cDNA; 459 BP.
DE Herpes virus CTLA-8 coding sequence.
PN US6043344-A.
PD 28-MAR-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 42.9% Conservative: 23
Best Local Similarity: 28.6% Mismatches: 57
Query Match: 15.0% Indels: 35
RESULT 1046
ID AEA28882 standard; cDNA; 459 BP.
DE Herpesvirus saimiri CTLA-8 (IL-17) cDNA, SEQ ID NO: 5.
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Percent Similarity: 42.9% Conservative: 23
Best Local Similarity: 28.6% Mismatches: 57
Query Match: 15.0% Indels: 35
RESULT 1047
ID ABA03786 standard; cDNA; 2520 BP.
DE Herpesvirus saimiri open reading frame ORF13.
PN US6274711-B1.
PD 14-AUG-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (SCHE) SCHERING CORP.
Percent Similarity: 42.9% Conservative: 23
Best Local Similarity: 28.6% Mismatches: 57
Query Match: 15.0% Indels: 35
RESULT 1048
ID ACA63322 standard; DNA; 2520 BP.
DE Saimiriine herpesvirus 2 ORF13 DNA.
PN US2003040603-A1.
PD 27-FEB-2003.
PA (GOLS/) GOLSTEIN P.
PA (ROUV/) ROUVIER E.
PA (FOSS/) FOSSIEZ F.
PA (LEBE/) LEBECQUE S J E.
PA (DJOS/) DJOSSOU O.
PA (BANC/) BANCHEREAU J.
Percent Similarity: 42.9% Conservative: 23
Best Local Similarity: 28.6% Mismatches: 57
Query Match: 15.0% Indels: 35
RESULT 1049
ID AAZ34282 standard; cDNA; 687 BP.
DE Human PRO1031 nucleotide sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1050
ID AAC58608 standard; cDNA; 687 BP.
DE Human PRO1031 protein UNQ516 encoding cDNA SEQ ID NO:149.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1051
ID AAZ29727 standard; cDNA; 687 BP.
DE Human Interleukin 17B, PRO1031 cDNA.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1052
ID AAC78577 standard; cDNA; 687 BP.
DE Human PRO1031 (UNQ516) nucleotide sequence SEQ ID NO:469.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1053
ID AAA75694 standard; cDNA; 687 BP.
DE cDNA clone DNA59294-1381 encoding a PRO1031 polypeptide.
PN WO200053752-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1054
ID AAS21466 standard; cDNA; 687 BP.
DE Human cDNA sequence encoding for PRO1031 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1055
ID AAS09509 standard; cDNA; 687 BP.
DE Human cDNA encoding Interleukin 17B ligand, IL-17B.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1056
ID AAC88961 standard; cDNA; 687 BP.
DE Human PRO1031 coding sequence.
PN WO200070050-A1.
PD 23-NOV-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1057
ID AAC91479 standard; cDNA; 687 BP.
DE Human PRO1031 cDNA.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1058
ID ACA63850 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1059
ID ACA03825 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1060
ID ACA72014 standard; cDNA; 687 BP.
DE Human secreted and transmembrane PRO polypeptide #26 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1061
ID ABX89363 standard; cDNA; 687 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1031.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1062
ID ABX92654 standard; cDNA; 687 BP.
DE cDNA encoding human PRO1031 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1063
ID ACD42017 standard; cDNA; 687 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #223.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1064
ID ACA89850 standard; cDNA; 687 BP.
DE Human cDNA (PRO1031) encoding h-IL17B.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1065
ID ACA66395 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1031.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1066
ID ACA04246 standard; cDNA; 687 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 445.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1067
ID ACA64634 standard; cDNA; 687 BP.
DE Human cDNA encoding IL-17 family member, PRO1031.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1068
ID ADA45964 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1069
ID ADA76395 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1070
ID ADA19045 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1071
ID ADA43224 standard; cDNA; 687 BP.
DE Human interleukin 17 related mammalian cytokine polypeptide cDNA #1.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1072
ID ADA61668 standard; cDNA; 687 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1073
ID ADB19453 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1074
ID ADB27994 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1075
ID ADA86473 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71

Query Match: 14.8% Indels: 21
RESULT 1076
ID ADB16037 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1077
ID ADA47823 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1078
ID ADA67618 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1079
ID ADB30625 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1080
ID ADA85921 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1081
ID ADA97133 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1082
ID ADA79437 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1083
ID ADA87576 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1084
ID ADB16778 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1085
ID ADA91870 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1086
ID ADB14933 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1087
ID ADA25008 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1088
ID ADB18894 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1089
ID ADA94109 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1090
ID ADB20005 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1091
ID ADB13317 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1092

ID ACD98646 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1093
ID ACD29996 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1094
ID ADA12669 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1031.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1095
ID ADA74571 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1096
ID ADB24804 standard; cDNA; 687 BP.
DE Human PRO polynucleotide SEQ ID NO 445.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1097
ID ADA82328 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1098
ID ADA75291 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1099
ID ADA85369 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1100
ID ADA84817 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1101
ID ADB30073 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1102
ID ADA80601 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1103
ID ADA75843 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1104
ID ADA47068 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1105
ID ADB25364 standard; cDNA; 687 BP.
DE Human PRO polynucleotide SEQ ID NO 445.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1106
ID ADA93540 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1107
ID ADB26890 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1108
ID ADB31177 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.

PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1109
ID ADA61105 standard; cDNA; 687 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1110
ID ADB24252 standard; cDNA; 687 BP.
DE Human PRO polynucleotide SEQ ID NO 445.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1111
ID ADA96581 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1112
ID ADA81153 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1113
ID ADA96029 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1114
ID ADB26338 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1115
ID ADB21823 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1116
ID ACD29411 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #120.
PN US2003049633-A1.
PD 13-MAR-2003.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1117
ID ADA77602 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1118
ID ADB18342 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1119
ID ADA87025 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1120
ID ADA88128 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1121
ID ADA46516 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1122
ID ADA49765 standard; cDNA; 687 BP.
DE Human interleukin-17/interleukin-17 receptor related PRO1031 cDNA.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1123
ID ADB28546 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1124
ID ADB29098 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1125
ID ADA77050 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1126
ID ADA26958 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #1.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1127
ID ADA88680 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1128
ID ADA97685 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1129
ID ADB27442 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003022239-A1.
PD 30-JAN-2003.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1130
ID ADB22375 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1131
ID ADA67066 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1132
ID ADB22927 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1133
ID ADB23700 standard; cDNA; 687 BP.
DE Human PRO polynucleotide SEQ ID NO 445.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1134
ID ADA92422 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1135
ID ADB15485 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1136
ID ADB38737 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1137
ID ADB38185 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1138
ID ADB66657 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1139
ID ADB89737 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1140
ID ADB90469 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1141

ID ADB39570 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1142
ID ADB73975 standard; cDNA; 687 BP.
DE Human PRO polynucleotide sequence #120.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1143
ID ADB47193 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1144
ID ADB86800 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1145
ID ADB76691 standard; cDNA; 687 BP.
DE Human PRO polynucleotide sequence #120.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1146
ID ADB77405 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1147
ID ADB34562 standard; cDNA; 687 BP.
DE Human PRO polynucleotide SEQ ID NO 445.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1148
ID ADB35666 standard; cDNA; 687 BP.
DE Human PRO polynucleotide SEQ ID NO 445.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1149
ID ADB66892 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #1.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1150
ID ADB34010 standard; cDNA; 687 BP.
DE Human PRO polynucleotide SEQ ID NO 445.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1151
ID ADB35114 standard; cDNA; 687 BP.
DE Human PRO polynucleotide SEQ ID NO 445.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1152
ID ADB36218 standard; cDNA; 687 BP.
DE Human PRO polynucleotide SEQ ID NO 445.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1153
ID ADB46613 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1154
ID ADC44117 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1155
ID ADC61877 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1156
ID ADC63841 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1157
ID ADC66941 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.

PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1158
ID ADC69065 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1159
ID ADC63125 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1160
ID ADC68190 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1161
ID ADC41510 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1162
ID ADC67565 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1163
ID ADC62501 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1164
ID ADC42134 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1165
ID ADC50486 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1166
ID ADC72033 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1167
ID ADC60012 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1168
ID ADC53019 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID445.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1169
ID ADC57373 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID445.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1170
ID ADC60564 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1171
ID ADC51039 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1172
ID ADC65566 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1173
ID ADC54664 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID445.
PN US2003087363-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1174
ID ADC53625 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID445.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1175
ID ADC59148 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID445.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1176
ID ADC56026 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID445.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1177
ID ADC58596 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID445.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1178
ID ADD03270 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1179
ID ADC90262 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1180
ID ADC69681 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1181
ID ADC48570 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1182
ID ADD10099 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1183
ID ADD04674 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1184
ID ADC80630 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1185
ID ADD11137 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1186
ID ADC48018 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1187
ID ADC80078 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1188
ID ADD09547 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1189
ID ADD41260 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25

Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1190
ID ADD52399 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1191
ID ADD53139 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1192
ID ADD53691 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1193
ID ADD51847 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1194
ID ADD02646 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1195
ID ADD02080 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1196
ID ADD54262 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1197
ID ADE49503 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1198
ID ADD92579 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1199
ID ADD91475 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1200
ID ADE04089 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1201
ID ADE32386 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1202
ID ADE22318 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1203
ID ADD79542 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1204
ID ADE35557 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1205
ID ADE16671 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21

RESULT 1206
ID ADD73286 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1207
ID ADE42078 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1208
ID ADE17895 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1209
ID ADD92027 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1210
ID ADE33490 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1211
ID ADE34042 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1212
ID ADD80094 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1213
ID ADD93131 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1214
ID ADD72644 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1215
ID ADE19551 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1216
ID ADE18999 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1217
ID ADE43195 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1218
ID ADD95984 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1219
ID ADE22870 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1220
ID ADD78988 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1221
ID ADE32938 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1222
ID ADE42630 standard; cDNA; 687 BP.

DE Human PRO polynucleotide #223.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1223
ID ADE17295 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1224
ID ADD80646 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1225
ID ADD89674 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1226
ID ADE40958 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1227
ID ADE04757 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1228
ID AAD63607 standard; cDNA; 687 BP.
DE Human IL-17B ligand (PRO1031) cDNA.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1229
ID ADE92886 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1230
ID ADF47309 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1231
ID ADG21595 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1232
ID ADG23236 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1233
ID ADF97571 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1234
ID ADG87376 standard; cDNA; 687 BP.
DE Human PRO1031 cDNA from clone DNA59294-1381-1.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1235
ID ADG80635 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1236
ID ADG53066 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1237
ID ADG60386 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1238
ID ADG80083 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207372-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1239
ID ADH55375 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1240
ID ADH55927 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1241
ID ADI61146 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1242
ID ADI64146 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1243
ID ADI65095 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1244
ID ADI63594 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1245
ID ADH82008 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1246
ID ADH81456 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1247
ID ACD24075 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1248
ID ACD42815 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1249
ID ACA67216 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1250
ID ADL16672 standard; cDNA; 687 BP.
DE cDNA encoding human PRO1031 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1251
ID ADM82625 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1252
ID ADN16024 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1253
ID ADN16653 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1254
ID ADN15472 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1255
ID ADN14920 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1256
ID ADC81182 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1257
ID ADD76630 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1258
ID ADD87994 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1259
ID ADD86398 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1260
ID ADE75846 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1261
ID ADE48803 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1262
ID ADE23422 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1263
ID ADE23974 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1264
ID ADE24617 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1265
ID ADD87442 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1266
ID ADE89308 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1267
ID ADE18447 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1268
ID ADE88756 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1269
ID ADE89904 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1270
ID ADF61544 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1271
ID ADF40236 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1272
ID ADF46032 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1273
ID ADE94776 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1274
ID ADE91187 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1275
ID ADE95328 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1276
ID ADE93438 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1277
ID ADF24428 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1278
ID ADF40860 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1279
ID ADF23804 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1280
ID ADF33787 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1281
ID ADF35019 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1282
ID ADF27254 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1283
ID ADF27890 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1284
ID ADE92334 standard; cDNA; 687 BP.

DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1285
ID ADE90635 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1286
ID ADF41484 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1287
ID ADF33163 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1288
ID ADF25529 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1289
ID ADF26630 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1290
ID ADF34419 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1291
ID ADF46656 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1292
ID ADE91782 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1293
ID ADG02361 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1294
ID ADG22147 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1295
ID ADG20217 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1296
ID ADF98123 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1297
ID ADG24340 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1298
ID ADF98694 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1299
ID ADG03525 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1300
ID ADF99246 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207353-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1301
ID ADG16831 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1302
ID ADG05290 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1303
ID ADG19557 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1304
ID ADG13394 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1305
ID ADG08451 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1306
ID ADG15621 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1307
ID ADF97019 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1308
ID ADG06204 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1309
ID ADG23788 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1310
ID ADG04077 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1311
ID ADG24978 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1312
ID ADG07275 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1313
ID ADG07827 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1314
ID ADG55322 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1315
ID ADG60986 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1316
ID ADG62090 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1317
ID ADG82291 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1318
ID ADG57530 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1319
ID ADG56978 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1320
ID ADG55874 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1321
ID ADG58634 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1322
ID ADG71000 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1323
ID ADG58082 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1324
ID ADG53666 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1325
ID ADG71552 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1326
ID ADG50642 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1327
ID ADG81739 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003207805-A1.
PD 06-NOV-2003.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1328
ID ADH30701 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1329
ID ADH12068 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1330
ID ADG50018 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1331
ID ADG51890 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1332
ID ADG52490 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21

RESULT 1333
ID ADG54218 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1334
ID ADG49394 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1335
ID ADG81187 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1336
ID ADG56426 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1337
ID ADH12692 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1338
ID ADG48770 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1339
ID ADG61538 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1340
ID ADH28625 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1341
ID ADG54770 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1342
ID ADG59810 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1343
ID ADG51266 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1344
ID ADG59210 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1345
ID ADG62666 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1346
ID ADI81234 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1347
ID ADH25691 standard; cDNA; 687 BP.
DE Human neurotrimin homologue related nucleotide sequence SEQ ID NO:469.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1348
ID ADG09977 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1349
ID ADI15448 standard; cDNA; 687 BP.

DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1350
ID ADG09325 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1351
ID ADI14780 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1352
ID ADI18375 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1353
ID ADL16633 standard; cDNA; 687 BP.
DE cDNA encoding human PRO1031 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1354
ID ADL71293 standard; cDNA; 687 BP.
DE Human IL-17B (PRO1031) encoding cDNA, DNA59294-1381.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1355
ID ADJ63656 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1356
ID ADJ77551 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1357
ID ADJ65673 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1358
ID ADM27809 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1359
ID ADM17468 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1360
ID ADL07302 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1361
ID ADM42533 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1362
ID ADM28395 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1363
ID ADI95877 standard; cDNA; 687 BP.
DE cDNA encoding human PRO polypeptide #223.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1364
ID ADI96429 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1365
ID ADS32381 standard; cDNA; 687 BP.
DE Novel human secreted and transmembrane protein PRO1031 cDNA.
PN US2004203125-A1.

PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1366
ID ADT03365 standard; cDNA; 687 BP.
DE Human PRO polynucleotide #223.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1367
ID ADU50424 standard; cDNA; 687 BP.
DE PRO1031 coding sequence, SEQ ID 469.
PN US2004223964-A1.
PD 11-NOV-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1368
ID ADW49703 standard; cDNA; 687 BP.
DE PRO1031 cDNA, SEQ ID 469.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1369
ID ADZ03416 standard; cDNA; 687 BP.
DE Human secreted/transmembrane PRO1031 cDNA.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1370
ID ADZ52364 standard; cDNA; 687 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1031.
PN US2005084935-A1.
PD 21-APR-2005.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1371
ID AEB14162 standard; cDNA; 687 BP.
DE Cancer cell diagnosis method-related human cDNA sequence - SEQ ID 445.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1372
ID AAH79255 standard; cDNA; 704 BP.
DE Human cell factor-CX1 protein related coding sequence.
PN CN1299823-A.
PD 20-JUN-2001.
PA (SHAN-) SHANGHAI HUACHEN BIOLOGICAL TECHNOLOGY I.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1373
ID AAX15870 standard; cDNA; 705 BP.
DE cDNA encoding interleukin-20.
PN WO9903982-A1.
PD 28-JAN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1374

ID AAA75787 standard; DNA; 705 BP.
DE DNA encoding a human interleukin 20 polypeptide.
PN WO200055204-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1375
ID AAA57516 standard; cDNA; 705 BP.
DE cDNA encoding a human interleukin-20 polypeptide.
PN WO200042189-A1.
PD 20-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1376
ID ADS88026 standard; DNA; 711 BP.
DE Tumour treatment-related human gene sequence SeqID62.
PN WO2004034995-A2.
PD 29-APR-2004.
PA (UYPI-) UNIV PITTSBURGH.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1377
ID ADQ23207 standard; DNA; 730 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6027.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1378
ID AAV83172 standard; cDNA; 736 BP.
DE Human Zcyto7 cDNA.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1379
ID AAD18295 standard; cDNA; 736 BP.
DE Human Zcyto7 cDNA.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1380
ID ABS57064 standard; cDNA; 736 BP.
DE Human cDNA encoding Zcyto7 protein.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1381
ID ABV72465 standard; DNA; 736 BP.
DE Nucleotide sequence of human interleukin 17B (IL-17B).
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1382
ID AAX84472 standard; DNA; 738 BP.
DE Human EDIRF I coding sequence.
PN WO9932632-A1.
PD 01-JUL-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1383
ID AAX84474 standard; DNA; 1259 BP.
DE Human EDIRF II coding sequence.
PN WO9932632-A1.
PD 01-JUL-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Percent Similarity: 44.2% Conservative: 25
Best Local Similarity: 29.1% Mismatches: 71
Query Match: 14.8% Indels: 21
RESULT 1384
ID AAX89401 standard; cDNA; 540 BP.
DE Human interleukin-17D polynucleotide.
PN WO9935267-A1.
PD 15-JUL-1999.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 44.6% Conservative: 25
Best Local Similarity: 28.7% Mismatches: 70
Query Match: 14.4% Indels: 17
RESULT 1385
ID ADV42754 standard; cDNA; 543 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 382.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 44.6% Conservative: 25
Best Local Similarity: 28.7% Mismatches: 70
Query Match: 14.4% Indels: 17
RESULT 1386
ID AAA95780 standard; cDNA; 689 BP.
DE Human immune system molecule cDNA from Incyte clone 3577142.
PN WO200060080-A2.
PD 12-OCT-2000.
PA (INCY-) INCYTE PHARM INC.
Percent Similarity: 43.6% Conservative: 25
Best Local Similarity: 28.5% Mismatches: 72
Query Match: 14.4% Indels: 21
RESULT 1387
ID ABK86567 standard; DNA; 771 BP.
DE Human cDNA encoding chondroleukin, IL-17B.
PN WO200238764-A2.
PD 16-MAY-2002.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 43.6% Conservative: 25
Best Local Similarity: 28.5% Mismatches: 72
Query Match: 14.4% Indels: 21
RESULT 1388
ID AAA59159 standard; cDNA; 620 BP.
DE cDNA encoding a murine interleukin-174 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 45.8% Conservative: 13
Best Local Similarity: 35.0% Mismatches: 52
Query Match: 14.1% Indels: 13
RESULT 1389
ID AAA58987 standard; cDNA; 620 BP.
DE cDNA encoding a murine interleukin (IL) 174 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 45.8% Conservative: 13
Best Local Similarity: 35.0% Mismatches: 52
Query Match: 14.1% Indels: 13
RESULT 1390

ID ADB32003 standard; cDNA; 620 BP.
DE Mouse partial cDNA encoding interleukin 174, IL-174.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 45.8% Conservative: 13
Best Local Similarity: 35.0% Mismatches: 52
Query Match: 14.1% Indels: 13
RESULT 1391
ID ADR13805 standard; cDNA; 620 BP.
DE Murine interleukin-174 (IL-174) partial cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 45.8% Conservative: 13
Best Local Similarity: 35.0% Mismatches: 52
Query Match: 14.1% Indels: 13
RESULT 1392
ID AAT33802 standard; cDNA to mRNA; 498 BP.
DE Murine CTLA8 (interleukin-17) cDNA.
PN WO9629408-A1.
PD 26-SEP-1996.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1393
ID AAX01923 standard; cDNA to mRNA; 498 BP.
DE Murine CTLA-8 cDNA.
PN US5869286-A.
PD 09-FEB-1999.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1394
ID AAA51989 standard; cDNA to mRNA; 498 BP.
DE Murine interleukin-17 (CTLA-8) coding sequence.
PN US6100235-A.
PD 08-AUG-2000.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1395
ID AAA52147 standard; cDNA to mRNA; 498 BP.
DE Murine interleukin-17 (CTLA-8) coding sequence.
PN US6096305-A.
PD 01-AUG-2000.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1396
ID AAA59872 standard; cDNA; 498 BP.
DE Fragment of murine CTLA8 (IL-17) nucleotide sequence.
PN US6072033-A.
PD 06-JUN-2000.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1397
ID AAA61239 standard; DNA; 498 BP.
DE Murine CTLA-8 DNA.
PN US6072037-A.
PD 06-JUN-2000.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1398
ID AAF57187 standard; cDNA; 498 BP.
DE Murine CTLA-8 polypeptide encoding cDNA.
PN US6197525-B1.
PD 06-MAR-2001.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1399
ID AAD02814 standard; DNA; 498 BP.
DE Murine Interleukin-17 (IL-17) or CTLA-8 protein DNA.
PN US6191104-B1.
PD 20-FEB-2001.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1400
ID ADJ88261 standard; cDNA to mRNA; 498 BP.
DE Murine IL-17 nucleic acid sequence.
PN US6680057-B1.
PD 20-JAN-2004.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1401
ID ADQ91248 standard; cDNA; 498 BP.
DE Mouse cDNA encoding CTLA-8.
PN US2004120898-A1.
PD 24-JUN-2004.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1402
ID ADR01304 standard; cDNA to mRNA; 498 BP.
DE Mouse CTLA-8 cDNA to mRNA.
PN US2004120899-A1.
PD 24-JUN-2004.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 43.4% Conservative: 20
Best Local Similarity: 30.8% Mismatches: 61
Query Match: 14.0% Indels: 29
RESULT 1403
ID AAA59152 standard; cDNA; 543 BP.
DE cDNA encoding a human interleukin-172 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 43.9% Conservative: 25
Best Local Similarity: 28.0% Mismatches: 71
Query Match: 14.0% Indels: 17
RESULT 1404
ID AAA58980 standard; cDNA; 543 BP.
DE cDNA encoding a human interleukin (IL) 172 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 43.9% Conservative: 25
Best Local Similarity: 28.0% Mismatches: 71
Query Match: 14.0% Indels: 17
RESULT 1405
ID ADB31989 standard; cDNA; 543 BP.
DE Human cDNA encoding interleukin 172, IL-172.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 43.9% Conservative: 25
Best Local Similarity: 28.0% Mismatches: 71
Query Match: 14.0% Indels: 17
RESULT 1406
ID ADR13791 standard; cDNA; 543 BP.
DE Human interleukin-172 (IL-172) cDNA.

PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 43.9% Conservative: 25
Best Local Similarity: 28.0% Mismatches: 71
Query Match: 14.0% Indels: 17
RESULT 1407
ID AAT61414 standard; cDNA; 461 BP.
DE Rat CTLA-8.
PN WO9704097-A2.
PD 06-FEB-1997.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 42.5% Conservative: 20
Best Local Similarity: 29.4% Mismatches: 55
Query Match: 13.8% Indels: 33
RESULT 1408
ID AAA59967 standard; cDNA; 461 BP.
DE Rat cytotoxic T lymphocyte antigen-8 (CTLA-8) cDNA sequence.
PN US6074849-A.
PD 13-JUN-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 42.5% Conservative: 20
Best Local Similarity: 29.4% Mismatches: 55
Query Match: 13.8% Indels: 33
RESULT 1409
ID AAA07430 standard; cDNA; 461 BP.
DE Rat CTLA-8 coding sequence.
PN US6043344-A.
PD 28-MAR-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 42.5% Conservative: 20
Best Local Similarity: 29.4% Mismatches: 55
Query Match: 13.8% Indels: 33
RESULT 1410
ID AEA28880 standard; cDNA; 461 BP.
DE Rat CTLA-8 cDNA, SEQ ID NO: 3.
PN US6902735-B1.
PD 07-JUN-2005.
PA (GEMY) GENETICS INST LLC.
Percent Similarity: 42.5% Conservative: 20
Best Local Similarity: 29.4% Mismatches: 55
Query Match: 13.8% Indels: 33
RESULT 1411
ID AAQ92881 standard; cDNA; 1080 BP.
DE Mouse CTLA-8 cDNA.
PN WO9518826-A2.
PD 13-JUL-1995.
PA (SCHE) SCHERING CORP.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
Percent Similarity: 42.5% Conservative: 20
Best Local Similarity: 29.4% Mismatches: 55
Query Match: 13.8% Indels: 33
RESULT 1412
ID AAH77241 standard; cDNA; 1080 BP.
DE Murine cytokine-like protein CTLA-8 coding sequence.
PN US6274711-B1.
PD 14-AUG-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (SCHE) SCHERING CORP.
Percent Similarity: 42.5% Conservative: 20
Best Local Similarity: 29.4% Mismatches: 55
Query Match: 13.8% Indels: 33
RESULT 1413
ID ACA63321 standard; cDNA; 1080 BP.
DE Mouse cytotoxic T-lymphocyte antigen CTLA-8 cDNA #1.
PN US2003040603-A1.
PD 27-FEB-2003.
PA (GOLS/) GOLSTEIN P.
PA (ROUV/) ROUVIER E.
PA (FOSS/) FOSSIEZ F.
PA (LEBE/) LEBECQUE S J E.
PA (DJOS/) DJOSSOU O.
PA (BANC/) BANCHEREAU J.
Percent Similarity: 42.5% Conservative: 20
Best Local Similarity: 29.4% Mismatches: 55
Query Match: 13.8% Indels: 33
RESULT 1414
ID ADC17316 standard; cDNA; 1080 BP.
DE Murine cytotoxic T lymphocyte-associated antigen (CTLA-8) cDNA.
PN US6562333-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 42.5% Conservative: 20
Best Local Similarity: 29.4% Mismatches: 55
Query Match: 13.8% Indels: 33
RESULT 1415
ID AAH77245 standard; cDNA; 1134 BP.
DE Mouse cytokine-like protein CTLA-8 fragment coding sequence.
PN US6274711-B1.
PD 14-AUG-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (SCHE) SCHERING CORP.
Percent Similarity: 42.0% Conservative: 22
Best Local Similarity: 29.0% Mismatches: 62
Query Match: 13.8% Indels: 36
RESULT 1416
ID AAS89507 standard; cDNA; 1196 BP.
DE DNA encoding novel human diagnostic protein #25311.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.0% Conservative: 16
Best Local Similarity: 31.3% Mismatches: 51
Query Match: 13.7% Indels: 36
RESULT 1417
ID AAS93559 standard; cDNA; 1355 BP.
DE DNA encoding novel human diagnostic protein #29363.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 41.4% Conservative: 15
Best Local Similarity: 32.8% Mismatches: 75
Query Match: 13.3% Indels: 29
RESULT 1418
ID ADU40516 standard; cDNA; 1355 BP.
DE Novel human polynucleotide seq id 301.
PN US2004219521-A1.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.
PA (WENG/) WENG G.
PA (BOYL/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Percent Similarity: 41.4% Conservative: 15
Best Local Similarity: 32.8% Mismatches: 75
Query Match: 13.3% Indels: 29
RESULT 1419
ID ACA63325 standard; cDNA; 1134 BP.
DE Mouse cytotoxic T-lymphocyte antigen CTLA-8 cDNA #2.
PN US2003040603-A1.
PD 27-FEB-2003.
PA (GOLS/) GOLSTEIN P.
PA (ROUV/) ROUVIER E.
PA (FOSS/) FOSSIEZ F.
PA (LEBE/) LEBECQUE S J E.
PA (DJOS/) DJOSSOU O.
PA (BANC/) BANCHEREAU J.
Percent Similarity: 41.4% Conservative: 22
Best Local Similarity: 28.4% Mismatches: 63
Query Match: 13.2% Indels: 36
RESULT 1420
ID AAA57556 standard; cDNA; 723 BP.
DE cDNA clone of a human interleukin-20.
PN WO200042189-A1.
PD 20-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 44.8% Conservative: 26
Best Local Similarity: 29.1% Mismatches: 70
Query Match: 12.9% Indels: 22
RESULT 1421
ID AAA57838 standard; cDNA; 723 BP.
DE cDNA clone of a human interleukin-20.
PN WO200042189-A1.
PD 20-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.8% Conservative: 26
Best Local Similarity: 29.1% Mismatches: 70
Query Match: 12.9% Indels: 22
RESULT 1422
ID AAI21746 standard; DNA; 258 BP.
DE Probe #11679 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 56.0% Conservative: 14
Best Local Similarity: 39.3% Mismatches: 23
Query Match: 12.7% Indels: 14
RESULT 1423
ID ABA66823 standard; DNA; 258 BP.
DE Human foetal liver single exon nucleic acid probe #15128.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 56.0% Conservative: 14
Best Local Similarity: 39.3% Mismatches: 23
Query Match: 12.7% Indels: 14
RESULT 1424
ID AAI47029 standard; DNA; 258 BP.
DE Probe #15715 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 56.0% Conservative: 14
Best Local Similarity: 39.3% Mismatches: 23
Query Match: 12.7% Indels: 14
RESULT 1425
ID ABA48904 standard; DNA; 258 BP.
DE Human breast cell single exon nucleic acid probe #7599.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 56.0% Conservative: 14
Best Local Similarity: 39.3% Mismatches: 23
Query Match: 12.7% Indels: 14
RESULT 1426
ID ABA33886 standard; DNA; 258 BP.
DE Probe #12352 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 56.0% Conservative: 14
Best Local Similarity: 39.3% Mismatches: 23
Query Match: 12.7% Indels: 14
RESULT 1427
ID AAK40974 standard; DNA; 258 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 15531.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 56.0% Conservative: 14
Best Local Similarity: 39.3% Mismatches: 23
Query Match: 12.7% Indels: 14
RESULT 1428
ID AAK15251 standard; DNA; 258 BP.
DE Human brain expressed single exon probe SEQ ID NO: 15242.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 56.0% Conservative: 14
Best Local Similarity: 39.3% Mismatches: 23
Query Match: 12.7% Indels: 14
RESULT 1429
ID ABS40560 standard; DNA; 258 BP.
DE Human liver single exon probe, SEQ ID No 15550.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 56.0% Conservative: 14
Best Local Similarity: 39.3% Mismatches: 23
Query Match: 12.7% Indels: 14
RESULT 1430
ID AAI07431 standard; DNA; 258 BP.
DE Probe #7422 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 56.0% Conservative: 14
Best Local Similarity: 39.3% Mismatches: 23
Query Match: 12.7% Indels: 14
RESULT 1431
ID AAV83181 standard; cDNA; 497 BP.
DE Murine Zcyto7 expressed sequence tag.
PN WO9849310-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 41.3% Conservative: 24
Best Local Similarity: 26.9% Mismatches: 65
Query Match: 12.6% Indels: 33
RESULT 1432
ID AAD18300 standard; cDNA; 497 BP.
DE Mouse Zcyto7 cDNA from EST clone 660242.
PN WO200164240-A2.
PD 07-SEP-2001.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 41.3% Conservative: 24
Best Local Similarity: 26.9% Mismatches: 65
Query Match: 12.6% Indels: 33
RESULT 1433
ID ABS57069 standard; cDNA; 497 BP.
DE Mouse Zcyto7 EST 660242.
PN US2002039568-A1.
PD 04-APR-2002.
PA (MOOR/) MOORE E E.
PA (NOVA/) NOVAK J E.
Percent Similarity: 41.3% Conservative: 24
Best Local Similarity: 26.9% Mismatches: 65
Query Match: 12.6% Indels: 33
RESULT 1434
ID ABV72470 standard; DNA; 497 BP.
DE Expressed sequence tag (EST) used to identify IL-17B.
PN WO200276386-A2.
PD 03-OCT-2002.
PA (ZYMO) ZYMOGENETICS INC.
PA (UNIW) UNIV WASHINGTON.
Percent Similarity: 41.3% Conservative: 24
Best Local Similarity: 26.9% Mismatches: 65
Query Match: 12.6% Indels: 33
RESULT 1435
ID AAA59154 standard; cDNA; 310 BP.
DE cDNA encoding a human interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 47.2% Conservative: 11
Best Local Similarity: 34.8% Mismatches: 44
Query Match: 12.1% Indels: 3
RESULT 1436
ID AAQ92883 standard; cDNA; 239 BP.
DE Human CTLA-8 exon cDNA.
PN WO9518826-A2.
PD 13-JUL-1995.
PA (SCHE) SCHERING CORP.

PA (INRM) INST NAT SANTE & RECH MEDICALE.
Percent Similarity: 50.6% Conservative: 8
Best Local Similarity: 40.7% Mismatches: 26
Query Match: 11.6% Indels: 14
RESULT 1437
ID AAH77243 standard; cDNA; 240 BP.
DE Human cytokine-like protein CTLA-8 fragment coding sequence.
PN US6274711-B1.
PD 14-AUG-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (SCHE) SCHERING CORP.
Percent Similarity: 50.6% Conservative: 8
Best Local Similarity: 40.7% Mismatches: 26
Query Match: 11.6% Indels: 14
RESULT 1438
ID ACA63323 standard; cDNA; 240 BP.
DE Human cytotoxic T-lymphocyte antigen CTLA-8 cDNA #1.
PN US2003040603-A1.
PD 27-FEB-2003.
PA (GOLS/) GOLSTEIN P.
PA (ROUV/) ROUVIER E.
PA (FOSS/) FOSSIEZ F.
PA (LEBE/) LEBECQUE S J E.
PA (DJOS/) DJOSSOU O.
PA (BANC/) BANCHEREAU J.
Percent Similarity: 50.6% Conservative: 8
Best Local Similarity: 40.7% Mismatches: 26
Query Match: 11.6% Indels: 14
RESULT 1439
ID ADC17320 standard; cDNA; 240 BP.
DE Human cytotoxic T lymphocyte-associated antigen (CTLA-8) exon 8 cDNA.
PN US6562333-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 50.6% Conservative: 8
Best Local Similarity: 40.7% Mismatches: 26
Query Match: 11.6% Indels: 14
RESULT 1440
ID ACH79791 standard; DNA; 501 BP.
DE Human genome derived single exon probe #12986.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Percent Similarity: 50.6% Conservative: 8
Best Local Similarity: 40.7% Mismatches: 26
Query Match: 11.6% Indels: 14
RESULT 1441
ID ACF81859 standard; DNA; 397 BP.
DE Human SIRS/sepsis diagnostic marker DNA fragment 719.
PN WO2004087949-A2.
PD 14-OCT-2004.
PA (SIRS-) SIRS LAB GMBH.
Percent Similarity: 51.0% Conservative: 16
Best Local Similarity: 35.0% Mismatches: 40
Query Match: 11.4% Indels: 10
RESULT 1442
ID AAV86024 standard; cDNA; 514 BP.
DE EST clone B18.
PN WO9845435-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 43.9% Conservative: 24
Best Local Similarity: 28.7% Mismatches: 53
Query Match: 11.4% Indels: 35
RESULT 1443
ID AAZ29729 standard; DNA; 830 BP.
DE Virtual DNA fragment DNA47332 used for isolation of human PRO1031 cDNA.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.7% Conservative: 25
Best Local Similarity: 27.8% Mismatches: 71
Query Match: 11.0% Indels: 19
RESULT 1444
ID ADQ85430 standard; cDNA; 3704 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2244.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 37.4% Conservative: 9
Best Local Similarity: 33.0% Mismatches: 62
Query Match: 10.5% Indels: 70
RESULT 1445
ID ADN05189 standard; cDNA; 4456 BP.
DE Antipsoriatic cDNA sequence #810.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 37.4% Conservative: 9
Best Local Similarity: 33.0% Mismatches: 62
Query Match: 10.5% Indels: 70
RESULT 1446
ID AAA59151 standard; cDNA; 403 BP.
DE cDNA encoding a human interleukin-175 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 58.5% Conservative: 8
Best Local Similarity: 43.4% Mismatches: 21
Query Match: 10.3% Indels: 1
RESULT 1447
ID AAA59150 standard; cDNA; 403 BP.
DE cDNA encoding a human interleukin-175 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 58.5% Conservative: 8
Best Local Similarity: 43.4% Mismatches: 21
Query Match: 10.3% Indels: 1
RESULT 1448
ID AAA58992 standard; cDNA; 403 BP.
DE cDNA encoding a human interleukin (IL) 175 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 58.5% Conservative: 8
Best Local Similarity: 43.4% Mismatches: 21
Query Match: 10.3% Indels: 1
RESULT 1449
ID AAA58993 standard; cDNA; 403 BP.
DE cDNA encoding a human interleukin (IL) 175 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Percent Similarity: 58.5% Conservative: 8
Best Local Similarity: 43.4% Mismatches: 21
Query Match: 10.3% Indels: 1
RESULT 1450
ID ADB32011 standard; cDNA; 403 BP.
DE Human partial cDNA encoding interleukin 175, IL-175.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 58.5% Conservative: 8
Best Local Similarity: 43.4% Mismatches: 21
Query Match: 10.3% Indels: 1
RESULT 1451
ID ADR13815 standard; cDNA; 403 BP.
DE Human interleukin-175 (IL-175) cDNA #2.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.

Percent Similarity: 58.5% Conservative: 8
Best Local Similarity: 43.4% Mismatches: 21
Query Match: 10.3% Indels: 1
RESULT 1452
ID ADR13814 standard; cDNA; 403 BP.
DE Human interleukin-175 (IL-175) cDNA #1.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Percent Similarity: 58.5% Conservative: 8
Best Local Similarity: 43.4% Mismatches: 21
Query Match: 10.3% Indels: 1
RESULT 1453
ID AAI12556 standard; DNA; 443 BP.
DE Probe #2489 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.6% Conservative: 21
Best Local Similarity: 27.1% Mismatches: 56
Query Match: 10.3% Indels: 36
RESULT 1454
ID ABA54259 standard; DNA; 443 BP.
DE Human foetal liver single exon nucleic acid probe #2564.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.6% Conservative: 21
Best Local Similarity: 27.1% Mismatches: 56
Query Match: 10.3% Indels: 36
RESULT 1455
ID AAI33904 standard; DNA; 443 BP.
DE Probe #2590 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.6% Conservative: 21
Best Local Similarity: 27.1% Mismatches: 56
Query Match: 10.3% Indels: 36
RESULT 1456
ID ABA43800 standard; DNA; 443 BP.
DE Human breast cell single exon nucleic acid probe #2495.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.6% Conservative: 21
Best Local Similarity: 27.1% Mismatches: 56
Query Match: 10.3% Indels: 36
RESULT 1457
ID ABA24010 standard; DNA; 443 BP.
DE Probe #2476 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.6% Conservative: 21
Best Local Similarity: 27.1% Mismatches: 56
Query Match: 10.3% Indels: 36
RESULT 1458
ID AAK27971 standard; DNA; 443 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 2528.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.6% Conservative: 21
Best Local Similarity: 27.1% Mismatches: 56
Query Match: 10.3% Indels: 36
RESULT 1459
ID AAK02535 standard; DNA; 443 BP.
DE Human brain expressed single exon probe SEQ ID NO: 2526.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.6% Conservative: 21
Best Local Similarity: 27.1% Mismatches: 56
Query Match: 10.3% Indels: 36
RESULT 1460
ID ABS27560 standard; DNA; 443 BP.
DE Human liver single exon probe, SEQ ID No 2550.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.6% Conservative: 21
Best Local Similarity: 27.1% Mismatches: 56
Query Match: 10.3% Indels: 36
RESULT 1461
ID AAI02461 standard; DNA; 443 BP.
DE Probe #2452 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 40.6% Conservative: 21
Best Local Similarity: 27.1% Mismatches: 56
Query Match: 10.3% Indels: 36
RESULT 1462
ID AAX84482 standard; DNA; 265 BP.
DE Probe for murine EDIRF II coding sequence.
PN WO9932632-A1.
PD 01-JUL-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Percent Similarity: 63.3% Conservative: 11
Best Local Similarity: 40.8% Mismatches: 18
Query Match: 10.2% Indels: 0
RESULT 1463
ID AAS86133 standard; cDNA; 2580 BP.
DE DNA encoding novel human diagnostic protein #21937.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 35.4% Conservative: 17
Best Local Similarity: 27.9% Mismatches: 66
Query Match: 9.9% Indels: 80
RESULT 1464
ID AAL61096 standard; DNA; 1356 BP.
DE Rabbit 11G05 CD83 antibody heavy chain DNA.
PN WO2003045318-A2.
PD 05-JUN-2003.
PA (CELL-) CELLTECH R & D INC.
PA (RAMS/) RAMSDELL F.
PA (PROL/) PROLL S C.
PA (STAE/) STAEHLING-HAMPTON K.
PA (APPE/) APPELBY M W.
PA (MART/) MARTINEZ L F G.
Percent Similarity: 31.3% Conservative: 17
Best Local Similarity: 23.8% Mismatches: 79
Query Match: 9.8% Indels: 77
RESULT 1465
ID ADO79094 standard; DNA; 1356 BP.
DE Rabbit anti-CD83 monoclonal antibody 11G05 heavy chain DNA, SEQ ID NO:18.
PN WO2004048552-A2.
PD 10-JUN-2004.
PA (CELL-) CELLTECH R & D INC.
PA (GARC/) GARCIA-MARTINEZ L F.
PA (CHEN/) CHEN Y.
Percent Similarity: 31.3% Conservative: 17
Best Local Similarity: 23.8% Mismatches: 79
Query Match: 9.8% Indels: 77
RESULT 1466
ID AAL61098 standard; DNA; 1362 BP.
DE Rabbit 14C12 CD83 antibody heavy chain DNA.
PN WO2003045318-A2.
PD 05-JUN-2003.
PA (CELL-) CELLTECH R & D INC.
PA (RAMS/) RAMSDELL F.
PA (PROL/) PROLL S C.
PA (STAE/) STAEHLING-HAMPTON K.
PA (APPE/) APPELBY M W.

PA (MART/) MARTINEZ L F G.
Percent Similarity: 31.3% Conservative: 17
Best Local Similarity: 23.8% Mismatches: 79
Query Match: 9.8% Indels: 77
RESULT 1467
ID AAL61094 standard; DNA; 1362 BP.
DE Rabbit 20D04 CD83 antibody heavy chain DNA.
PN WO2003045318-A2.
PD 05-JUN-2003.
PA (CELL-) CELLTECH R & D INC.
PA (RAMS/) RAMSDELL F.
PA (PROL/) PROLL S C.
PA (STAE/) STAEHLING-HAMPTON K.
PA (APPE/) APPELBY M W.
PA (MART/) MARTINEZ L F G.
Percent Similarity: 31.3% Conservative: 17
Best Local Similarity: 23.8% Mismatches: 79
Query Match: 9.8% Indels: 77
RESULT 1468
ID ADO79090 standard; DNA; 1362 BP.
DE Rabbit anti-CD83 monoclonal antibody 20D04 heavy chain DNA, SEQ ID NO:14.
PN WO2004048552-A2.
PD 10-JUN-2004.
PA (CELL-) CELLTECH R & D INC.
PA (GARC/) GARCIA-MARTINEZ L F.
PA (CHEN/) CHEN Y.
Percent Similarity: 31.3% Conservative: 17
Best Local Similarity: 23.8% Mismatches: 79
Query Match: 9.8% Indels: 77
RESULT 1469
ID ADW68153 standard; DNA; 1362 BP.
DE Rabbit anti-CD83 monoclonal antibody 14C12 heavy chain DNA, SEQ ID NO:22.
PN WO2004048552-A2.
PD 10-JUN-2004.
PA (CLLT) CELLTECH R & D INC.
PA (GARC/) GARCIA-MARTINEZ L F.
PA (CHEN/) CHEN Y.
Percent Similarity: 31.3% Conservative: 17
Best Local Similarity: 23.8% Mismatches: 79
Query Match: 9.8% Indels: 77
RESULT 1470
ID AAL61100 standard; DNA; 1368 BP.
DE Rabbit M83 020B08H CD83 antibody heavy chain DNA.
PN WO2003045318-A2.
PD 05-JUN-2003.
PA (CELL-) CELLTECH R & D INC.
PA (RAMS/) RAMSDELL F.
PA (PROL/) PROLL S C.
PA (STAE/) STAEHLING-HAMPTON K.
PA (APPE/) APPELBY M W.
PA (MART/) MARTINEZ L F G.
Percent Similarity: 31.3% Conservative: 17
Best Local Similarity: 23.8% Mismatches: 79
Query Match: 9.8% Indels: 77
RESULT 1471
ID ADO79134 standard; DNA; 1368 BP.
DE Rabbit anti-CD83 monoclonal antibody M83 020B08H heavy chain DNA, SEQ:61.
PN WO2004048552-A2.
PD 10-JUN-2004.
PA (CELL-) CELLTECH R & D INC.
PA (GARC/) GARCIA-MARTINEZ L F.
PA (CHEN/) CHEN Y.
Percent Similarity: 31.3% Conservative: 17
Best Local Similarity: 23.8% Mismatches: 79
Query Match: 9.8% Indels: 77
RESULT 1472
ID AAL61102 standard; DNA; 1377 BP.
DE Rabbit M83 006G05L CD83 antibody heavy chain DNA.
PN WO2003045318-A2.
PD 05-JUN-2003.
PA (CELL-) CELLTECH R & D INC.
PA (RAMS/) RAMSDELL F.
PA (PROL/) PROLL S C.
PA (STAE/) STAEHLING-HAMPTON K.
PA (APPE/) APPELBY M W.
PA (MART/) MARTINEZ L F G.
Percent Similarity: 31.3% Conservative: 17
Best Local Similarity: 23.8% Mismatches: 79
Query Match: 9.8% Indels: 77
RESULT 1473
ID ADO79138 standard; DNA; 1377 BP.
DE Rabbit anti-CD83 monoclonal antibody M83 006G05L heavy chain DNA, SEQ:65.
PN WO2004048552-A2.
PD 10-JUN-2004.
PA (CELL-) CELLTECH R & D INC.
PA (GARC/) GARCIA-MARTINEZ L F.
PA (CHEN/) CHEN Y.
Percent Similarity: 31.3% Conservative: 17
Best Local Similarity: 23.8% Mismatches: 79
Query Match: 9.8% Indels: 77
RESULT 1474
ID ADO82611 standard; cDNA; 1971 BP.
DE Plant full length insert polynucleotide seqid 1331.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Percent Similarity: 36.6% Conservative: 15
Best Local Similarity: 29.9% Mismatches: 83
Query Match: 9.7% Indels: 59
RESULT 1475
ID ACN44758 standard; DNA; 172569 BP.
DE Human genomic sequence hCG20145.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 37.7% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 79
Query Match: 9.7% Indels: 62
RESULT 1476
ID ABQ54582 standard; cDNA; 1095 BP.
DE Human ovarian antigen HVVBD93 cDNA, SEQ ID NO:462.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 31.8% Conservative: 12
Best Local Similarity: 26.3% Mismatches: 70
Query Match: 9.6% Indels: 78
RESULT 1477
ID ABL15291 standard; cDNA; 2721 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40355.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 29.2% Conservative: 15
Best Local Similarity: 23.2% Mismatches: 77
Query Match: 9.6% Indels: 100
RESULT 1478
ID ABQ61214 standard; cDNA; 2751 BP.
DE FLJ10300 fis clone NT2RM2000030 encoding sequence.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 35.8% Conservative: 21
Best Local Similarity: 26.1% Mismatches: 82
Query Match: 9.6% Indels: 58
RESULT 1479
ID ABD32811 standard; DNA; 161051 BP.
DE Human cancer-associated genomic DNA HD16-063.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.

Percent Similarity: 35.9% Conservative: 21
Best Local Similarity: 25.7% Mismatches: 78
Query Match: 9.6% Indels: 54
RESULT 1480
ID AEB11612 standard; cDNA; 1256 BP.
DE Human tumor necrosis factor ligand Ztnf12 PCR amplicon.
PN WO2005058957-A2.
PD 30-JUN-2005.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 43.2% Conservative: 9
Best Local Similarity: 35.1% Mismatches: 27
Query Match: 9.5% Indels: 36
RESULT 1481
ID AEB11640 standard; cDNA; 1256 BP.
DE Human tumor necrosis factor ligand Ztnf12 PCR amplicon.
PN WO2005058957-A2.
PD 30-JUN-2005.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 43.2% Conservative: 9
Best Local Similarity: 35.1% Mismatches: 27
Query Match: 9.5% Indels: 36
RESULT 1482
ID AEB11595 standard; cDNA; 1650 BP.
DE Human tumor necrosis factor ligand Ztnf12x1 coding sequence.
PN WO2005058957-A2.
PD 30-JUN-2005.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 43.2% Conservative: 9
Best Local Similarity: 35.1% Mismatches: 27
Query Match: 9.5% Indels: 36
RESULT 1483
ID AEB11609 standard; cDNA; 1664 BP.
DE Human tumor necrosis factor ligand Ztnf12x2 coding sequence.
PN WO2005058957-A2.
PD 30-JUN-2005.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 43.2% Conservative: 9
Best Local Similarity: 35.1% Mismatches: 27
Query Match: 9.5% Indels: 36
RESULT 1484
ID AEB11627 standard; cDNA; 2292 BP.
DE Tumor necrosis factor ligand Ztnf12-MBP fusion protein coding sequence.
PN WO2005058957-A2.
PD 30-JUN-2005.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 43.2% Conservative: 9
Best Local Similarity: 35.1% Mismatches: 27
Query Match: 9.5% Indels: 36
RESULT 1485
ID ADS89074 standard; DNA; 5425 BP.
DE Human PSA gene SEQ ID NO:90.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 30.8% Conservative: 20
Best Local Similarity: 23.3% Mismatches: 73
Query Match: 9.5% Indels: 111
RESULT 1486
ID ADS89108 standard; DNA; 6001 BP.
DE Human gene SEQ ID NO:124.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 30.8% Conservative: 20
Best Local Similarity: 23.3% Mismatches: 73
Query Match: 9.5% Indels: 111
RESULT 1487
ID ACD19239 standard; DNA; 12848 BP.
DE E. coli 0157 unique DNA sequence OZID_252.
PN US2003023075-A1.
PD 30-JAN-2003.
PA (BLAT/) BLATTNER F R.
PA (BURL/) BURLAND V D.
PA (PERN/) PERNA N T.
PA (PLUN/) PLUNKETT G.
PA (WELC/) WELCH R.
Percent Similarity: 33.3% Conservative: 21
Best Local Similarity: 23.5% Mismatches: 74
Query Match: 9.5% Indels: 68
RESULT 1488
ID ADC00831 standard; DNA; 39824 BP.
DE Enterohaemorragic E. coli 0157:H7-specific nucleic acid SEQ ID NO: 876.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Percent Similarity: 33.3% Conservative: 21
Best Local Similarity: 23.5% Mismatches: 74
Query Match: 9.5% Indels: 68
RESULT 1489
ID AAH16550 standard; cDNA; 1988 BP.
DE Human cDNA sequence SEQ ID NO:15608.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 37.6% Conservative: 24
Best Local Similarity: 26.2% Mismatches: 75
Query Match: 9.5% Indels: 57
RESULT 1490
ID ADR14627 standard; DNA; 1988 BP.
DE Human NF-kappaB pathway-associated gene SeqID628.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Percent Similarity: 37.6% Conservative: 24
Best Local Similarity: 26.2% Mismatches: 75
Query Match: 9.5% Indels: 57
RESULT 1491
ID AAH17583 standard; cDNA; 2322 BP.
DE Human cDNA sequence SEQ ID NO:17075.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 37.6% Conservative: 24
Best Local Similarity: 26.2% Mismatches: 75
Query Match: 9.5% Indels: 57
RESULT 1492
ID AAD51680 standard; cDNA; 2344 BP.
DE Human nucleic acid associated protein (NAAP)-6 encoding cDNA.
PN WO200299115-A2.
PD 12-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
PA (YUEH/) YUE H.
Percent Similarity: 37.6% Conservative: 24
Best Local Similarity: 26.2% Mismatches: 75
Query Match: 9.5% Indels: 57
RESULT 1493
ID ADC30765 standard; cDNA; 2702 BP.
DE Human novel cDNA sequence, SEQ ID NO:847.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.6% Conservative: 24
Best Local Similarity: 26.2% Mismatches: 75
Query Match: 9.5% Indels: 57
RESULT 1494
ID AAK83412 standard; DNA; 4156 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38224.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 37.6% Conservative: 24
Best Local Similarity: 26.2% Mismatches: 75
Query Match: 9.5% Indels: 57
RESULT 1495
ID ACL64586 standard; DNA; 10182 BP.
DE M. xanthus DNA fragment, seq id 1049.

PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Percent Similarity: 34.2% Conservative: 15
Best Local Similarity: 28.0% Mismatches: 73
Query Match: 9.5% Indels: 87
RESULT 1496
ID AAD58977 standard; DNA; 83450 BP.
DE Human phosphatase genomic DNA.
Percent Similarity: 34.4% Conservative: 14
Best Local Similarity: 27.2% Mismatches: 77
Query Match: 9.5% Indels: 51
RESULT 1497
ID ADG88582 standard; DNA; 83450 BP.
DE Human phosphatase gene.
Percent Similarity: 34.4% Conservative: 14
Best Local Similarity: 27.2% Mismatches: 77
Query Match: 9.5% Indels: 51
RESULT 1498
ID AEB47870 standard; DNA; 83450 BP.
DE Human novel splice form phosphatase genomic DNA.
Percent Similarity: 34.4% Conservative: 14
Best Local Similarity: 27.2% Mismatches: 77
Query Match: 9.5% Indels: 51
RESULT 1499
ID ABQ81842 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 genomic sequence SEQ ID NO:1.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Percent Similarity: 41.5% Conservative: 19
Best Local Similarity: 30.4% Mismatches: 79
Query Match: 9.4% Indels: 23
RESULT 1500
ID ACL30126 standard; cDNA; 828 BP.
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:4082.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 40.1% Conservative: 19
Best Local Similarity: 29.9% Mismatches: 64
Query Match: 9.4% Indels: 48

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2006, 17:57:06 ; Search time 214 Seconds
(without alignments)
1636.353 Million cell updates/sec

Title: US-09-854-280-3
Perfect score: 1073
Sequence: 1 MTLLPGLLFLTWLHTCLAHH.....FHTEFIHVPVGCTCVLPRSV 197

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US09854280/runat_27042006_101650_27704/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=1500 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US09854280_@CGN_1_1_512_@runat_27042006_101650_27704
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1073	100.0	1047	3	US-09-747-259-3	Sequence 3, Appli
	2	1073	100.0	1047	3	US-09-949-016-5387	Sequence 5387, Ap
	3	1073	100.0	1107	3	US-09-480-297A-22	Sequence 22, Appl
	4	969	90.3	5884	3	US-09-949-016-17129	Sequence 17129, A
c	5	454	42.3	601	3	US-09-949-016-188268	Sequence 188268,
	6	446	41.6	521	3	US-09-480-297A-19	Sequence 19, Appl
	7	446	41.6	521	3	US-09-480-297A-20	Sequence 20, Appl
c	8	203	18.9	601	3	US-09-949-016-188267	Sequence 188267,
	9	202	18.8	1385	3	US-09-480-297A-7	Sequence 7, Appli
	10	201.5	18.8	1754	3	US-09-747-259-7	Sequence 7, Appli
	11	193	18.0	985	3	US-09-480-297A-17	Sequence 17, Appl
	12	193	18.0	985	3	US-09-836-385-3	Sequence 3, Appli
	13	192.5	17.9	1143	3	US-09-480-297A-11	Sequence 11, Appl
	14	192.5	17.9	1258	3	US-09-724-864-2	Sequence 2, Appli
	15	192	17.9	454	3	US-09-480-297A-5	Sequence 5, Appli
	16	175	16.3	813	2	US-08-514-014-11	Sequence 11, Appl
	17	175	16.3	813	2	US-08-833-823-11	Sequence 11, Appl
	18	175	16.3	813	3	US-09-034-810-1	Sequence 1, Appli
	19	175	16.3	813	3	US-08-685-239-1	Sequence 1, Appli
	20	175	16.3	813	3	US-10-102-080-1	Sequence 1, Appli
	21	173	16.1	559	3	US-09-747-259-9	Sequence 9, Appli
	22	173	16.1	692	3	US-09-620-956-11	Sequence 11, Appl
	23	173	16.1	692	3	US-09-611-152-11	Sequence 11, Appl
	24	173	16.1	692	3	US-09-794-705A-6	Sequence 6, Appli
	25	173	16.1	692	3	US-09-631-531-11	Sequence 11, Appl
	26	169	15.8	504	3	US-09-480-297A-13	Sequence 13, Appl
	27	169	15.8	504	3	US-09-836-385-1	Sequence 1, Appli
	28	169	15.8	1317	3	US-09-949-016-3137	Sequence 3137, Ap
	29	169	15.8	1320	3	US-09-747-259-5	Sequence 5, Appli
	30	168.5	15.7	543	3	US-09-480-297A-3	Sequence 3, Appli
	31	161	15.0	510	3	US-08-432-994A-7	Sequence 7, Appli
	32	161	15.0	510	3	US-08-250-846-7	Sequence 7, Appli
	33	161	15.0	510	3	US-09-929-612A-7	Sequence 7, Appli
	34	161	15.0	1859	3	US-09-949-016-1459	Sequence 1459, Ap
	35	161	15.0	1874	3	US-09-023-655-891	Sequence 891, App
	36	160.5	15.0	456	3	US-08-432-994A-3	Sequence 3, Appli
	37	160.5	15.0	456	3	US-08-250-846-3	Sequence 3, Appli
	38	160.5	15.0	459	3	US-09-034-810-5	Sequence 5, Appli
	39	160.5	15.0	459	3	US-08-685-239-5	Sequence 5, Appli
	40	160.5	15.0	459	3	US-10-102-080-5	Sequence 5, Appli
	41	160.5	15.0	2520	3	US-09-929-612A-3	Sequence 3, Appli
	42	158.5	14.8	687	3	US-09-747-259-1	Sequence 1, Appli
	43	158.5	14.8	687	3	US-09-999-833A-469	Sequence 469, App
	44	158.5	14.8	687	3	US-10-020-445A-469	Sequence 469, App
	45	158.5	14.8	688	3	US-09-949-016-4320	Sequence 4320, Ap
	46	158.5	14.8	705	3	US-09-231-788-1	Sequence 1, Appli
	47	158.5	14.8	705	3	US-09-796-844-34	Sequence 34, Appl
	48	158.5	14.8	736	3	US-09-620-956-1	Sequence 1, Appli
	49	158.5	14.8	736	3	US-09-611-152-1	Sequence 1, Appli
	50	158.5	14.8	736	3	US-09-794-705A-1	Sequence 1, Appli
	51	158.5	14.8	736	3	US-09-631-531-1	Sequence 1, Appli
	52	151	14.1	620	3	US-09-480-297A-15	Sequence 15, Appl
	53	150.5	14.0	498	2	US-08-620-694A-6	Sequence 6, Appli
	54	150.5	14.0	498	3	US-09-022-255-6	Sequence 6, Appli
	55	150.5	14.0	498	3	US-09-022-696-6	Sequence 6, Appli
	56	150.5	14.0	498	3	US-09-022-253-6	Sequence 6, Appli
	57	150.5	14.0	498	3	US-09-022-260-6	Sequence 6, Appli
	58	150.5	14.0	498	3	US-09-022-259-6	Sequence 6, Appli
	59	150.5	14.0	498	3	US-09-022-257-6	Sequence 6, Appli
	60	150.5	14.0	498	3	US-09-549-679-6	Sequence 6, Appli
	61	150.5	14.0	543	3	US-09-480-297A-1	Sequence 1, Appli
	62	148.5	13.8	461	3	US-09-034-810-3	Sequence 3, Appli
	63	148.5	13.8	461	3	US-08-685-239-3	Sequence 3, Appli
	64	148.5	13.8	461	3	US-10-102-080-3	Sequence 3, Appli
	65	148.5	13.8	1080	3	US-08-432-994A-1	Sequence 1, Appli
	66	148.5	13.8	1080	3	US-08-250-846-1	Sequence 1, Appli
	67	148.5	13.8	1080	3	US-09-929-612A-1	Sequence 1, Appli
	68	148.5	13.8	1134	3	US-08-432-994A-9	Sequence 9, Appli
	69	148.5	13.8	1134	3	US-09-929-612A-9	Sequence 9, Appli
	70	138.5	12.9	723	3	US-09-231-788-28	Sequence 28, Appl
c	71	138.5	12.9	723	3	US-09-231-788-29	Sequence 29, Appl
	72	135.5	12.6	497	3	US-09-620-956-13	Sequence 13, Appl
	73	135.5	12.6	497	3	US-09-611-152-13	Sequence 13, Appl
	74	135.5	12.6	497	3	US-09-794-705A-8	Sequence 8, Appli
	75	135.5	12.6	497	3	US-09-631-531-13	Sequence 13, Appl
	76	125	11.6	237	3	US-09-929-612A-5	Sequence 5, Appli
	77	125	11.6	240	3	US-08-432-994A-5	Sequence 5, Appli
	78	125	11.6	240	3	US-08-250-846-5	Sequence 5, Appli
	79	125	11.6	8252	3	US-09-949-016-13201	Sequence 13201, A
	80	124	11.6	7546	3	US-09-949-016-14879	Sequence 14879, A
	81	119	11.1	601	3	US-09-949-016-113731	Sequence 113731,
c	82	113	10.5	50229	3	US-09-949-016-15499	Sequence 15499, A

	83	112	10.4	9003	3	US-09-949-016-16062 Sequence 16062, A
	84	110.5	10.3	403	3	US-09-480-297A-24 Sequence 24, Appl
	85	110.5	10.3	403	3	US-09-480-297A-25 Sequence 25, Appl
c	86	106	9.9	35969	3	US-09-949-016-15562 Sequence 15562, A
	87	105	9.8	4622	3	US-08-509-024-6 Sequence 6, Appli
	88	105	9.8	4622	3	US-09-333-279-6 Sequence 6, Appli
	89	105	9.8	4622	3	US-09-631-780-6 Sequence 6, Appli
	90	102	9.5	12848	3	US-09-453-702B-252 Sequence 252, App
	91	102	9.5	12848	3	US-10-114-170-252 Sequence 252, App
c	92	101.5	9.5	10182	3	US-09-902-540-1049 Sequence 1049, Ap
	93	101.5	9.5	83450	3	US-09-811-469-3 Sequence 3, Appli
	94	101.5	9.5	83450	3	US-10-370-659-3 Sequence 3, Appli
	95	101	9.4	601	3	US-09-949-016-138655 Sequence 138655,
	96	100	9.3	601	3	US-09-949-016-138656 Sequence 138656,
	97	100	9.3	1194	3	US-09-902-540-9110 Sequence 9110, Ap
	98	100	9.3	8820	3	US-09-902-540-974 Sequence 974, App
c	99	99.5	9.3	20099	3	US-09-949-016-13784 Sequence 13784, A
c	100	99.5	9.3	154746	3	US-09-827-688-8 Sequence 8, Appli
	101	99	9.2	601	3	US-09-949-016-138657 Sequence 138657,
c	102	99	9.2	9191	3	US-09-902-540-918 Sequence 918, App
	103	99	9.2	194889	3	US-09-949-016-15654 Sequence 15654, A
c	104	99	9.2	198632	3	US-09-949-016-12781 Sequence 12781, A
c	105	99	9.2	198637	3	US-09-949-016-17393 Sequence 17393, A
c	106	98.5	9.2	750	3	US-09-813-453B-62 Sequence 62, Appl
c	107	98.5	9.2	38261	3	US-09-949-016-13802 Sequence 13802, A
	108	98	9.1	1953	3	US-10-104-047-938 Sequence 938, App
	109	98	9.1	3223	3	US-09-949-016-2058 Sequence 2058, Ap
	110	98	9.1	3252	3	US-10-327-189-3 Sequence 3, Appli
	111	98	9.1	3252	3	US-09-949-016-438 Sequence 438, App
	112	97.5	9.1	146039	3	US-09-949-016-12449 Sequence 12449, A
	113	97	9.0	3048	2	US-08-188-228-47 Sequence 47, Appl
	114	97	9.0	3048	2	US-08-332-643-41 Sequence 41, Appl
	115	97	9.0	3048	2	US-08-332-638-47 Sequence 47, Appl
c	116	97	9.0	7760	3	US-09-902-540-845 Sequence 845, App
	117	97	9.0	49144	3	US-09-949-016-15343 Sequence 15343, A
	118	96	8.9	4992	3	US-09-902-540-635 Sequence 635, App
c	119	96	8.9	16047	3	US-09-902-540-1136 Sequence 1136, Ap
	120	95.5	8.9	981	3	US-09-252-991A-13867 Sequence 13867, A
c	121	95.5	8.9	1278	3	US-09-252-991A-13473 Sequence 13473, A
	122	95.5	8.9	1530	3	US-09-252-991A-13672 Sequence 13672, A
	123	95.5	8.9	13117	3	US-09-949-016-15804 Sequence 15804, A
	124	95.5	8.9	23501	3	US-09-949-016-17517 Sequence 17517, A
c	125	95.5	8.9	92344	3	US-09-949-016-16802 Sequence 16802, A
	126	95.5	8.9	152331	3	US-09-128-155-16 Sequence 16, Appl
	127	95.5	8.9	176373	3	US-09-128-155-17 Sequence 17, Appl
	128	95	8.9	3310	3	US-10-104-047-545 Sequence 545, App
	129	95	8.9	11778	3	US-09-902-540-1020 Sequence 1020, Ap
	130	94.5	8.8	1114	3	US-09-270-767-3661 Sequence 3661, Ap
	131	94.5	8.8	1114	3	US-09-270-767-18943 Sequence 18943, A
c	132	94.5	8.8	2005	3	US-10-104-047-288 Sequence 288, App
	133	94.5	8.8	28194	3	US-09-902-540-1250 Sequence 1250, Ap
c	134	94.5	8.8	31713	3	US-09-949-016-16960 Sequence 16960, A
c	135	94.5	8.8	37875	3	US-09-949-016-13182 Sequence 13182, A
	136	94.5	8.8	70308	3	US-09-949-016-15601 Sequence 15601, A
	137	94	8.8	783	3	US-09-902-540-6650 Sequence 6650, Ap
	138	94	8.8	3132	3	US-09-902-540-516 Sequence 516, App
	139	94	8.8	3626	3	US-09-620-312D-93 Sequence 93, Appl
c	140	94	8.8	4403765	3	US-09-103-840A-2 Sequence 2, Appli
c	141	94	8.8	4411529	3	US-09-103-840A-1 Sequence 1, Appli
	142	93.5	8.7	601	3	US-09-949-016-146836 Sequence 146836,
c	143	93.5	8.7	47741	3	US-09-949-002-785 Sequence 785, App
c	144	93.5	8.7	96340	3	US-09-949-016-15863 Sequence 15863, A
	145	93	8.7	50	3	US-10-131-827-4768 Sequence 4768, Ap
	146	93	8.7	1669	3	US-10-104-047-1679 Sequence 1679, Ap
c	147	93	8.7	1953	3	US-09-976-594-231 Sequence 231, App
	148	93	8.7	18955	3	US-09-949-016-13343 Sequence 13343, A
	149	93	8.7	30678	3	US-09-949-016-12818 Sequence 12818, A
c	150	93	8.7	72455	3	US-09-949-016-13793 Sequence 13793, A
c	151	93	8.7	104475	3	US-09-949-016-12115 Sequence 12115, A
c	152	93	8.7	325034	3	US-09-949-016-14957 Sequence 14957, A
c	153	93	8.7	389504	3	US-09-949-016-11774 Sequence 11774, A
	154	92.5	8.6	2217	3	US-09-023-655-381 Sequence 381, App
	155	92.5	8.6	20936	3	US-09-949-002-657 Sequence 657, App
	156	92.5	8.6	20937	3	US-09-949-002-818 Sequence 818, App
c	157	92	8.6	2208	3	US-09-252-991A-13998 Sequence 13998, A
	158	92	8.6	2439	3	US-09-252-991A-14139 Sequence 14139, A
	159	92	8.6	2860	3	US-10-104-047-951 Sequence 951, App
	160	92	8.6	2994	3	US-09-252-991A-14228 Sequence 14228, A
	161	92	8.6	5051	3	US-09-902-540-806 Sequence 806, App
c	162	92	8.6	17050	3	US-09-949-016-12784 Sequence 12784, A
c	163	92	8.6	17050	3	US-09-949-016-13680 Sequence 13680, A
c	164	92	8.6	43414	3	US-09-949-016-12839 Sequence 12839, A
c	165	92	8.6	43415	3	US-09-949-016-16491 Sequence 16491, A
	166	91.5	8.5	601	3	US-09-949-016-69920 Sequence 69920, A
c	167	91.5	8.5	700	3	US-09-735-271-996 Sequence 996, App
	168	91.5	8.5	732	3	US-09-252-991A-2003 Sequence 2003, Ap
	169	91.5	8.5	792	3	US-09-252-991A-13931 Sequence 13931, A
	170	91.5	8.5	1221	3	US-09-252-991A-2160 Sequence 2160, Ap
c	171	91.5	8.5	1284	3	US-09-252-991A-13528 Sequence 13528, A
c	172	91.5	8.5	1482	3	US-09-252-991A-1723 Sequence 1723, Ap
c	173	91.5	8.5	8939	3	US-09-949-016-12703 Sequence 12703, A
c	174	91.5	8.5	9076	3	US-09-949-016-17368 Sequence 17368, A
	175	91.5	8.5	9316	3	US-09-949-016-16181 Sequence 16181, A
c	176	91.5	8.5	9521	3	US-09-902-540-953 Sequence 953, App
	177	91.5	8.5	13782	3	US-09-949-016-14992 Sequence 14992, A
c	178	91.5	8.5	63183	3	US-09-949-016-13047 Sequence 13047, A
c	179	91.5	8.5	63183	3	US-09-949-016-13048 Sequence 13048, A
c	180	91.5	8.5	111282	3	US-09-754-250-3 Sequence 3, Appli
c	181	91.5	8.5	111282	3	US-10-094-989-3 Sequence 3, Appli
c	182	91	8.5	1311	3	US-09-902-540-2371 Sequence 2371, Ap
c	183	91	8.5	1968	3	US-09-902-540-9206 Sequence 9206, Ap
c	184	91	8.5	2433	3	US-09-902-540-5148 Sequence 5148, Ap
	185	91	8.5	2514	3	US-09-902-540-2072 Sequence 2072, Ap
	186	91	8.5	4234	3	US-09-976-594-513 Sequence 513, App
c	187	91	8.5	10301	3	US-09-902-540-985 Sequence 985, App
	188	91	8.5	13579	3	US-09-902-540-1101 Sequence 1101, Ap
c	189	91	8.5	18079	3	US-09-949-016-13344 Sequence 13344, A
c	190	91	8.5	29559	3	US-09-902-540-1254 Sequence 1254, Ap
c	191	90.5	8.4	601	3	US-09-949-016-95232 Sequence 95232, A
c	192	90.5	8.4	601	3	US-09-949-016-95410 Sequence 95410, A
c	193	90.5	8.4	601	3	US-09-949-016-95588 Sequence 95588, A
c	194	90.5	8.4	601	3	US-09-949-016-95766 Sequence 95766, A
c	195	90.5	8.4	601	3	US-09-949-016-191525 Sequence 191525,
c	196	90.5	8.4	601	3	US-09-949-016-191703 Sequence 191703,
c	197	90.5	8.4	601	3	US-09-949-016-191881 Sequence 191881,
c	198	90.5	8.4	601	3	US-09-949-016-192059 Sequence 192059,
c	199	90.5	8.4	1287	3	US-09-902-540-7428 Sequence 7428, Ap
	200	90.5	8.4	1578	3	US-09-902-540-8956 Sequence 8956, Ap
c	201	90.5	8.4	3914	5	US-08-117-373-11 Sequence 11, Appl
c	202	90.5	8.4	5504	3	US-09-902-540-716 Sequence 716, App
c	203	90.5	8.4	7866	3	US-09-949-016-12072 Sequence 12072, A
c	204	90.5	8.4	7872	3	US-09-949-016-16771 Sequence 16771, A
c	205	90.5	8.4	8316	3	US-09-902-540-956 Sequence 956, App
c	206	90.5	8.4	20093	3	US-09-949-016-15207 Sequence 15207, A
	207	90.5	8.4	50937	3	US-09-428-517-1 Sequence 1, Appli
c	208	90.5	8.4	60990	3	US-09-949-016-14080 Sequence 14080, A
c	209	90.5	8.4	63319	3	US-09-949-016-16579 Sequence 16579, A
	210	90.5	8.4	77772	3	US-09-949-016-17417 Sequence 17417, A
	211	90.5	8.4	77997	3	US-09-949-016-12249 Sequence 12249, A
c	212	90.5	8.4	203475	3	US-09-949-016-14516 Sequence 14516, A
c	213	90.5	8.4	203475	3	US-09-949-016-14517 Sequence 14517, A
c	214	90.5	8.4	203475	3	US-09-949-016-14518 Sequence 14518, A
c	215	90.5	8.4	203475	3	US-09-949-016-14519 Sequence 14519, A
c	216	90.5	8.4	203475	3	US-09-949-016-17226 Sequence 17226, A
c	217	90.5	8.4	203475	3	US-09-949-016-17227 Sequence 17227, A
c	218	90.5	8.4	203475	3	US-09-949-016-17228 Sequence 17228, A
c	219	90.5	8.4	203475	3	US-09-949-016-17229 Sequence 17229, A
c	220	90	8.4	1521	3	US-09-902-540-2540 Sequence 2540, Ap
	221	90	8.4	2250	3	US-09-902-540-4529 Sequence 4529, Ap
	222	90	8.4	3196	2	US-09-096-982-4 Sequence 4, Appli
	223	90	8.4	3196	2	US-08-653-650A-4 Sequence 4, Appli
	224	90	8.4	7065	3	US-09-949-016-17586 Sequence 17586, A
	225	90	8.4	7065	3	US-09-949-002-851 Sequence 851, App
	226	90	8.4	7065	3	US-09-949-002-852 Sequence 852, App
	227	90	8.4	7065	3	US-09-949-002-853 Sequence 853, App
	228	90	8.4	7066	3	US-09-949-016-14840 Sequence 14840, A

	229	90	8.4	7066	3	US-09-949-002-754	Sequence 754, App
	230	90	8.4	7066	3	US-09-949-002-755	Sequence 755, App
	231	90	8.4	7066	3	US-09-949-002-756	Sequence 756, App
	232	90	8.4	7100	3	US-09-949-016-17587	Sequence 17587, A
	233	90	8.4	7100	3	US-09-949-002-854	Sequence 854, App
	234	90	8.4	7100	3	US-09-949-002-855	Sequence 855, App
	235	90	8.4	7100	3	US-09-949-002-856	Sequence 856, App
	236	90	8.4	7104	3	US-09-949-016-14841	Sequence 14841, A
	237	90	8.4	7104	3	US-09-949-002-757	Sequence 757, App
	238	90	8.4	7104	3	US-09-949-002-758	Sequence 758, App
	239	90	8.4	7104	3	US-09-949-002-759	Sequence 759, App
	240	90	8.4	15312	3	US-09-902-540-1115	Sequence 1115, Ap
	241	90	8.4	25497	3	US-09-902-540-1224	Sequence 1224, Ap
c	242	90	8.4	71989	3	US-09-443-501A-2	Sequence 2, Appli
c	243	90	8.4	71989	3	US-09-724-889A-2	Sequence 2, Appli
c	244	90	8.4	71989	3	US-09-724-876-2	Sequence 2, Appli
c	245	90	8.4	87352	3	US-09-949-016-12053	Sequence 12053, A
c	246	90	8.4	87352	3	US-09-949-016-12721	Sequence 12721, A
c	247	90	8.4	87352	3	US-09-949-016-15692	Sequence 15692, A
c	248	90	8.4	87352	3	US-09-949-016-15693	Sequence 15693, A
c	249	89.5	8.3	601	3	US-09-949-016-173024	Sequence 173024,
	250	89.5	8.3	601	3	US-09-949-016-204403	Sequence 204403,
	251	89.5	8.3	765	3	US-09-252-991A-15050	Sequence 15050, A
	252	89.5	8.3	1329	3	US-09-252-991A-14932	Sequence 14932, A
	253	89.5	8.3	5121	3	US-09-252-991A-15189	Sequence 15189, A
c	254	89.5	8.3	8256	3	US-09-949-016-16951	Sequence 16951, A
	255	89.5	8.3	50453	3	US-09-949-016-16642	Sequence 16642, A
	256	89.5	8.3	51242	3	US-09-949-016-12486	Sequence 12486, A
	257	89.5	8.3	57559	3	US-09-949-016-13077	Sequence 13077, A
	258	89.5	8.3	57560	3	US-09-949-016-12536	Sequence 12536, A
	259	89.5	8.3	117807	3	US-09-949-016-15525	Sequence 15525, A
	260	89	8.3	601	3	US-09-949-016-198538	Sequence 198538,
	261	89	8.3	1155	3	US-09-902-540-7960	Sequence 7960, Ap
c	262	89	8.3	1386	3	US-09-902-540-4598	Sequence 4598, Ap
	263	89	8.3	1656	3	US-10-033-109-13	Sequence 13, Appl
	264	89	8.3	2010	3	US-09-949-002-105	Sequence 105, App
	265	89	8.3	2010	3	US-09-949-002-247	Sequence 247, App
	266	89	8.3	2817	3	US-09-023-655-859	Sequence 859, App
	267	89	8.3	2851	3	US-09-535-521-1	Sequence 1, Appli
c	268	89	8.3	2851	3	US-09-535-521-3	Sequence 3, Appli
	269	89	8.3	3021	3	US-09-023-655-1259	Sequence 1259, Ap
	270	89	8.3	3043	3	US-09-008-271A-14	Sequence 14, Appl
	271	89	8.3	3043	3	US-09-968-415-14	Sequence 14, Appl
c	272	89	8.3	6134	3	US-09-902-540-805	Sequence 805, App
c	273	89	8.3	18632	3	US-09-949-016-16574	Sequence 16574, A
c	274	89	8.3	19025	3	US-09-849-334-3	Sequence 3, Appli
c	275	89	8.3	19025	3	US-10-274-878-3	Sequence 3, Appli
c	276	89	8.3	19025	3	US-10-697-266-3	Sequence 3, Appli
c	277	89	8.3	19326	3	US-09-949-016-16776	Sequence 16776, A
	278	89	8.3	24741	3	US-09-949-016-15547	Sequence 15547, A
	279	89	8.3	27707	3	US-09-902-540-1226	Sequence 1226, Ap
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	281	89	8.3	56963	3	US-09-949-016-12966	Sequence 12966, A
	282	89	8.3	56968	3	US-09-949-016-11888	Sequence 11888, A
c	283	89	8.3	95122	3	US-09-949-016-17235	Sequence 17235, A
c	284	89	8.3	137949	3	US-09-949-016-12196	Sequence 12196, A
c	285	89	8.3	137956	3	US-09-949-016-17260	Sequence 17260, A
c	286	89	8.3	767677	3	US-09-949-016-12147	Sequence 12147, A
c	287	89	8.3	767677	3	US-09-949-016-17361	Sequence 17361, A
	288	88.5	8.2	1110	3	US-09-902-540-2360	Sequence 2360, Ap
c	289	88.5	8.2	1630	3	US-09-023-655-598	Sequence 598, App
	290	88.5	8.2	1930	3	US-09-724-864-9	Sequence 9, Appli
c	291	88.5	8.2	4286	3	US-09-899-634C-1	Sequence 1, Appli
c	292	88.5	8.2	5759	3	US-09-954-483B-14	Sequence 14, Appl
c	293	88.5	8.2	6148	3	US-09-954-483B-13	Sequence 13, Appl
c	294	88.5	8.2	6663	3	US-09-335-011-15	Sequence 15, Appl
c	295	88.5	8.2	6714	3	US-09-299-141-6	Sequence 6, Appli
c	296	88.5	8.2	6924	3	US-09-299-141-9	Sequence 9, Appli
c	297	88.5	8.2	6924	3	US-09-299-141-10	Sequence 10, Appl
c	298	88.5	8.2	6924	3	US-09-299-141-11	Sequence 11, Appl
c	299	88.5	8.2	7223	3	US-09-335-011-8	Sequence 8, Appli
	300	88.5	8.2	7594	3	US-09-949-016-17582	Sequence 17582, A
c	301	88.5	8.2	8033	3	US-09-574-779B-134	Sequence 134, App
c	302	88.5	8.2	15209	3	US-09-902-540-1104	Sequence 1104, Ap
c	303	88.5	8.2	15447	3	US-09-902-540-1100	Sequence 1100, Ap
	304	88.5	8.2	16265	3	US-09-902-540-1126	Sequence 1126, Ap
c	305	88.5	8.2	18472	3	US-09-949-016-12891	Sequence 12891, A
c	306	88.5	8.2	18478	3	US-09-949-016-15925	Sequence 15925, A
c	307	88.5	8.2	39376	3	US-09-949-016-17536	Sequence 17536, A
c	308	88.5	8.2	119032	3	US-09-949-016-12160	Sequence 12160, A
c	309	88.5	8.2	119032	3	US-09-949-016-17268	Sequence 17268, A
c	310	88.5	8.2	258775	3	US-09-949-016-16435	Sequence 16435, A
c	311	88	8.2	601	3	US-09-949-016-55190	Sequence 55190, A
	312	88	8.2	601	3	US-09-949-016-170577	Sequence 170577,
	313	88	8.2	753	3	US-08-998-416-567	Sequence 567, App
c	314	88	8.2	1335	3	US-09-354-221-3	Sequence 3, Appli
c	315	88	8.2	1386	3	US-09-489-039A-5081	Sequence 5081, Ap
	316	88	8.2	1506	3	US-09-489-039A-5052	Sequence 5052, Ap
c	317	88	8.2	1572	3	US-09-902-540-8613	Sequence 8613, Ap
	318	88	8.2	2885	3	US-09-949-016-1936	Sequence 1936, Ap
	319	88	8.2	2913	3	US-09-976-594-368	Sequence 368, App
c	320	88	8.2	3609	3	US-09-902-540-632	Sequence 632, App
	321	88	8.2	7645	3	US-09-949-016-16559	Sequence 16559, A
c	322	88	8.2	7659	3	US-09-902-540-910	Sequence 910, App
c	323	88	8.2	9884	3	US-09-949-016-12548	Sequence 12548, A
c	324	88	8.2	9889	3	US-09-949-016-16116	Sequence 16116, A
	325	88	8.2	10103	2	US-08-457-273B-7	Sequence 7, Appli
c	326	88	8.2	10143	3	US-09-949-016-12090	Sequence 12090, A
c	327	88	8.2	10143	3	US-09-949-016-14396	Sequence 14396, A
c	328	88	8.2	10143	3	US-09-949-016-14397	Sequence 14397, A
c	329	88	8.2	11085	3	US-09-949-016-12795	Sequence 12795, A
c	330	88	8.2	11085	3	US-09-949-016-13917	Sequence 13917, A
c	331	88	8.2	11085	3	US-09-949-016-13918	Sequence 13918, A
	332	88	8.2	17592	3	US-09-902-540-1138	Sequence 1138, Ap
	333	88	8.2	18037	3	US-09-949-016-13678	Sequence 13678, A
	334	88	8.2	26729	3	US-10-283-247-6	Sequence 6, Appli
c	335	88	8.2	35122	3	US-09-949-016-11873	Sequence 11873, A
	336	88	8.2	70383	3	US-10-283-247-3	Sequence 3, Appli
c	337	88	8.2	70383	3	US-10-283-247-3	Sequence 3, Appli
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	339	88	8.2	77536	3	US-09-940-316B-1	Sequence 1, Appli
	340	87.5	8.2	601	3	US-09-949-016-32723	Sequence 32723, A
	341	87.5	8.2	601	3	US-09-949-016-137257	Sequence 137257,
	342	87.5	8.2	601	3	US-09-949-016-142336	Sequence 142336,
	343	87.5	8.2	601	3	US-09-949-016-178697	Sequence 178697,
c	344	87.5	8.2	1385	3	US-08-932-411A-17	Sequence 17, Appl
c	345	87.5	8.2	1385	3	US-09-585-645A-30	Sequence 30, Appl
c	346	87.5	8.2	1412	3	US-09-585-645A-6	Sequence 6, Appli
c	347	87.5	8.2	1412	3	US-09-585-645A-37	Sequence 37, Appl
	348	87.5	8.2	1482	3	US-09-252-991A-354	Sequence 354, App
	349	87.5	8.2	2089	3	US-10-104-047-1055	Sequence 1055, Ap
c	350	87.5	8.2	2337	3	US-09-252-991A-301	Sequence 301, App
c	351	87.5	8.2	3581	3	US-09-949-016-4965	Sequence 4965, Ap
c	352	87.5	8.2	3680	3	US-10-012-231A-32	Sequence 32, Appl
c	353	87.5	8.2	3680	3	US-10-015-389A-32	Sequence 32, Appl
c	354	87.5	8.2	3680	3	US-10-006-768A-32	Sequence 32, Appl
c	355	87.5	8.2	3680	3	US-10-015-671A-32	Sequence 32, Appl
c	356	87.5	8.2	3680	3	US-10-015-393A-32	Sequence 32, Appl
c	357	87.5	8.2	3680	3	US-10-011-833A-32	Sequence 32, Appl
c	358	87.5	8.2	3680	3	US-10-006-041A-32	Sequence 32, Appl
c	359	87.5	8.2	3680	3	US-10-012-064A-32	Sequence 32, Appl
	360	87.5	8.2	6099	3	US-09-854-856-41	Sequence 41, Appl
	361	87.5	8.2	6099	3	US-10-010-720-41	Sequence 41, Appl
c	362	87.5	8.2	6274	3	US-09-949-016-335	Sequence 335, App
	363	87.5	8.2	6279	3	US-09-854-856-9	Sequence 9, Appli
	364	87.5	8.2	6279	3	US-10-010-720-9	Sequence 9, Appli
	365	87.5	8.2	6510	3	US-09-854-856-39	Sequence 39, Appl
	366	87.5	8.2	6510	3	US-10-010-720-39	Sequence 39, Appl
	367	87.5	8.2	6690	3	US-09-854-856-7	Sequence 7, Appli
	368	87.5	8.2	6690	3	US-10-010-720-7	Sequence 7, Appli
	369	87.5	8.2	7398	3	US-09-949-016-15901	Sequence 15901, A
	370	87.5	8.2	19019	3	US-09-902-540-1171	Sequence 1171, Ap
	371	87.5	8.2	19728	3	US-09-949-016-12506	Sequence 12506, A
	372	87.5	8.2	19728	3	US-09-949-016-15767	Sequence 15767, A
c	373	87.5	8.2	126200	3	US-09-949-016-11824	Sequence 11824, A
c	374	87.5	8.2	126200	3	US-09-949-016-13193	Sequence 13193, A

c 375	87.5	8.2	129327	3	US-09-949-016-12257	Sequence 12257, A
c 376	87.5	8.2	129327	3	US-09-949-016-15368	Sequence 15368, A
377	87.5	8.2	134008	3	US-09-949-016-13841	Sequence 13841, A
378	87	8.1	601	3	US-09-949-016-71116	Sequence 71116, A
c 379	87	8.1	810	3	US-09-252-991A-15221	Sequence 15221, A
c 380	87	8.1	831	2	US-07-882-329-1	Sequence 1, Appli
c 381	87	8.1	831	2	US-08-183-213-1	Sequence 1, Appli
382	87	8.1	954	3	US-09-252-991A-15232	Sequence 15232, A
c 383	87	8.1	1000	3	US-09-949-016-944	Sequence 944, App
c 384	87	8.1	1120	2	US-07-882-329-3	Sequence 3, Appli
c 385	87	8.1	1120	2	US-08-183-213-3	Sequence 3, Appli
c 386	87	8.1	1149	3	US-09-252-991A-7156	Sequence 7156, Ap
c 387	87	8.1	1329	2	US-07-882-329-4	Sequence 4, Appli
c 388	87	8.1	1329	2	US-08-183-213-4	Sequence 4, Appli
389	87	8.1	1350	3	US-09-252-991A-7337	Sequence 7337, Ap
c 390	87	8.1	1434	3	US-09-252-991A-15227	Sequence 15227, A
c 391	87	8.1	1525	3	US-09-964-895-3	Sequence 3, Appli
c 392	87	8.1	1525	3	US-10-651-013-3	Sequence 3, Appli
393	87	8.1	1980	2	US-08-109-106-4	Sequence 4, Appli
c 394	87	8.1	1995	3	US-09-902-540-9209	Sequence 9209, Ap
395	87	8.1	2240	3	US-10-104-047-2	Sequence 2, Appli
c 396	87	8.1	2598	3	US-09-902-540-507	Sequence 507, App
c 397	87	8.1	2667	3	US-09-252-991A-7216	Sequence 7216, Ap
398	87	8.1	2733	3	US-09-902-540-9152	Sequence 9152, Ap
c 399	87	8.1	6012	3	US-09-902-540-808	Sequence 808, App
c 400	87	8.1	9164	3	US-09-814-915A-80	Sequence 80, Appl
c 401	87	8.1	9710	3	US-09-902-540-978	Sequence 978, App
402	87	8.1	14823	3	US-09-902-540-1087	Sequence 1087, Ap
c 403	87	8.1	16438	3	US-09-949-016-16165	Sequence 16165, A
404	87	8.1	16720	3	US-09-902-540-1168	Sequence 1168, Ap
405	87	8.1	40586	3	US-09-949-016-16965	Sequence 16965, A
c 406	87	8.1	109690	3	US-09-949-016-13525	Sequence 13525, A
c 407	87	8.1	134008	3	US-09-949-016-13841	Sequence 13841, A
408	86.5	8.1	601	3	US-09-949-016-26052	Sequence 26052, A
409	86.5	8.1	601	3	US-09-949-016-198198	Sequence 198198,
410	86.5	8.1	759	3	US-09-902-540-5997	Sequence 5997, Ap
411	86.5	8.1	1476	3	US-09-902-540-220	Sequence 220, App
412	86.5	8.1	1573	3	US-09-799-451-51	Sequence 51, Appl
413	86.5	8.1	1623	3	US-09-902-540-2480	Sequence 2480, Ap
c 414	86.5	8.1	2150	3	US-10-104-047-1786	Sequence 1786, Ap
415	86.5	8.1	2458	3	US-09-071-101-5	Sequence 5, Appli
416	86.5	8.1	2458	3	US-09-369-618-6	Sequence 6, Appli
417	86.5	8.1	2458	3	US-09-369-617-6	Sequence 6, Appli
418	86.5	8.1	3490	2	US-08-841-483-3	Sequence 3, Appli
419	86.5	8.1	3490	3	US-09-382-911-3	Sequence 3, Appli
c 420	86.5	8.1	4063	3	US-09-902-540-595	Sequence 595, App
421	86.5	8.1	4094	2	US-08-841-483-5	Sequence 5, Appli
422	86.5	8.1	4094	3	US-09-382-911-5	Sequence 5, Appli
c 423	86.5	8.1	5725	3	US-09-949-016-1964	Sequence 1964, Ap
424	86.5	8.1	6254	3	US-08-927-219-126	Sequence 126, App
425	86.5	8.1	7928	3	US-09-548-473B-5	Sequence 5, Appli
426	86.5	8.1	8544	3	US-09-902-540-917	Sequence 917, App
427	86.5	8.1	9080	3	US-09-902-540-1963	Sequence 1963, Ap
428	86.5	8.1	9779	3	US-09-949-016-15370	Sequence 15370, A
429	86.5	8.1	12028	3	US-09-902-540-1071	Sequence 1071, Ap
c 430	86.5	8.1	15209	3	US-09-902-540-1110	Sequence 1110, Ap
431	86.5	8.1	15847	3	US-09-949-016-13736	Sequence 13736, A
432	86.5	8.1	15847	3	US-09-949-016-13737	Sequence 13737, A
433	86.5	8.1	15847	3	US-09-949-016-13738	Sequence 13738, A
434	86.5	8.1	15847	3	US-09-949-016-13739	Sequence 13739, A
435	86.5	8.1	15847	3	US-09-949-016-13740	Sequence 13740, A
436	86.5	8.1	16629	3	US-09-949-016-14737	Sequence 14737, A
437	86.5	8.1	16629	3	US-09-949-016-14738	Sequence 14738, A
438	86.5	8.1	16629	3	US-09-949-016-14739	Sequence 14739, A
439	86.5	8.1	16629	3	US-09-949-016-14740	Sequence 14740, A
440	86.5	8.1	16629	3	US-09-949-016-14741	Sequence 14741, A
441	86.5	8.1	16629	3	US-09-949-016-14742	Sequence 14742, A
442	86.5	8.1	16629	3	US-09-949-016-14743	Sequence 14743, A
443	86.5	8.1	16629	3	US-09-949-016-14744	Sequence 14744, A
444	86.5	8.1	16629	3	US-09-949-016-14745	Sequence 14745, A
445	86.5	8.1	16629	3	US-09-949-016-14746	Sequence 14746, A
446	86.5	8.1	16629	3	US-09-949-016-14752	Sequence 14752, A
447	86.5	8.1	16629	3	US-09-949-016-14753	Sequence 14753, A
448	86.5	8.1	16629	3	US-09-949-016-14754	Sequence 14754, A
449	86.5	8.1	16629	3	US-09-949-016-14755	Sequence 14755, A
450	86.5	8.1	16629	3	US-09-949-016-14756	Sequence 14756, A
451	86.5	8.1	16803	3	US-09-949-016-14747	Sequence 14747, A
452	86.5	8.1	16803	3	US-09-949-016-14748	Sequence 14748, A
453	86.5	8.1	16803	3	US-09-949-016-14749	Sequence 14749, A
454	86.5	8.1	16803	3	US-09-949-016-14750	Sequence 14750, A
455	86.5	8.1	16803	3	US-09-949-016-14751	Sequence 14751, A
c 456	86.5	8.1	18660	3	US-09-477-962-2	Sequence 2, Appli
c 457	86.5	8.1	38155	3	US-09-453-702B-79	Sequence 79, Appl
c 458	86.5	8.1	38155	3	US-10-114-170-79	Sequence 79, Appl
c 459	86.5	8.1	41768	3	US-09-902-540-1266	Sequence 1266, Ap
c 460	86.5	8.1	44377	2	US-08-804-227C-7	Sequence 7, Appli
c 461	86.5	8.1	44377	2	US-08-804-198-1	Sequence 1, Appli
c 462	86.5	8.1	49603	3	US-09-949-016-13706	Sequence 13706, A
c 463	86.5	8.1	53722	3	US-09-949-016-12077	Sequence 12077, A
c 464	86.5	8.1	80161	3	US-09-036-987A-1	Sequence 1, Appli
c 465	86.5	8.1	80161	3	US-09-370-700-1	Sequence 1, Appli
c 466	86.5	8.1	80161	3	US-09-603-207-1	Sequence 1, Appli
467	86.5	8.1	455726	3	US-09-949-016-14157	Sequence 14157, A
468	86.5	8.1	481115	3	US-09-949-016-11940	Sequence 11940, A
c 469	86	8.0	601	3	US-09-949-016-53326	Sequence 53326, A
c 470	86	8.0	601	3	US-09-949-016-53327	Sequence 53327, A
471	86	8.0	1461	3	US-09-902-540-7265	Sequence 7265, Ap
472	86	8.0	1708	3	US-10-104-047-1901	Sequence 1901, Ap
473	86	8.0	1843	3	US-09-620-312D-402	Sequence 402, App
474	86	8.0	2064	3	US-09-178-109-3	Sequence 3, Appli
475	86	8.0	2064	3	US-10-062-879-3	Sequence 3, Appli
476	86	8.0	2072	3	US-09-142-791A-3	Sequence 3, Appli
477	86	8.0	2104	3	US-09-142-791A-1	Sequence 1, Appli
478	86	8.0	2104	3	US-09-142-791A-5	Sequence 5, Appli
479	86	8.0	2121	3	US-09-178-109-1	Sequence 1, Appli
480	86	8.0	2121	3	US-10-062-879-1	Sequence 1, Appli
c 481	86	8.0	2611	3	US-10-104-047-330	Sequence 330, App
c 482	86	8.0	2831	3	US-09-949-016-2020	Sequence 2020, Ap
c 483	86	8.0	4094	3	US-09-902-540-665	Sequence 665, App
484	86	8.0	4324	3	US-09-902-540-684	Sequence 684, App
485	86	8.0	9036	3	US-09-949-016-16866	Sequence 16866, A
c 486	86	8.0	12250	3	US-09-949-016-17580	Sequence 17580, A
c 487	86	8.0	13637	3	US-09-902-540-1097	Sequence 1097, Ap
488	86	8.0	17879	3	US-09-949-016-12992	Sequence 12992, A
489	86	8.0	28958	2	US-08-258-261B-6	Sequence 6, Appli
490	86	8.0	28958	2	US-08-456-837-6	Sequence 6, Appli
491	86	8.0	28958	2	US-08-457-342-6	Sequence 6, Appli
492	86	8.0	28958	2	US-08-457-646A-6	Sequence 6, Appli
493	86	8.0	28958	2	US-08-458-076A-6	Sequence 6, Appli
494	86	8.0	28958	2	US-08-764-233A-4	Sequence 4, Appli
495	86	8.0	28958	2	US-08-457-335A-6	Sequence 6, Appli
496	86	8.0	28958	2	US-08-729-214-6	Sequence 6, Appli
497	86	8.0	28958	3	US-09-028-934-6	Sequence 6, Appli
498	86	8.0	49377	2	US-08-764-233A-1	Sequence 1, Appli
c 499	86	8.0	49677	3	US-09-949-002-817	Sequence 817, App
500	86	8.0	139936	3	US-09-949-016-11782	Sequence 11782, A
501	86	8.0	139952	3	US-09-949-016-13280	Sequence 13280, A
c 502	86	8.0	222691	3	US-09-949-016-11762	Sequence 11762, A
c 503	86	8.0	222697	3	US-09-949-016-15842	Sequence 15842, A
504	86	8.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
505	86	8.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 506	85.5	8.0	888	3	US-09-902-540-5511	Sequence 5511, Ap
507	85.5	8.0	1335	3	US-09-252-991A-973	Sequence 973, App
c 508	85.5	8.0	1653	3	US-09-252-991A-1111	Sequence 1111, Ap
c 509	85.5	8.0	1943	3	US-10-104-047-1892	Sequence 1892, Ap
c 510	85.5	8.0	1947	3	US-09-199-637A-220	Sequence 220, App
511	85.5	8.0	1995	3	US-09-902-540-9209	Sequence 9209, Ap
512	85.5	8.0	3187	2	US-08-910-856-9	Sequence 9, Appli
513	85.5	8.0	3187	2	US-08-910-856-10	Sequence 10, Appl
514	85.5	8.0	3187	3	US-09-672-749-16	Sequence 16, Appl
515	85.5	8.0	4524	2	US-08-845-998-7	Sequence 7, Appli
516	85.5	8.0	4524	3	US-09-206-537-7	Sequence 7, Appli
517	85.5	8.0	4524	3	US-09-430-854-7	Sequence 7, Appli
518	85.5	8.0	4563	3	US-09-252-991A-930	Sequence 930, App
519	85.5	8.0	4659	3	US-08-264-578-10	Sequence 10, Appl
520	85.5	8.0	4659	3	US-08-217-704C-9	Sequence 9, Appli

	521	85.5	8.0	4659	3	US-08-164-487A-1	Sequence 1, Appli
	522	85.5	8.0	5692	3	US-09-902-540-783	Sequence 783, App
	523	85.5	8.0	10301	3	US-09-902-540-985	Sequence 985, App
	524	85.5	8.0	34621	3	US-09-949-002-700	Sequence 700, App
	525	85.5	8.0	38371	3	US-09-949-016-12061	Sequence 12061, A
	526	85.5	8.0	38371	3	US-09-949-016-12488	Sequence 12488, A
	527	85.5	8.0	38371	3	US-09-949-016-15596	Sequence 15596, A
	528	85.5	8.0	38371	3	US-09-949-016-15597	Sequence 15597, A
	529	85.5	8.0	40653	3	US-09-949-002-640	Sequence 640, App
c	530	85.5	8.0	41927	3	US-09-902-540-1268	Sequence 1268, Ap
c	531	85.5	8.0	42235	3	US-09-199-637A-1	Sequence 1, Appli
	532	85.5	8.0	45684	3	US-09-949-016-16539	Sequence 16539, A
c	533	85.5	8.0	47981	3	US-09-679-279-1	Sequence 1, Appli
	534	85.5	8.0	49225	3	US-09-902-540-1269	Sequence 1269, Ap
c	535	85.5	8.0	70563	3	US-09-949-016-16743	Sequence 16743, A
c	536	85.5	8.0	77772	3	US-09-949-016-17417	Sequence 17417, A
c	537	85.5	8.0	77997	3	US-09-949-016-12249	Sequence 12249, A
	538	85.5	8.0	109690	3	US-09-949-016-13525	Sequence 13525, A
c	539	85.5	8.0	212139	3	US-09-949-016-16065	Sequence 16065, A
	540	85	7.9	423	3	US-09-489-039A-720	Sequence 720, App
c	541	85	7.9	996	3	US-09-902-540-9593	Sequence 9593, Ap
c	542	85	7.9	1005	3	US-09-949-016-5687	Sequence 5687, Ap
	543	85	7.9	1197	3	US-09-602-787A-485	Sequence 485, App
c	544	85	7.9	1476	3	US-09-489-039A-665	Sequence 665, App
	545	85	7.9	1551	3	US-09-489-039A-489	Sequence 489, App
	546	85	7.9	1677	3	US-09-252-991A-337	Sequence 337, App
	547	85	7.9	2358	3	US-10-104-047-1084	Sequence 1084, Ap
c	548	85	7.9	2685	3	US-09-252-991A-4555	Sequence 4555, Ap
c	549	85	7.9	3719	3	US-09-949-016-1060	Sequence 1060, Ap
	550	85	7.9	3924	3	US-09-252-991A-4296	Sequence 4296, Ap
	551	85	7.9	7546	3	US-09-902-540-801	Sequence 801, App
	552	85	7.9	13346	3	US-09-902-540-1089	Sequence 1089, Ap
c	553	85	7.9	17896	3	US-09-949-016-11986	Sequence 11986, A
c	554	85	7.9	18343	3	US-09-949-016-16413	Sequence 16413, A
c	555	85	7.9	18551	3	US-09-902-540-1187	Sequence 1187, Ap
	556	85	7.9	23802	3	US-09-949-016-12107	Sequence 12107, A
	557	85	7.9	23803	3	US-09-949-016-15878	Sequence 15878, A
	558	85	7.9	36223	3	US-09-949-016-14417	Sequence 14417, A
	559	85	7.9	40546	3	US-09-949-016-12847	Sequence 12847, A
	560	85	7.9	40546	3	US-09-949-016-12915	Sequence 12915, A
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	562	85	7.9	50341	2	US-09-075-904-1	Sequence 1, Appli
	563	85	7.9	52297	3	US-09-426-436-1	Sequence 1, Appli
	564	85	7.9	52297	3	US-08-705-557-1	Sequence 1, Appli
c	565	85	7.9	64377	3	US-09-949-016-15212	Sequence 15212, A
c	566	85	7.9	64377	3	US-09-949-016-15213	Sequence 15213, A
c	567	85	7.9	64377	3	US-09-949-016-15214	Sequence 15214, A
c	568	85	7.9	64377	3	US-09-949-016-15215	Sequence 15215, A
c	569	85	7.9	64377	3	US-09-949-016-15216	Sequence 15216, A
c	570	85	7.9	86414	3	US-09-949-016-12345	Sequence 12345, A
c	571	85	7.9	86414	3	US-09-949-016-15758	Sequence 15758, A
	572	85	7.9	105413	3	US-10-427-923-3	Sequence 3, Appli
	573	85	7.9	112219	3	US-09-949-016-12453	Sequence 12453, A
	574	85	7.9	112222	3	US-09-949-016-14324	Sequence 14324, A
	575	85	7.9	113186	3	US-09-949-016-17572	Sequence 17572, A
c	576	85	7.9	154600	3	US-09-949-016-14757	Sequence 14757, A
c	577	84.5	7.9	601	3	US-09-949-016-57639	Sequence 57639, A
c	578	84.5	7.9	798	3	US-09-902-540-4013	Sequence 4013, Ap
c	579	84.5	7.9	1164	3	US-09-252-991A-7162	Sequence 7162, Ap
c	580	84.5	7.9	1293	3	US-09-902-540-5585	Sequence 5585, Ap
c	581	84.5	7.9	1494	3	US-09-902-540-3058	Sequence 3058, Ap
c	582	84.5	7.9	1641	3	US-09-252-991A-8049	Sequence 8049, Ap
	583	84.5	7.9	1749	3	US-09-516-914-22	Sequence 22, Appl
	584	84.5	7.9	1989	3	US-09-534-228B-6	Sequence 6, Appli
	585	84.5	7.9	2151	3	US-09-252-991A-14112	Sequence 14112, A
c	586	84.5	7.9	2223	3	US-09-252-991A-14116	Sequence 14116, A
c	587	84.5	7.9	2226	3	US-08-951-260A-1	Sequence 1, Appli
c	588	84.5	7.9	2226	3	US-09-430-626A-1	Sequence 1, Appli
c	589	84.5	7.9	2226	3	US-10-243-687-1	Sequence 1, Appli
c	590	84.5	7.9	2615	3	US-10-104-047-1280	Sequence 1280, Ap
	591	84.5	7.9	3159	3	US-09-252-991A-14020	Sequence 14020, A
c	592	84.5	7.9	3202	3	US-09-287-354-1	Sequence 1, Appli
c	593	84.5	7.9	3492	3	US-09-023-655-1219	Sequence 1219, Ap
c	594	84.5	7.9	3677	3	US-09-949-016-1969	Sequence 1969, Ap
c	595	84.5	7.9	5051	3	US-09-902-540-628	Sequence 628, App
c	596	84.5	7.9	5140	3	US-09-333-214-2	Sequence 2, Appli
c	597	84.5	7.9	5808	3	US-09-902-540-794	Sequence 794, App
	598	84.5	7.9	5894	3	US-08-665-259-24	Sequence 24, Appl
	599	84.5	7.9	5894	3	US-08-762-500-24	Sequence 24, Appl
	600	84.5	7.9	6447	3	US-09-949-016-4925	Sequence 4925, Ap
	601	84.5	7.9	6525	3	US-08-762-500-74	Sequence 74, Appl
	602	84.5	7.9	14272	3	US-09-516-914-23	Sequence 23, Appl
c	603	84.5	7.9	15602	3	US-09-844-634-17	Sequence 17, Appl
c	604	84.5	7.9	16187	3	US-09-902-540-1093	Sequence 1093, Ap
	605	84.5	7.9	26533	3	US-09-902-540-1199	Sequence 1199, Ap
c	606	84.5	7.9	27578	3	US-09-949-016-12167	Sequence 12167, A
c	607	84.5	7.9	27579	3	US-09-949-016-15005	Sequence 15005, A
c	608	84.5	7.9	46253	3	US-09-949-016-11890	Sequence 11890, A
c	609	84.5	7.9	46257	3	US-09-949-016-13711	Sequence 13711, A
c	610	84.5	7.9	56963	3	US-09-949-016-12966	Sequence 12966, A
c	611	84.5	7.9	56968	3	US-09-949-016-11888	Sequence 11888, A
c	612	84.5	7.9	110585	3	US-09-949-016-13427	Sequence 13427, A
c	613	84.5	7.9	136058	3	US-09-949-016-12565	Sequence 12565, A
c	614	84.5	7.9	136480	3	US-09-949-016-17064	Sequence 17064, A
	615	84.5	7.9	203475	3	US-09-949-016-14516	Sequence 14516, A
	616	84.5	7.9	203475	3	US-09-949-016-14517	Sequence 14517, A
	617	84.5	7.9	203475	3	US-09-949-016-14518	Sequence 14518, A
	618	84.5	7.9	203475	3	US-09-949-016-14519	Sequence 14519, A
	619	84.5	7.9	203475	3	US-09-949-016-17226	Sequence 17226, A
	620	84.5	7.9	203475	3	US-09-949-016-17227	Sequence 17227, A
	621	84.5	7.9	203475	3	US-09-949-016-17228	Sequence 17228, A
	622	84.5	7.9	203475	3	US-09-949-016-17229	Sequence 17229, A
	623	84.5	7.9	325034	3	US-09-949-016-14957	Sequence 14957, A
	624	84.5	7.9	389504	3	US-09-949-016-11774	Sequence 11774, A
	625	84	7.8	908	3	US-09-972-800A-11	Sequence 11, Appl
	626	84	7.8	1094	3	US-09-302-769-9	Sequence 9, Appli
	627	84	7.8	1094	3	US-08-962-560C-9	Sequence 9, Appli
	628	84	7.8	1590	3	US-09-252-991A-15269	Sequence 15269, A
	629	84	7.8	1962	3	US-09-148-545-111	Sequence 111, App
	630	84	7.8	1962	3	US-09-621-011-111	Sequence 111, App
	631	84	7.8	2082	3	US-09-774-528-367	Sequence 367, App
	632	84	7.8	2082	3	US-10-120-988-367	Sequence 367, App
	633	84	7.8	2351	3	US-09-949-016-3250	Sequence 3250, Ap
	634	84	7.8	2377	3	US-09-920-668-3	Sequence 3, Appli
c	635	84	7.8	2480	3	US-09-064-199-15	Sequence 15, Appl
c	636	84	7.8	2513	3	US-09-949-016-983	Sequence 983, App
c	637	84	7.8	2876	3	US-09-601-844B-3	Sequence 3, Appli
c	638	84	7.8	2876	3	US-09-949-016-982	Sequence 982, App
c	639	84	7.8	2960	3	US-09-601-844B-1	Sequence 1, Appli
c	640	84	7.8	2960	3	US-09-949-016-645	Sequence 645, App
c	641	84	7.8	3117	2	US-08-747-536-1	Sequence 1, Appli
c	642	84	7.8	3393	2	US-08-295-502-1	Sequence 1, Appli
c	643	84	7.8	3393	6	PCT-US95-10691-1	Sequence 1, Appli
c	644	84	7.8	3936	3	US-09-902-540-7211	Sequence 7211, Ap
c	645	84	7.8	4346	3	US-09-064-199-12	Sequence 12, Appl
c	646	84	7.8	4366	3	US-09-064-199-14	Sequence 14, Appl
c	647	84	7.8	4418	3	US-09-064-199-13	Sequence 13, Appl
c	648	84	7.8	4431	3	US-09-064-199-8	Sequence 8, Appli
c	649	84	7.8	4441	3	US-09-641-999-2	Sequence 2, Appli
c	650	84	7.8	4441	3	US-09-064-199-10	Sequence 10, Appl
c	651	84	7.8	4543	2	US-08-519-547A-5	Sequence 5, Appli
c	652	84	7.8	4549	3	US-09-064-199-9	Sequence 9, Appli
c	653	84	7.8	4564	3	US-09-064-199-2	Sequence 2, Appli
c	654	84	7.8	4649	3	US-09-064-199-11	Sequence 11, Appl
c	655	84	7.8	4746	3	US-09-064-199-7	Sequence 7, Appli
c	656	84	7.8	4892	3	US-09-620-312D-492	Sequence 492, App
c	657	84	7.8	5105	3	US-09-064-199-3	Sequence 3, Appli
c	658	84	7.8	5237	3	US-09-949-002-264	Sequence 264, App
	659	84	7.8	5353	3	US-09-902-540-672	Sequence 672, App
c	660	84	7.8	5463	3	US-09-064-199-1	Sequence 1, Appli
	661	84	7.8	6394	3	US-09-949-016-14380	Sequence 14380, A
	662	84	7.8	6439	3	US-09-902-540-813	Sequence 813, App
c	663	84	7.8	6672	3	US-09-949-002-9	Sequence 9, Appli
c	664	84	7.8	6771	3	US-09-949-016-15294	Sequence 15294, A
	665	84	7.8	7553	3	US-09-902-540-920	Sequence 920, App
c	666	84	7.8	14097	3	US-09-949-016-13661	Sequence 13661, A

c 667	84	7.8	16802	3	US-09-949-016-12622	Sequence 12622, A
c 668	84	7.8	17000	3	US-09-691-220-3	Sequence 3, Appli
c 669	84	7.8	18082	3	US-09-949-016-12586	Sequence 12586, A
c 670	84	7.8	18083	3	US-09-949-016-15711	Sequence 15711, A
671	84	7.8	28172	3	US-09-902-540-1221	Sequence 1221, Ap
c 672	84	7.8	30528	3	US-09-949-016-14049	Sequence 14049, A
c 673	84	7.8	34589	3	US-09-949-002-836	Sequence 836, App
c 674	84	7.8	59258	3	US-09-949-002-581	Sequence 581, App
675	84	7.8	68702	3	US-09-949-016-16328	Sequence 16328, A
676	83.5	7.8	999	3	US-09-902-540-7970	Sequence 7970, Ap
677	83.5	7.8	1521	2	US-08-496-855A-3	Sequence 3, Appli
678	83.5	7.8	1521	2	US-07-938-154-9	Sequence 9, Appli
679	83.5	7.8	1521	6	PCT-US91-02311-9	Sequence 9, Appli
c 680	83.5	7.8	1569	3	US-09-252-991A-12675	Sequence 12675, A
c 681	83.5	7.8	1593	3	US-09-902-540-8792	Sequence 8792, Ap
c 682	83.5	7.8	1602	3	US-09-902-540-7421	Sequence 7421, Ap
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684	83.5	7.8	1779	3	US-09-252-991A-11083	Sequence 11083, A
685	83.5	7.8	1781	3	US-09-461-325-21	Sequence 21, Appl
686	83.5	7.8	1781	3	US-10-012-542-21	Sequence 21, Appl
687	83.5	7.8	1781	3	US-10-115-123-21	Sequence 21, Appl
688	83.5	7.8	1961	3	US-09-509-902A-15	Sequence 15, Appl
689	83.5	7.8	1961	3	US-10-024-828-15	Sequence 15, Appl
690	83.5	7.8	2004	3	US-09-188-930-230	Sequence 230, App
691	83.5	7.8	2004	3	US-09-312-283C-230	Sequence 230, App
692	83.5	7.8	2334	3	US-09-602-787A-181	Sequence 181, App
693	83.5	7.8	2448	3	US-08-487-596-13	Sequence 13, Appl
694	83.5	7.8	2448	3	US-08-660-451A-13	Sequence 13, Appl
695	83.5	7.8	2448	3	US-09-703-951A-13	Sequence 13, Appl
696	83.5	7.8	2450	2	US-08-466-589-9	Sequence 9, Appli
697	83.5	7.8	2450	2	US-08-700-636-9	Sequence 9, Appli
698	83.5	7.8	2450	3	US-08-467-574-9	Sequence 9, Appli
699	83.5	7.8	2450	3	US-09-217-345-9	Sequence 9, Appli
700	83.5	7.8	2450	3	US-09-892-985-9	Sequence 9, Appli
c 701	83.5	7.8	2643	3	US-09-252-991A-11170	Sequence 11170, A
c 702	83.5	7.8	2655	3	US-09-902-540-6674	Sequence 6674, Ap
c 703	83.5	7.8	2838	3	US-09-252-991A-14128	Sequence 14128, A
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705	83.5	7.8	3010	3	US-09-990-444-313	Sequence 313, App
706	83.5	7.8	3010	3	US-09-997-333-313	Sequence 313, App
707	83.5	7.8	3010	3	US-09-992-598-313	Sequence 313, App
708	83.5	7.8	3391	3	US-09-902-540-530	Sequence 530, App
709	83.5	7.8	3798	3	US-09-902-540-523	Sequence 523, App
710	83.5	7.8	3897	3	US-09-252-991A-14008	Sequence 14008, A
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c 714	83.5	7.8	4394	3	US-08-471-869-1	Sequence 1, Appli
c 715	83.5	7.8	4394	3	US-09-342-563-1	Sequence 1, Appli
c 716	83.5	7.8	4394	6	PCT-US94-08267-1	Sequence 1, Appli
717	83.5	7.8	4908	3	US-10-001-887-33	Sequence 33, Appl
718	83.5	7.8	6085	3	US-09-029-603-4	Sequence 4, Appli
c 719	83.5	7.8	6375	3	US-10-418-036-13	Sequence 13, Appl
c 720	83.5	7.8	7317	3	US-09-902-540-715	Sequence 715, App
c 721	83.5	7.8	7822	3	US-09-949-016-13339	Sequence 13339, A
722	83.5	7.8	7950	3	US-09-902-540-934	Sequence 934, App
723	83.5	7.8	10622	3	US-10-198-053-569	Sequence 569, App
c 724	83.5	7.8	11982	3	US-09-949-016-17084	Sequence 17084, A
c 725	83.5	7.8	17353	3	US-09-949-016-13437	Sequence 13437, A
c 726	83.5	7.8	22761	3	US-09-902-540-1219	Sequence 1219, Ap
c 727	83.5	7.8	25010	3	US-09-949-016-14070	Sequence 14070, A
c 728	83.5	7.8	30690	3	US-09-914-286-1	Sequence 1, Appli
c 729	83.5	7.8	39920	3	US-09-949-016-16316	Sequence 16316, A
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731	83.5	7.8	41170	3	US-09-902-540-1267	Sequence 1267, Ap
732	83.5	7.8	48908	3	US-09-453-702B-137	Sequence 137, App
733	83.5	7.8	48908	3	US-10-114-170-137	Sequence 137, App
734	83.5	7.8	62463	3	US-09-949-016-16071	Sequence 16071, A
735	83.5	7.8	141115	3	US-09-949-016-17490	Sequence 17490, A
736	83.5	7.8	142783	3	US-09-949-016-15127	Sequence 15127, A
737	83	7.7	474	3	US-09-893-737-17	Sequence 17, Appl
c 738	83	7.7	601	3	US-09-949-016-95233	Sequence 95233, A
c 739	83	7.7	601	3	US-09-949-016-95411	Sequence 95411, A
c 740	83	7.7	601	3	US-09-949-016-95589	Sequence 95589, A
c 741	83	7.7	601	3	US-09-949-016-95767	Sequence 95767, A
c 742	83	7.7	601	3	US-09-949-016-108857	Sequence 108857,
c 743	83	7.7	601	3	US-09-949-016-108858	Sequence 108858,
c 744	83	7.7	601	3	US-09-949-016-191526	Sequence 191526,
c 745	83	7.7	601	3	US-09-949-016-191704	Sequence 191704,
c 746	83	7.7	601	3	US-09-949-016-191882	Sequence 191882,
c 747	83	7.7	601	3	US-09-949-016-192060	Sequence 192060,
748	83	7.7	601	3	US-09-949-016-198537	Sequence 198537,
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750	83	7.7	775	3	US-09-270-767-4440	Sequence 4440, Ap
751	83	7.7	775	3	US-09-270-767-19722	Sequence 19722, A
c 752	83	7.7	888	3	US-09-902-540-9238	Sequence 9238, Ap
753	83	7.7	960	3	US-09-170-496D-195	Sequence 195, App
c 754	83	7.7	1252	3	US-09-902-540-6749	Sequence 6749, Ap
755	83	7.7	1293	3	US-09-252-991A-1655	Sequence 1655, Ap
756	83	7.7	1342	3	US-09-799-451-266	Sequence 266, App
757	83	7.7	1382	3	US-09-016-434-1256	Sequence 1256, Ap
758	83	7.7	1401	3	US-09-902-540-6962	Sequence 6962, Ap
759	83	7.7	1477	3	US-09-280-116-15	Sequence 15, Appl
c 760	83	7.7	1479	2	US-08-644-271-31	Sequence 31, Appl
c 761	83	7.7	1479	3	US-09-077-955-35	Sequence 35, Appl
c 762	83	7.7	1479	3	US-10-016-283-35	Sequence 35, Appl
c 763	83	7.7	1732	3	US-09-430-564-1	Sequence 1, Appli
c 764	83	7.7	1816	3	US-09-762-258-1	Sequence 1, Appli
c 765	83	7.7	2081	3	US-09-799-451-925	Sequence 925, App
766	83	7.7	2099	3	US-10-104-047-1394	Sequence 1394, Ap
c 767	83	7.7	2165	3	US-09-799-451-926	Sequence 926, App
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769	83	7.7	2197	3	US-09-905-125A-11	Sequence 11, Appl
770	83	7.7	2197	3	US-09-902-775A-11	Sequence 11, Appl
771	83	7.7	2197	3	US-09-906-700-11	Sequence 11, Appl
772	83	7.7	2197	3	US-09-903-603A-11	Sequence 11, Appl
773	83	7.7	2197	3	US-09-904-920A-11	Sequence 11, Appl
774	83	7.7	2197	3	US-09-909-064-11	Sequence 11, Appl
775	83	7.7	2197	3	US-09-905-381A-11	Sequence 11, Appl
776	83	7.7	2197	3	US-09-906-618-11	Sequence 11, Appl
777	83	7.7	2197	3	US-09-906-646-11	Sequence 11, Appl
778	83	7.7	2197	3	US-09-904-462-11	Sequence 11, Appl
779	83	7.7	2197	3	US-09-902-736A-11	Sequence 11, Appl
780	83	7.7	2197	3	US-09-906-722A-11	Sequence 11, Appl
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782	83	7.7	2558	3	US-08-999-733-3	Sequence 3, Appli
783	83	7.7	2558	3	US-10-271-311-3	Sequence 3, Appli
c 784	83	7.7	3222	3	US-09-252-991A-13746	Sequence 13746, A
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786	83	7.7	3435	6	PCT-US96-00005-1	Sequence 1, Appli
c 787	83	7.7	4050	3	US-09-902-540-604	Sequence 604, App
788	83	7.7	4142	3	US-09-902-540-546	Sequence 546, App
789	83	7.7	5103	3	US-09-252-991A-5192	Sequence 5192, Ap
790	83	7.7	5191	2	US-08-340-428B-1	Sequence 1, Appli
791	83	7.7	5191	6	PCT-US93-07306-1	Sequence 1, Appli
c 792	83	7.7	6420	3	US-09-937-837-2	Sequence 2, Appli
c 793	83	7.7	6876	3	US-09-252-991A-5283	Sequence 5283, Ap
794	83	7.7	7127	3	US-09-949-002-586	Sequence 586, App
795	83	7.7	7311	3	US-09-949-002-844	Sequence 844, App
c 796	83	7.7	9818	3	US-09-902-540-987	Sequence 987, App
797	83	7.7	10302	3	US-09-949-016-17492	Sequence 17492, A
798	83	7.7	12732	3	US-09-060-756-1	Sequence 1, Appli
799	83	7.7	12732	3	US-09-670-314-1	Sequence 1, Appli
800	83	7.7	15945	3	US-09-949-016-17271	Sequence 17271, A
c 801	83	7.7	20757	3	US-09-902-540-1189	Sequence 1189, Ap
c 802	83	7.7	28804	2	US-08-592-874-1	Sequence 1, Appli
c 803	83	7.7	28804	3	US-09-096-942-2	Sequence 2, Appli
c 804	83	7.7	28804	3	US-09-096-867-2	Sequence 2, Appli
c 805	83	7.7	31422	3	US-09-914-286-2	Sequence 2, Appli
c 806	83	7.7	33061	3	US-09-949-016-16848	Sequence 16848, A
c 807	83	7.7	44120	3	US-09-949-016-14151	Sequence 14151, A
c 808	83	7.7	44120	3	US-09-949-016-14152	Sequence 14152, A
c 809	83	7.7	44120	3	US-09-949-016-14153	Sequence 14153, A
c 810	83	7.7	44120	3	US-09-949-016-14154	Sequence 14154, A
c 811	83	7.7	44120	3	US-09-949-016-14155	Sequence 14155, A
c 812	83	7.7	44120	3	US-09-949-016-14156	Sequence 14156, A

c 813	83	7.7	55674	3	US-09-949-016-12563	Sequence 12563, A
c 814	83	7.7	55675	3	US-09-949-016-15706	Sequence 15706, A
c 815	83	7.7	84916	3	US-09-949-016-14736	Sequence 14736, A
c 816	83	7.7	118136	3	US-09-949-016-12439	Sequence 12439, A
c 817	83	7.7	190078	3	US-09-949-016-12707	Sequence 12707, A
c 818	83	7.7	190078	3	US-09-949-016-17026	Sequence 17026, A
819	82.5	7.7	576	3	US-09-893-737-223	Sequence 223, App
820	82.5	7.7	601	3	US-09-949-016-26913	Sequence 26913, A
c 821	82.5	7.7	601	3	US-09-949-016-127812	Sequence 127812,
c 822	82.5	7.7	601	3	US-09-949-016-128149	Sequence 128149,
823	82.5	7.7	601	3	US-09-949-016-182954	Sequence 182954,
c 824	82.5	7.7	681	3	US-09-902-540-3124	Sequence 3124, Ap
c 825	82.5	7.7	813	3	US-09-902-540-4621	Sequence 4621, Ap
c 826	82.5	7.7	888	3	US-09-902-540-3619	Sequence 3619, Ap
827	82.5	7.7	897	3	US-09-252-991A-12134	Sequence 12134, A
c 828	82.5	7.7	1001	3	US-09-671-317-342	Sequence 342, App
c 829	82.5	7.7	1051	3	US-09-919-172-2	Sequence 2, Appli
c 830	82.5	7.7	1119	3	US-09-902-540-5726	Sequence 5726, Ap
831	82.5	7.7	1122	3	US-09-622-439-5	Sequence 5, Appli
832	82.5	7.7	1122	3	US-10-318-142-5	Sequence 5, Appli
833	82.5	7.7	1122	3	US-09-875-076-19	Sequence 19, Appl
c 834	82.5	7.7	1431	3	US-09-252-991A-12608	Sequence 12608, A
c 835	82.5	7.7	1563	3	US-09-221-017B-238	Sequence 238, App
836	82.5	7.7	1607	3	US-09-328-857A-1	Sequence 1, Appli
837	82.5	7.7	1608	3	US-09-252-991A-9091	Sequence 9091, Ap
838	82.5	7.7	1647	3	US-09-902-540-5609	Sequence 5609, Ap
839	82.5	7.7	1710	3	US-09-252-991A-9011	Sequence 9011, Ap
c 840	82.5	7.7	1920	3	US-09-252-991A-8999	Sequence 8999, Ap
c 841	82.5	7.7	2106	3	US-09-270-767-11012	Sequence 11012, A
c 842	82.5	7.7	2109	3	US-09-902-540-8825	Sequence 8825, Ap
843	82.5	7.7	2137	3	US-09-907-794A-58	Sequence 58, Appl
844	82.5	7.7	2137	3	US-09-905-125A-58	Sequence 58, Appl
845	82.5	7.7	2137	3	US-09-902-775A-58	Sequence 58, Appl
846	82.5	7.7	2137	3	US-09-906-700-58	Sequence 58, Appl
847	82.5	7.7	2137	3	US-09-903-603A-58	Sequence 58, Appl
848	82.5	7.7	2137	3	US-09-904-920A-58	Sequence 58, Appl
849	82.5	7.7	2137	3	US-09-909-064-58	Sequence 58, Appl
850	82.5	7.7	2137	3	US-09-905-381A-58	Sequence 58, Appl
851	82.5	7.7	2137	3	US-09-906-618-58	Sequence 58, Appl
852	82.5	7.7	2137	3	US-09-906-646-58	Sequence 58, Appl
853	82.5	7.7	2137	3	US-09-904-462-58	Sequence 58, Appl
854	82.5	7.7	2137	3	US-09-902-736A-58	Sequence 58, Appl
855	82.5	7.7	2137	3	US-09-906-722A-58	Sequence 58, Appl
c 856	82.5	7.7	2240	3	US-10-104-047-2	Sequence 2, Appli
857	82.5	7.7	2608	3	US-09-904-615-16	Sequence 16, Appl
858	82.5	7.7	2608	3	US-10-054-988-16	Sequence 16, Appl
c 859	82.5	7.7	3201	3	US-10-104-047-1526	Sequence 1526, Ap
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861	82.5	7.7	3705	3	US-09-146-249A-64	Sequence 64, Appl
862	82.5	7.7	3705	3	US-08-206-188B-64	Sequence 64, Appl
863	82.5	7.7	3705	3	US-09-917-254-42	Sequence 42, Appl
c 864	82.5	7.7	6203	3	US-09-902-540-811	Sequence 811, App
865	82.5	7.7	6599	3	US-09-902-540-724	Sequence 724, App
c 866	82.5	7.7	8025	3	US-09-902-540-877	Sequence 877, App
c 867	82.5	7.7	8765	3	US-09-902-540-939	Sequence 939, App
c 868	82.5	7.7	15268	3	US-09-902-540-1142	Sequence 1142, Ap
869	82.5	7.7	18848	3	US-09-902-540-1174	Sequence 1174, Ap
c 870	82.5	7.7	18848	3	US-09-902-540-1174	Sequence 1174, Ap
c 871	82.5	7.7	24205	3	US-09-949-016-15385	Sequence 15385, A
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c 873	82.5	7.7	41737	3	US-09-949-016-12204	Sequence 12204, A
c 874	82.5	7.7	41741	3	US-09-949-016-16983	Sequence 16983, A
c 875	82.5	7.7	43267	3	US-09-949-016-17117	Sequence 17117, A
c 876	82.5	7.7	54484	3	US-09-902-540-1272	Sequence 1272, Ap
877	82.5	7.7	81927	3	US-09-949-016-15623	Sequence 15623, A
878	82.5	7.7	86414	3	US-09-949-016-12345	Sequence 12345, A
879	82.5	7.7	86414	3	US-09-949-016-15758	Sequence 15758, A
c 880	82.5	7.7	228851	3	US-09-949-016-13781	Sequence 13781, A
881	82.5	7.7	304533	3	US-09-949-016-15371	Sequence 15371, A
882	82.5	7.7	304533	3	US-09-949-016-15372	Sequence 15372, A
c 883	82	7.6	601	3	US-09-949-016-185413	Sequence 185413,
884	82	7.6	601	3	US-09-949-016-187880	Sequence 187880,
c 885	82	7.6	601	3	US-09-949-002-8167	Sequence 8167, Ap
886	82	7.6	807	3	US-09-489-039A-5230	Sequence 5230, Ap
887	82	7.6	822	3	US-09-902-540-6560	Sequence 6560, Ap
c 888	82	7.6	834	3	US-09-902-540-7570	Sequence 7570, Ap
889	82	7.6	912	3	US-09-252-991A-10695	Sequence 10695, A
890	82	7.6	942	3	US-09-949-016-2731	Sequence 2731, Ap
891	82	7.6	957	3	US-09-902-540-3584	Sequence 3584, Ap
c 892	82	7.6	959	3	US-09-902-540-102	Sequence 102, App
893	82	7.6	960	3	US-09-130-749-1	Sequence 1, Appli
894	82	7.6	960	3	US-09-130-749-1	Sequence 1, Appli
895	82	7.6	1151	2	US-08-807-044-2	Sequence 2, Appli
c 896	82	7.6	1401	3	US-09-902-540-9594	Sequence 9594, Ap
897	82	7.6	1485	3	US-09-252-991A-10594	Sequence 10594, A
c 898	82	7.6	1495	3	US-09-938-035B-3	Sequence 3, Appli
899	82	7.6	1509	3	US-09-252-991A-3614	Sequence 3614, Ap
900	82	7.6	1577	3	US-09-902-540-172	Sequence 172, App
901	82	7.6	1666	2	US-08-666-367B-3	Sequence 3, Appli
902	82	7.6	1666	3	US-09-143-438-3	Sequence 3, Appli
c 903	82	7.6	1707	3	US-09-949-016-2100	Sequence 2100, Ap
c 904	82	7.6	1833	3	US-09-902-540-4884	Sequence 4884, Ap
c 905	82	7.6	1929	3	US-09-146-950-1	Sequence 1, Appli
c 906	82	7.6	1929	3	US-09-934-289A-1	Sequence 1, Appli
907	82	7.6	2058	3	US-09-489-039A-5810	Sequence 5810, Ap
c 908	82	7.6	2129	3	US-09-799-451-417	Sequence 417, App
c 909	82	7.6	2200	3	US-09-504-358-27	Sequence 27, Appl
c 910	82	7.6	2200	3	US-09-954-314-27	Sequence 27, Appl
c 911	82	7.6	2200	3	US-10-230-562-27	Sequence 27, Appl
912	82	7.6	3027	3	US-08-818-112-110	Sequence 110, App
913	82	7.6	3027	3	US-08-818-111-105	Sequence 105, App
914	82	7.6	3027	3	US-09-056-556-110	Sequence 110, App
915	82	7.6	3027	3	US-09-072-596-105	Sequence 105, App
916	82	7.6	3027	3	US-09-072-967-110	Sequence 110, App
917	82	7.6	3027	3	US-10-193-002-105	Sequence 105, App
918	82	7.6	3027	3	US-10-084-843-110	Sequence 110, App
919	82	7.6	3661	3	US-08-718-388-5	Sequence 5, Appli
c 920	82	7.6	4190	3	US-08-938-291A-2	Sequence 2, Appli
c 921	82	7.6	4190	3	US-09-589-619-2	Sequence 2, Appli
c 922	82	7.6	4329	3	US-09-902-540-2431	Sequence 2431, Ap
923	82	7.6	4389	3	US-09-023-655-991	Sequence 991, App
924	82	7.6	4521	3	US-09-902-540-3633	Sequence 3633, Ap
c 925	82	7.6	4779	3	US-09-902-540-778	Sequence 778, App
926	82	7.6	5424	3	US-09-902-540-840	Sequence 840, App
c 927	82	7.6	6201	3	US-09-902-540-740	Sequence 740, App
c 928	82	7.6	6220	3	US-09-600-087-1	Sequence 1, Appli
c 929	82	7.6	6220	3	US-09-949-016-470	Sequence 470, App
c 930	82	7.6	6221	3	US-09-949-016-5229	Sequence 5229, Ap
931	82	7.6	6260	3	US-09-902-540-781	Sequence 781, App
932	82	7.6	6350	3	US-09-949-016-14473	Sequence 14473, A
c 933	82	7.6	6363	3	US-09-023-655-879	Sequence 879, App
934	82	7.6	6664	3	US-09-949-016-14970	Sequence 14970, A
935	82	7.6	7824	3	US-08-718-388-6	Sequence 6, Appli
c 936	82	7.6	8137	3	US-09-949-016-14012	Sequence 14012, A
c 937	82	7.6	8716	3	US-09-949-016-12854	Sequence 12854, A
c 938	82	7.6	11471	3	US-09-504-358-16	Sequence 16, Appl
c 939	82	7.6	11471	3	US-09-954-314-16	Sequence 16, Appl
c 940	82	7.6	11471	3	US-10-230-562-16	Sequence 16, Appl
c 941	82	7.6	13145	3	US-09-949-016-13083	Sequence 13083, A
c 942	82	7.6	14899	3	US-09-902-540-1107	Sequence 1107, Ap
943	82	7.6	15209	3	US-09-902-540-1104	Sequence 1104, Ap
944	82	7.6	16382	3	US-08-718-388-8	Sequence 8, Appli
945	82	7.6	19269	3	US-09-902-540-1175	Sequence 1175, Ap
c 946	82	7.6	21968	3	US-09-851-985-3	Sequence 3, Appli
947	82	7.6	22123	3	US-09-949-016-12376	Sequence 12376, A
948	82	7.6	22124	3	US-09-949-016-14666	Sequence 14666, A
949	82	7.6	22459	3	US-09-973-278-883	Sequence 883, App
c 950	82	7.6	25621	3	US-09-902-540-1253	Sequence 1253, Ap
951	82	7.6	28509	3	US-09-902-540-1240	Sequence 1240, Ap
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c 953	82	7.6	30001	2	US-08-474-933-1	Sequence 1, Appli
c 954	82	7.6	34621	3	US-09-949-002-700	Sequence 700, App
c 955	82	7.6	40653	3	US-09-949-002-640	Sequence 640, App
956	82	7.6	43267	3	US-09-949-016-17117	Sequence 17117, A
957	82	7.6	137226	3	US-09-949-016-13763	Sequence 13763, A
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c 960	81.5	7.6	533	3	US-09-542-615A-210	Sequence 210, App
c 961	81.5	7.6	533	3	US-09-606-421B-210	Sequence 210, App
c 962	81.5	7.6	533	3	US-09-466-396A-210	Sequence 210, App
c 963	81.5	7.6	533	3	US-09-476-496A-210	Sequence 210, App
c 964	81.5	7.6	533	3	US-09-630-940B-210	Sequence 210, App
c 965	81.5	7.6	533	3	US-10-007-700-210	Sequence 210, App
966	81.5	7.6	601	3	US-09-949-016-80788	Sequence 80788, A
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968	81.5	7.6	601	3	US-09-949-002-7706	Sequence 7706, Ap
969	81.5	7.6	601	3	US-09-949-002-7716	Sequence 7716, Ap
c 970	81.5	7.6	801	3	US-09-489-039A-313	Sequence 313, App
971	81.5	7.6	890	3	US-09-917-254-21	Sequence 21, Appl
972	81.5	7.6	894	3	US-09-902-540-6908	Sequence 6908, Ap
973	81.5	7.6	942	3	US-09-252-991A-10909	Sequence 10909, A
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c 975	81.5	7.6	1026	3	US-09-270-767-12480	Sequence 12480, A
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c 977	81.5	7.6	1197	3	US-09-494-921-29	Sequence 29, Appl
c 978	81.5	7.6	1197	3	US-09-734-237B-29	Sequence 29, Appl
979	81.5	7.6	1272	3	US-09-902-540-8799	Sequence 8799, Ap
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c 981	81.5	7.6	1278	3	US-09-252-991A-11277	Sequence 11277, A
982	81.5	7.6	1377	3	US-09-585-173B-43	Sequence 43, Appl
c 983	81.5	7.6	1623	3	US-09-252-991A-3844	Sequence 3844, Ap
984	81.5	7.6	1695	3	US-09-252-991A-1686	Sequence 1686, Ap
985	81.5	7.6	1707	3	US-09-724-797-15	Sequence 15, Appl
c 986	81.5	7.6	1722	3	US-09-902-540-9668	Sequence 9668, Ap
c 987	81.5	7.6	1740	3	US-09-252-991A-1492	Sequence 1492, Ap
c 988	81.5	7.6	1806	3	US-09-252-991A-11213	Sequence 11213, A
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990	81.5	7.6	1929	3	US-09-899-642A-1	Sequence 1, Appli
991	81.5	7.6	2218	2	US-08-985-090-4	Sequence 4, Appli
992	81.5	7.6	2218	3	US-09-165-543-31	Sequence 31, Appl
993	81.5	7.6	2262	2	US-07-689-008-3	Sequence 3, Appli
c 994	81.5	7.6	2457	3	US-09-016-434-1106	Sequence 1106, Ap
c 995	81.5	7.6	2590	3	US-09-620-312D-67	Sequence 67, Appl
996	81.5	7.6	2700	3	US-09-891-053-5	Sequence 5, Appli
997	81.5	7.6	3050	3	US-10-104-047-262	Sequence 262, App
998	81.5	7.6	3089	3	US-10-104-047-914	Sequence 914, App
999	81.5	7.6	3232	3	US-09-333-214-3	Sequence 3, Appli
1000	81.5	7.6	3244	3	US-09-165-543-4	Sequence 4, Appli
1001	81.5	7.6	3322	3	US-10-104-047-373	Sequence 373, App
1002	81.5	7.6	3743	3	US-10-104-047-273	Sequence 273, App
1003	81.5	7.6	4167	3	US-09-252-991A-3666	Sequence 3666, Ap
c1004	81.5	7.6	4213	3	US-09-711-619-8	Sequence 8, Appli
1005	81.5	7.6	4235	3	US-09-949-016-4975	Sequence 4975, Ap
1006	81.5	7.6	5069	3	US-09-902-540-591	Sequence 591, App
1007	81.5	7.6	5176	3	US-09-182-024A-1	Sequence 1, Appli
1008	81.5	7.6	5299	3	US-09-902-540-645	Sequence 645, App
1009	81.5	7.6	6566	3	US-09-902-540-734	Sequence 734, App
c1010	81.5	7.6	6827	3	US-09-711-619-7	Sequence 7, Appli
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1012	81.5	7.6	7553	3	US-09-902-540-8197	Sequence 8197, Ap
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1016	81.5	7.6	10391	3	US-09-902-540-958	Sequence 958, App
1017	81.5	7.6	14555	3	US-09-902-540-1096	Sequence 1096, Ap
c1018	81.5	7.6	17472	3	US-09-949-016-12217	Sequence 12217, A
c1019	81.5	7.6	17476	3	US-09-949-016-16865	Sequence 16865, A
1020	81.5	7.6	22357	3	US-09-949-002-779	Sequence 779, App
1021	81.5	7.6	22357	3	US-09-949-002-780	Sequence 780, App
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1028	81.5	7.6	44377	2	US-08-804-198-1	Sequence 1, Appli
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1031	81.5	7.6	72048	3	US-09-949-002-684	Sequence 684, App
1032	81.5	7.6	76962	3	US-09-949-016-17482	Sequence 17482, A
1033	81.5	7.6	126237	3	US-09-949-016-16674	Sequence 16674, A
1034	81.5	7.6	126237	3	US-09-949-016-16675	Sequence 16675, A
1035	81.5	7.6	146307	3	US-09-949-016-14881	Sequence 14881, A
1036	81.5	7.6	146307	3	US-09-949-016-14882	Sequence 14882, A
1037	81.5	7.6	146307	3	US-09-949-016-14883	Sequence 14883, A
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1039	81.5	7.6	146307	3	US-09-949-016-14885	Sequence 14885, A
1040	81.5	7.6	146307	3	US-09-949-016-14886	Sequence 14886, A
1041	81.5	7.6	146307	3	US-09-949-016-14887	Sequence 14887, A
1042	81.5	7.6	146307	3	US-09-949-016-14888	Sequence 14888, A
1043	81.5	7.6	148405	3	US-09-949-016-11747	Sequence 11747, A
1044	81.5	7.6	148405	3	US-09-949-016-12835	Sequence 12835, A
1045	81.5	7.6	148405	3	US-09-949-016-12836	Sequence 12836, A
1046	81.5	7.6	148405	3	US-09-949-016-12837	Sequence 12837, A
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1050	81	7.5	1053	3	US-09-252-991A-11337	Sequence 11337, A
1051	81	7.5	1059	3	US-09-902-540-8429	Sequence 8429, Ap
c1052	81	7.5	1119	3	US-09-894-844-53	Sequence 53, Appl
1053	81	7.5	1299	3	US-09-252-991A-5223	Sequence 5223, Ap
1054	81	7.5	1344	3	US-09-902-540-5946	Sequence 5946, Ap
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c1056	81	7.5	1356	2	US-08-520-519-5	Sequence 5, Appli
c1057	81	7.5	1356	3	US-09-039-798-5	Sequence 5, Appli
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c1059	81	7.5	1417	2	US-08-520-519-4	Sequence 4, Appli
c1060	81	7.5	1417	3	US-09-039-798-4	Sequence 4, Appli
c1061	81	7.5	1417	3	US-09-016-434-1403	Sequence 1403, Ap
1062	81	7.5	1428	3	US-09-252-991A-16235	Sequence 16235, A
1063	81	7.5	1479	3	US-09-252-991A-7048	Sequence 7048, Ap
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c1065	81	7.5	1498	2	US-08-520-519-6	Sequence 6, Appli
c1066	81	7.5	1498	3	US-09-039-798-6	Sequence 6, Appli
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c1070	81	7.5	1724	3	US-09-333-279-1	Sequence 1, Appli
c1071	81	7.5	1724	3	US-09-631-780-1	Sequence 1, Appli
c1072	81	7.5	1724	3	US-09-934-289A-14	Sequence 14, Appl
c1073	81	7.5	1724	6	PCT-US96-12374-1	Sequence 1, Appli
1074	81	7.5	1806	3	US-09-252-991A-5253	Sequence 5253, Ap
1075	81	7.5	1908	3	US-09-417-197-124	Sequence 124, App
c1076	81	7.5	1910	3	US-09-310-463-13	Sequence 13, Appl
c1077	81	7.5	1910	3	US-08-842-248A-13	Sequence 13, Appl
c1078	81	7.5	1910	3	US-09-949-016-894	Sequence 894, App
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1080	81	7.5	1958	3	US-09-949-016-1420	Sequence 1420, Ap
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1082	81	7.5	2025	3	US-09-506-859-1	Sequence 1, Appli
1083	81	7.5	2025	6	PCT-US95-15428-1	Sequence 1, Appli
c1084	81	7.5	2187	3	US-09-252-991A-7042	Sequence 7042, Ap
1085	81	7.5	2325	3	US-09-252-991A-218	Sequence 218, App
c1086	81	7.5	2511	3	US-09-774-528-123	Sequence 123, App
c1087	81	7.5	2511	3	US-10-120-988-123	Sequence 123, App
1088	81	7.5	2620	2	US-08-459-194-1	Sequence 1, Appli
1089	81	7.5	2620	2	US-07-968-953-1	Sequence 1, Appli
1090	81	7.5	2620	3	US-09-047-645-1	Sequence 1, Appli
1091	81	7.5	2707	2	US-08-709-874A-9	Sequence 9, Appli
1092	81	7.5	2707	3	US-09-104-382-9	Sequence 9, Appli
1093	81	7.5	2707	3	US-09-833-555-9	Sequence 9, Appli
c1094	81	7.5	2784	3	US-09-252-991A-194	Sequence 194, App
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1096	81	7.5	2922	3	US-09-252-991A-4815	Sequence 4815, Ap
1097	81	7.5	2946	3	US-09-252-991A-227	Sequence 227, App
1098	81	7.5	2993	3	US-09-949-016-5836	Sequence 5836, Ap
1099	81	7.5	3345	3	US-09-894-998A-49	Sequence 49, Appl
1100	81	7.5	3345	3	US-10-237-551-49	Sequence 49, Appl
1101	81	7.5	3345	3	US-10-237-551-189	Sequence 189, App
1102	81	7.5	3402	3	US-09-252-991A-1374	Sequence 1374, Ap
1103	81	7.5	3438	3	US-10-104-047-521	Sequence 521, App
c1104	81	7.5	3687	3	US-09-252-991A-1193	Sequence 1193, Ap

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1106	81	7.5	4047	3	US-09-999-201B-3	Sequence 3, Appli
1107	81	7.5	4047	3	US-10-281-673A-3	Sequence 3, Appli
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c1109	81	7.5	4266	3	US-09-252-991A-1234	Sequence 1234, Ap
1110	81	7.5	4695	2	US-08-231-193A-57	Sequence 57, Appl
1111	81	7.5	4695	2	US-08-486-273A-57	Sequence 57, Appl
1112	81	7.5	4695	3	US-08-940-086A-57	Sequence 57, Appl
1113	81	7.5	4695	3	US-08-940-035A-57	Sequence 57, Appl
1114	81	7.5	4695	3	US-08-935-105A-57	Sequence 57, Appl
1115	81	7.5	4695	3	US-09-648-797-57	Sequence 57, Appl
1116	81	7.5	4695	3	US-09-386-123-57	Sequence 57, Appl
1117	81	7.5	4695	3	US-10-038-937-57	Sequence 57, Appl
1118	81	7.5	4695	3	US-10-007-747-57	Sequence 57, Appl
1119	81	7.5	4695	3	US-09-945-901-57	Sequence 57, Appl
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1123	81	7.5	8037	3	US-09-774-528-209	Sequence 209, App
1124	81	7.5	8037	3	US-10-120-988-209	Sequence 209, App
1125	81	7.5	8379	3	US-09-949-016-5683	Sequence 5683, Ap
1126	81	7.5	10023	3	US-09-252-991A-6997	Sequence 6997, Ap
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1129	81	7.5	10838	3	US-09-902-540-1013	Sequence 1013, Ap
c1130	81	7.5	10892	3	US-09-902-540-962	Sequence 962, App
c1131	81	7.5	10968	3	US-09-867-753-3	Sequence 3, Appli
c1132	81	7.5	11732	3	US-09-902-540-1061	Sequence 1061, Ap
c1133	81	7.5	16265	3	US-09-902-540-1126	Sequence 1126, Ap
c1134	81	7.5	18686	3	US-09-902-540-1206	Sequence 1206, Ap
1135	81	7.5	18722	3	US-09-949-016-15892	Sequence 15892, A
1136	81	7.5	30172	3	US-09-949-002-660	Sequence 660, App
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1139	81	7.5	42898	3	US-09-949-016-15904	Sequence 15904, A
c1140	81	7.5	48318	3	US-09-949-016-15717	Sequence 15717, A
c1141	81	7.5	49407	3	US-09-949-016-12532	Sequence 12532, A
c1142	81	7.5	49408	3	US-09-949-016-17045	Sequence 17045, A
c1143	81	7.5	49487	3	US-09-949-016-15721	Sequence 15721, A
1144	81	7.5	57280	3	US-09-949-016-11796	Sequence 11796, A
1145	81	7.5	57280	3	US-09-949-016-12843	Sequence 12843, A
1146	81	7.5	57280	3	US-09-949-016-12844	Sequence 12844, A
1147	81	7.5	57280	3	US-09-949-016-12846	Sequence 12846, A
1148	81	7.5	57280	3	US-09-949-016-13542	Sequence 13542, A
1149	81	7.5	57280	3	US-09-949-016-13543	Sequence 13543, A
1150	81	7.5	57280	3	US-09-949-016-13544	Sequence 13544, A
1151	81	7.5	57280	3	US-09-949-016-13545	Sequence 13545, A
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1154	81	7.5	57280	3	US-09-949-016-14635	Sequence 14635, A
1155	81	7.5	57280	3	US-09-949-016-14636	Sequence 14636, A
1156	81	7.5	57280	3	US-09-949-016-14637	Sequence 14637, A
1157	81	7.5	57280	3	US-09-949-016-14638	Sequence 14638, A
1158	81	7.5	57280	3	US-09-949-016-14639	Sequence 14639, A
1159	81	7.5	57280	3	US-09-949-016-14640	Sequence 14640, A
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1162	81	7.5	136058	3	US-09-949-016-12565	Sequence 12565, A
1163	81	7.5	136480	3	US-09-949-016-17064	Sequence 17064, A
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1165	80.5	7.5	651	3	US-09-949-016-2335	Sequence 2335, Ap
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1167	80.5	7.5	765	3	US-09-252-991A-6200	Sequence 6200, Ap
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1169	80.5	7.5	864	3	US-09-180-271-1	Sequence 1, Appli
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c1171	80.5	7.5	957	3	US-09-902-540-4213	Sequence 4213, Ap
c1172	80.5	7.5	1045	3	US-09-602-777A-219	Sequence 219, App
c1173	80.5	7.5	1066	3	US-09-602-777A-217	Sequence 217, App
1174	80.5	7.5	1074	3	US-09-516-914-16	Sequence 16, Appl
1175	80.5	7.5	1152	3	US-09-252-991A-6038	Sequence 6038, Ap
c1176	80.5	7.5	1185	3	US-09-252-991A-11261	Sequence 11261, A
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1178	80.5	7.5	1281	3	US-09-902-540-2838	Sequence 2838, Ap
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c1180	80.5	7.5	1371	3	US-10-029-180-23	Sequence 23, Appl
c1181	80.5	7.5	1380	3	US-09-902-540-6690	Sequence 6690, Ap
1182	80.5	7.5	1395	3	US-09-252-991A-10988	Sequence 10988, A
1183	80.5	7.5	1455	3	US-09-902-540-5175	Sequence 5175, Ap
c1184	80.5	7.5	1458	3	US-09-252-991A-14586	Sequence 14586, A
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1186	80.5	7.5	1536	3	US-09-252-991A-3483	Sequence 3483, Ap
1187	80.5	7.5	1566	3	US-09-489-039A-6221	Sequence 6221, Ap
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1195	80.5	7.5	1956	3	US-08-867-352-20	Sequence 20, Appl
1196	80.5	7.5	2088	3	US-10-104-047-1629	Sequence 1629, Ap
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1215	80.5	7.5	4120	2	US-08-316-950-11	Sequence 11, Appl
1216	80.5	7.5	4120	6	PCT-US95-12642-11	Sequence 11, Appl
1217	80.5	7.5	4190	3	US-08-924-345-1	Sequence 1, Appli
1218	80.5	7.5	4296	2	US-08-316-950-15	Sequence 15, Appl
1219	80.5	7.5	4296	6	PCT-US95-12642-15	Sequence 15, Appl
1220	80.5	7.5	4352	2	US-08-316-950-16	Sequence 16, Appl
1221	80.5	7.5	4352	6	PCT-US95-12642-16	Sequence 16, Appl
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1224	80.5	7.5	5464	3	US-09-902-540-717	Sequence 717, App
1225	80.5	7.5	6047	2	US-08-316-950-12	Sequence 12, Appl
1226	80.5	7.5	6047	6	PCT-US95-12642-12	Sequence 12, Appl
1227	80.5	7.5	6155	3	US-09-902-540-737	Sequence 737, App
1228	80.5	7.5	6171	2	US-08-316-950-17	Sequence 17, Appl
1229	80.5	7.5	6171	6	PCT-US95-12642-17	Sequence 17, Appl
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1231	80.5	7.5	6407	2	US-07-977-630-2	Sequence 2, Appli
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1249	80.5	7.5	23847	3	US-09-902-540-1177	Sequence 1177, Ap
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1257	80.5	7.5	43555	3	US-09-949-016-13993	Sequence 13993, A
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1267	80.5	7.5	97196	3	US-09-949-016-16971	Sequence 16971, A
1268	80.5	7.5	112874	3	US-09-949-016-13180	Sequence 13180, A
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1277	80	7.5	943	3	US-09-762-027-7	Sequence 7, Appli
1278	80	7.5	1047	3	US-09-252-991A-6949	Sequence 6949, Ap
1279	80	7.5	1170	3	US-09-252-991A-5049	Sequence 5049, Ap
1280	80	7.5	1263	3	US-09-252-991A-13340	Sequence 13340, A
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1283	80	7.5	1444	2	US-08-258-442-9	Sequence 9, Appli
1284	80	7.5	1444	2	US-08-328-809-4	Sequence 4, Appli
1285	80	7.5	1444	3	US-08-866-840-4	Sequence 4, Appli
1286	80	7.5	1444	6	PCT-US92-11107-9	Sequence 9, Appli
1287	80	7.5	1476	3	US-09-252-991A-15187	Sequence 15187, A
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1290	80	7.5	1793	3	US-09-521-109-1	Sequence 1, Appli
1291	80	7.5	1793	3	US-09-562-332-1	Sequence 1, Appli
1292	80	7.5	1793	3	US-09-949-016-565	Sequence 565, App
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1294	80	7.5	1800	3	US-09-949-016-2041	Sequence 2041, Ap
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1296	80	7.5	1860	3	US-09-252-991A-5014	Sequence 5014, Ap
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1300	80	7.5	1898	3	US-08-866-840-3	Sequence 3, Appli
1301	80	7.5	1898	6	PCT-US92-11107-8	Sequence 8, Appli
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1307	80	7.5	2839	2	US-08-258-442-6	Sequence 6, Appli
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1310	80	7.5	2839	3	US-08-866-840-1	Sequence 1, Appli
1311	80	7.5	2839	6	PCT-US92-11107-6	Sequence 6, Appli
1312	80	7.5	2959	3	US-09-023-655-141	Sequence 141, App
1313	80	7.5	3205	3	US-09-976-594-171	Sequence 171, App
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1315	80	7.5	3486	3	US-09-976-594-1018	Sequence 1018, Ap
1316	80	7.5	3508	3	US-09-902-540-8762	Sequence 8762, Ap
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1318	80	7.5	3777	3	US-09-902-540-2062	Sequence 2062, Ap
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1320	80	7.5	3966	3	US-09-949-016-2932	Sequence 2932, Ap
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1322	80	7.5	4843	3	US-09-949-016-15195	Sequence 15195, A
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1324	80	7.5	4979	3	US-09-949-016-238	Sequence 238, App
c1325	80	7.5	7617	3	US-09-902-540-881	Sequence 881, App
1326	80	7.5	7960	3	US-09-949-016-15600	Sequence 15600, A
1327	80	7.5	8205	3	US-09-949-016-1500	Sequence 1500, Ap
1328	80	7.5	8220	3	US-09-949-016-932	Sequence 932, App
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1330	80	7.5	8607	3	US-09-949-016-13657	Sequence 13657, A
1331	80	7.5	8608	3	US-09-949-016-12184	Sequence 12184, A
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c1333	80	7.5	9162	3	US-09-973-278-841	Sequence 841, App
1334	80	7.5	9333	3	US-09-902-540-930	Sequence 930, App
1335	80	7.5	11726	3	US-09-949-016-16968	Sequence 16968, A
1336	80	7.5	11726	3	US-09-949-016-16969	Sequence 16969, A
1337	80	7.5	11726	3	US-09-949-002-834	Sequence 834, App
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1339	80	7.5	13018	3	US-09-949-016-14767	Sequence 14767, A
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1341	80	7.5	13090	3	US-09-949-016-14372	Sequence 14372, A
1342	80	7.5	13160	3	US-09-949-016-12520	Sequence 12520, A
1343	80	7.5	13197	3	US-09-949-016-16223	Sequence 16223, A
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c1345	80	7.5	13284	3	US-09-949-016-15900	Sequence 15900, A
c1346	80	7.5	13821	3	US-09-949-016-13690	Sequence 13690, A
c1347	80	7.5	14101	3	US-09-902-540-1080	Sequence 1080, Ap
c1348	80	7.5	15132	3	US-09-902-540-1137	Sequence 1137, Ap
1349	80	7.5	15239	2	US-08-390-878-17	Sequence 17, Appl
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1351	80	7.5	16340	3	US-09-949-002-583	Sequence 583, App
1352	80	7.5	16341	3	US-09-949-016-14579	Sequence 14579, A
1353	80	7.5	16341	3	US-09-949-016-14580	Sequence 14580, A
1354	80	7.5	16341	3	US-09-949-002-747	Sequence 747, App
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c1356	80	7.5	17584	3	US-09-949-016-13743	Sequence 13743, A
1357	80	7.5	19598	3	US-09-902-540-1143	Sequence 1143, Ap
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1359	80	7.5	23856	3	US-09-949-016-15732	Sequence 15732, A
1360	80	7.5	28054	3	US-09-902-540-1248	Sequence 1248, Ap
1361	80	7.5	31623	3	US-09-949-016-15945	Sequence 15945, A
1362	80	7.5	34794	3	US-09-713-678-39	Sequence 39, Appl
1363	80	7.5	34794	3	US-10-164-085-39	Sequence 39, Appl
1364	80	7.5	34794	3	US-09-573-740A-82	Sequence 82, Appl
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1367	80	7.5	44393	3	US-09-949-016-14944	Sequence 14944, A
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1369	80	7.5	44393	3	US-09-949-016-14946	Sequence 14946, A
1370	80	7.5	44393	3	US-09-949-016-16911	Sequence 16911, A
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c1372	80	7.5	53337	3	US-09-949-016-16092	Sequence 16092, A
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c1378	80	7.5	68750	3	US-09-568-486-1	Sequence 1, Appli
c1379	80	7.5	68750	3	US-09-568-472-1	Sequence 1, Appli
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1382	80	7.5	95122	3	US-09-949-016-17235	Sequence 17235, A
1383	80	7.5	100928	3	US-09-949-016-16926	Sequence 16926, A
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1385	80	7.5	120727	3	US-09-949-016-15788	Sequence 15788, A
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c1387	80	7.5	133157	3	US-09-949-016-12541	Sequence 12541, A
1388	79.5	7.4	601	3	US-09-949-016-76457	Sequence 76457, A
c1389	79.5	7.4	601	3	US-09-949-016-203528	Sequence 203528,
1390	79.5	7.4	705	3	US-09-902-540-7841	Sequence 7841, Ap
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1393	79.5	7.4	894	3	US-09-949-016-1145	Sequence 1145, Ap
1394	79.5	7.4	894	3	US-09-949-016-5310	Sequence 5310, Ap
1395	79.5	7.4	899	3	US-09-548-130-4	Sequence 4, Appli
c1396	79.5	7.4	899	3	US-09-548-130-5	Sequence 5, Appli

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1398	79.5	7.4	1128	3	US-09-902-540-2422	Sequence 2422, Ap
1399	79.5	7.4	1242	3	US-09-902-540-6329	Sequence 6329, Ap
c1400	79.5	7.4	1284	3	US-09-902-540-7113	Sequence 7113, Ap
1401	79.5	7.4	1344	3	US-08-705-771-8	Sequence 8, Appli
1402	79.5	7.4	1344	3	US-09-417-540-8	Sequence 8, Appli
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1406	79.5	7.4	1705	3	US-09-227-595-23	Sequence 23, Appl
1407	79.5	7.4	1705	3	US-08-595-590B-23	Sequence 23, Appl
1408	79.5	7.4	1765	3	US-09-799-451-275	Sequence 275, App
c1409	79.5	7.4	1859	3	US-09-286-529-19	Sequence 19, Appl
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1412	79.5	7.4	2007	3	US-09-252-991A-4970	Sequence 4970, Ap
1413	79.5	7.4	2009	2	US-08-109-106-5	Sequence 5, Appli
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1415	79.5	7.4	2290	3	US-10-104-047-8	Sequence 8, Appli
1416	79.5	7.4	2304	3	US-09-799-451-340	Sequence 340, App
1417	79.5	7.4	2341	3	US-09-902-540-395	Sequence 395, App
c1418	79.5	7.4	2447	3	US-09-949-016-5274	Sequence 5274, Ap
1419	79.5	7.4	2558	3	US-09-902-540-6342	Sequence 6342, Ap
1420	79.5	7.4	2560	3	US-09-902-540-400	Sequence 400, App
1421	79.5	7.4	2748	3	US-09-949-016-2211	Sequence 2211, Ap
1422	79.5	7.4	2763	3	US-09-575-081B-11	Sequence 11, Appl
1423	79.5	7.4	2770	3	US-09-227-595-29	Sequence 29, Appl
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1427	79.5	7.4	3633	3	US-09-221-017B-362	Sequence 362, App
1428	79.5	7.4	4079	3	US-09-016-434-1237	Sequence 1237, Ap
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c1437	79.5	7.4	6317	2	US-08-920-812-21	Sequence 21, Appl
c1438	79.5	7.4	6317	2	US-08-920-827-21	Sequence 21, Appl
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1446	79.5	7.4	8134	3	US-09-949-016-13953	Sequence 13953, A
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1454	79.5	7.4	9564	3	US-09-902-540-1026	Sequence 1026, Ap
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1472	79.5	7.4	37292	3	US-09-949-016-15382	Sequence 15382, A
c1473	79.5	7.4	39243	3	US-09-949-016-12316	Sequence 12316, A
c1474	79.5	7.4	39243	3	US-09-949-016-15443	Sequence 15443, A
1475	79.5	7.4	49301	3	US-09-949-016-16296	Sequence 16296, A
1476	79.5	7.4	55827	3	US-09-813-133A-3	Sequence 3, Appli
1477	79.5	7.4	55827	3	US-10-212-877-3	Sequence 3, Appli
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c1479	79.5	7.4	64047	3	US-09-949-016-15781	Sequence 15781, A
c1480	79.5	7.4	67002	3	US-09-949-016-16803	Sequence 16803, A
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c1487	79.5	7.4	240157	3	US-09-949-016-16264	Sequence 16264, A
c1488	79.5	7.4	536165	3	US-09-214-808-1	Sequence 1, Appli
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c1492	79	7.4	601	3	US-09-949-016-192797	Sequence 192797,
c1493	79	7.4	601	3	US-09-949-016-192798	Sequence 192798,
c1494	79	7.4	601	3	US-09-949-016-202984	Sequence 202984,
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c1496	79	7.4	628	3	US-09-533-559-2840	Sequence 2840, Ap
1497	79	7.4	720	2	US-08-722-349-4	Sequence 4, Appli
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c1499	79	7.4	720	3	US-09-252-991A-4679	Sequence 4679, Ap
1500	79	7.4	729	3	US-09-902-540-8856	Sequence 8856, Ap

ALIGNMENTS

RESULT 1
US-09-747-259-3
; Sequence 3, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Fong,Sherman
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Li,Hanzhong
; APPLICANT: Hillan,Kenneth
; APPLICANT: Tumas,Daniel
; APPLICANT: VanLookeren,Menno
; APPLICANT: Vandlen,Richard
; APPLICANT: Watanabe,Colin
; APPLICANT: Williams,P.Mickey
; APPLICANT: Wood,William
; APPLICANT: Yansura,Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02

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;  PRIOR APPLICATION NUMBER: US 60/191,007
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/07532
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/15264
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: US 60/213,087
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: US 09/644,848
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/242,837
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: PCT/US00/30873
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: US 60/253,646
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 3
;   LENGTH: 1047
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-747-259-3

Alignment Scores:
Pred. No.:              1.63e-93        Length:         1047
Score:                  1073.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-09-854-280-3 (1-197) x US-09-747-259-3 (1-1047)

Qy          1 MetThrLeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHis 20
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Db         50 ATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCAT 109

Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
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Db        110 GACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAG 169

Qy         41 GluLeuProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGln 60
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Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Db        470 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 529

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RESULT 2
US-09-949-016-5387
; Sequence 5387, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5387
;   LENGTH: 1047
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5387

Alignment Scores:
Pred. No.:              1.63e-93        Length:         1047
Score:                  1073.00         Matches:        197
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     3               Gaps:           0

US-09-854-280-3 (1-197) x US-09-949-016-5387 (1-1047)

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Qy         21 AspProSerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGlu 40
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Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
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Qy         81 ArgProSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAsp 100
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RESULT 3
US-09-480-297A-22
; Sequence 22, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)..(705)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (166)..()
; OTHER INFORMATION:
US-09-480-297A-22

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Score:	1073.00	Matches:	197
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
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US-09-854-280-3 (1-197) x US-09-480-297A-22 (1-1107)

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Qy         61 AlaLeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        101 ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArgTyr 120
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Qy        121 ProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 CCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGC 534

Qy        141 ArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 CGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGC 594

Qy        161 ArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACC 654

Qy        181 GluPheIleHisValProValGlyCysThrCysValLeuProArgSerVal 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 GAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTG 705
```

RESULT 4
US-09-949-016-17129
; Sequence 17129, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17129
; LENGTH: 5884
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17129

Alignment Scores:

Pred. No.:	1.58e-82	Length:	5884
Score:	969.00	Matches:	195
Percent Similarity:	53.7%	Conservative:	0
Best Local Similarity:	53.7%	Mismatches:	0
Query Match:	90.3%	Indels:	168
DB:	3	Gaps:	1

US-09-854-280-3 (1-197) x US-09-949-016-17129 (1-5884)

```
Qy          3 LeuLeuProGlyLeuLeuPheLeuThrTrpLeuHisThrCysLeuAlaHisHisAspPro 22
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2389 CTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCC 2448

Qy         23 SerLeuArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGluGluLeu 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2449 TCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTG 2508

Qy         43 ProLeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeu 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2509 CCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTG 2568

Qy         63 ProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArgPro 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2569 CCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCC 2628

Qy         83 SerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGluAlaAspThrHis 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2629 TCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCAC 2688

Qy        103 GlnArgSerIleSerProTrpArgTyrArg---------------------------- 112
              ||||||||||||||||||||||||||||
Db       2689 CAGCGCTCCATCTCACCCTGGAGATACCGGTGAGGACCTGGGGATTCCGCTGTGGCGTGG 2748

Qy        112 ------------------------------------------------------------ 112
```

```
Db       2749 GGCTGCCCCTCCCCTGGCGGGGCCCTGACTGCCCGGAGAGCTCTCTGGGCCTTGGCGGTT 2808

Qy        112 ------------------------------------------------------------ 112

Db       2809 CTCACCTGTCAAGTGGGCGTGGCCACCTGAGCTCCCTCCCTCCGGCCCTCCTGACCTGGA 2868

Qy        112 ------------------------------------------------------------ 112

Db       2869 CGGCTGAGCTGCTGCTTGCGGCTGGCCGTGCCCTGCCTCCCACTGTCCTAGGTGGCCAGG 2928

Qy        112 ------------------------------------------------------------ 112

Db       2929 GTCCCCTGGGGAAATTCTGGGCCCGTCACCTGAGCTCCTGCAGAAGTGGGGCTGGGTGAT 2988

Qy        112 ------------------------------------------------------------ 112

Db       2989 GAAGTGGAAGGGAGGCTCCTAGAGGCCTCCGGACCCTGCTCTGTGCTCTTGGAGGGCCCT 3048

Qy        112 ------------------------------------------------------------ 112

Db       3049 GGGGAGACGTGGATTACCACCACATGTGAGCCCGACTGCACCCCAAGCCCGTGTGGCTCA 3108

Qy        112 ------------------------------------------------------------ 112

Db       3109 GCCCTCGCTGCCTCAGGTCCTATCCTGAGTACACGGAGAGGGGCCCTGAGGGGAGAGGGG 3168

Qy        113 ----------------------------------------------------------ValAsp 114
                                                                       ||||||
Db       3169 CCTCCAGGAGGACAGGGTAGGGCCAGAGACTCACTGTGCACCCCGTCCCGCAGTGTGGAC 3228

Qy        115 ThrAspGluAspArgTyrProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCys 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3229 ACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGT 3288

Qy        135 IleAspAlaArgThrGlyArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSer 154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3289 ATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGC 3348

Qy        155 LeuLeuValLeuArgArgArgProCysSerArgAspGlySerGlyLeuProThrProGly 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3349 CTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGG 3408

Qy        175 AlaPheAlaPheHisThrGluPheIleHisValProValGlyCysThrCysValLeuPro 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3409 GCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCC 3468

Qy        195 ArgSerVal 197
              |||||||||
Db       3469 CGTTCAGTG 3477
```

RESULT 5
US-09-949-016-188268/c
; Sequence 188268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188268
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-188268

Alignment Scores:

Pred. No.:	1.48e-34	Length:	601
Score:	454.00	Matches:	85
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	42.3%	Indels:	0
DB:	3	Gaps:	0

US-09-854-280-3 (1-197) x US-09-949-016-188268 (1-601)

```
Qy        113 ValAspThrAspGluAspArgTyrProGlnLysLeuAlaPheAlaGluCysLeuCysArg 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGA 349

Qy        133 GlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLeuAsnSerValArgLeuLeu 152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCYGTGCGGCTGCTC 289

Qy        153 GlnSerLeuLeuValLeuArgArgArgProCysSerArgAspGlySerGlyLeuProThr 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACA 229

Qy        173 ProGlyAlaPheAlaPheHisThrGluPheIleHisValProValGlyCysThrCysVal 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 CCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTG 169

Qy        193 LeuProArgSerVal 197
              ||||||||||||||
Db        168 CTGCCCCGTTCAGTG 154
```

RESULT 6
US-09-480-297A-19
; Sequence 19, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (281)..(281)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (367)..(367)
; OTHER INFORMATION: unkonwn amino
; NAME/KEY: misc_feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (462)..(462)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc_feature
; LOCATION: (468)..(468)
; OTHER INFORMATION: unknown amino
US-09-480-297A-19

Alignment Scores:

Pred. No.:	7.12e-34	Length:	521
Score:	446.00	Matches:	83

```
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            41.6%           Indels:        0
DB:                     3               Gaps:          0

US-09-854-280-3 (1-197) x US-09-480-297A-19 (1-521)

Qy        114 AspThrAspGluAspArgTyrProGlnLysLeuAlaPheAlaGluCysLeuCysArgGly 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGC 60

Qy        134 CysIleAspAlaArgThrGlyArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGln 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAG 120

Qy        154 SerLeuLeuValLeuArgArgArgProCysSerArgAspGlySerGlyLeuProThrPro 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCT 180

Qy        174 GlyAlaPheAlaPheHisThrGluPheIleHisValProValGlyCysThrCysValLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTG 240

Qy        194 ProArgSer 196
              |||||||||
Db        241 CCCCGTTCA 249

RESULT 7
US-09-480-297A-20
; Sequence 20, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 521
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(369)
;   OTHER INFORMATION:
;   NAME/KEY: misc_feature
;   LOCATION: (281)..(281)
;   OTHER INFORMATION: unkown amino
;   NAME/KEY: misc_feature
;   LOCATION: (367)..(367)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (437)..(437)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (462)..(462)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (468)..(468)
;   OTHER INFORMATION: unknown amino
US-09-480-297A-20

Alignment Scores:
Pred. No.:              7.12e-34        Length:        521
Score:                  446.00          Matches:       83
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            41.6%           Indels:        0
DB:                     3               Gaps:          0

US-09-854-280-3 (1-197) x US-09-480-297A-20 (1-521)

Qy        114 AspThrAspGluAspArgTyrProGlnLysLeuAlaPheAlaGluCysLeuCysArgGly 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGC 60

Qy        134 CysIleAspAlaArgThrGlyArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGln 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAG 120

Qy        154 SerLeuLeuValLeuArgArgArgProCysSerArgAspGlySerGlyLeuProThrPro 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCT 180

Qy        174 GlyAlaPheAlaPheHisThrGluPheIleHisValProValGlyCysThrCysValLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTG 240

Qy        194 ProArgSer 196
              |||||||||
Db        241 CCCCGTTCA 249

RESULT 8
US-09-949-016-188267/c
; Sequence 188267, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188267
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-188267

Alignment Scores:
Pred. No.:              1.63e-10        Length:        601
Score:                  203.00          Matches:       37
Percent Similarity:     100.0%          Conservative:  0
Best Local Similarity:  100.0%          Mismatches:    0
Query Match:            18.9%           Indels:        0
DB:                     3               Gaps:          0

US-09-854-280-3 (1-197) x US-09-949-016-188267 (1-601)

Qy         76 ArgGlyArgHisGluArgProSerAlaThrThrGlnCysProValLeuArgProGluGlu 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 AGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAG 541

Qy         96 ValLeuGluAlaAspThrHisGlnArgSerIleSerProTrpArgTyrArg 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    ·   540 GTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCTGGAGATACCGG 490

RESULT 9
US-09-480-297A-7
; Sequence 7, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
```

```
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 1385
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (59)..(664)
;   OTHER INFORMATION:
;   NAME/KEY: mat_peptide
;   LOCATION: (110)..()
;   OTHER INFORMATION:
US-09-480-297A-7

Alignment Scores:
Pred. No.:              6.34e-10        Length:         1385
Score:                  202.00          Matches:        61
Percent Similarity:     40.2%           Conservative:   17
Best Local Similarity:  31.4%           Mismatches:     61
Query Match:            18.8%           Indels:         55
DB:                     3               Gaps:           6

US-09-854-280-3 (1-197) x US-09-480-297A-7 (1-1385)

Qy         44 LeuGlyGlnAlaProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeuPro 63
Db         19 CTCGCTCAGTCGGCTTCTCGGTCCAAGTCCCCGGGTCTGGATGCTGGTAGCCGGCTTCCT 78

Qy         64 -ValAlaLeuValSerSerLeuGluAlaAlaSerHisArg---GlyArgHisGluArgPr 82
Db         79 GCTGGCGCTGCCGCCGAGCTGGGCCGCGGGCGCCCCGAGGGCGGGCAGG------CGCCC 132

Qy         82 oSerAlaThrThrGlnCysProValLeuArgProGluGluValLeuGlu---------- 98
Db        133 CGCGCGGCCGCGGGGCTGC---GCGGACCGGCCGGAGGAGCTACTGGAGCAGCTGTACGG 189

Qy         98 ---------------------------------------------------------- 98
Db        190 GCGCCTGGCGGCCGGCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGA 249

Qy         99 ----------------------------------------AlaAsp------------- 100
Db        250 GCAGGCGCGCAACGCGAGCTGCCCGGCAGGGGGCAGGCCCGCCGACCGCCGCTTCCGGCC 309

Qy        101 ----ThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspAr 119
Db        310 GCCCACCAACCTGCGCAGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAG 369

Qy        119 gTyrProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgTh 139
Db        370 GTACCCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTT 429

Qy        139 rGlyArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuAr 159
Db        430 CGGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCG 489

Qy        159 gArgArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHi 179
Db        490 CCGCACCCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCC------------- 535

Qy        179 sThrGluPheIleHisValProValGlyCysThrCysVal 192
Db        536 -------TACGTCACCATCCCCGTGGGCTGCACCTGCGTC 568
```

```
RESULT 10
US-09-747-259-7
; Sequence 7, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Chen, Jian
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Li,Hanzhong
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  VanLookeren,Menno
;  APPLICANT:  Vandlen,Richard
;  APPLICANT:  Watanabe,Colin
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William
;  APPLICANT:  Yansura,Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P1(US)
;  CURRENT APPLICATION NUMBER: US/09/747,259
;  CURRENT FILING DATE:  2000-12-20
;  PRIOR APPLICATION NUMBER: US 09/311,832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US 60/172,096
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: PCT/US99/31274
;  PRIOR FILING DATE: 1999-12-30
;  PRIOR APPLICATION NUMBER: US 60/175,481
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/191,007
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/07532
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/15264
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: US 60/213,087
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: US 09/644,848
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/242,837
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: PCT/US00/30873
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: US 60/253,646
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 7
;   LENGTH: 1754
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-747-259-7

Alignment Scores:
Pred. No.:              9.77e-10        Length:         1754
Score:                  201.50          Matches:        58
Percent Similarity:     38.5%           Conservative:   14
Best Local Similarity:  31.0%           Mismatches:     65
Query Match:            18.8%           Indels:         50
DB:                     3               Gaps:           5
```

```
US-09-854-280-3 (1-197) x US-09-747-259-7 (1-1754)

Qy          25 ArgGlyHisProHisSerHisGlyThrProHisCysTyrSerAlaGluGluLeuProLeu 44
               ||||||  |||             |||       :::           |||
Db          45 CGCGGGCGCCCCCAGGGCGGGCAGGCGCCCCGCGCGGCCGCGGGGCTGCGCGGACCGGCC 104

Qy          45 GlyGlnAla-------------------------------------------------Pro 48
               |||  |||                                                  |||
Db         105 GGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGGCCGGCGTGCTCAGTGCCTTCCA 164

Qy          49 ProHisLeuLeuAlaArgGlyAlaLysTrpGly------GlnAlaLeuProValAlaLeu 66
               ||||||     |||      |||      |||      :::   ||||||
Db         165 CCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCGAGCTGCCC--------- 215

Qy          67 ValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArgProSerAlaThrThr 86
                                    ||||||:::     ||||||
Db         216 ------------------------GGCAGGGGGCAGGCCCGGCGACCGCCG--------- 242

Qy          87 GlnCysProValLeuArgProGluGluValLeuGluAla-AspThrHisGlnArgSerIl 106
                                   |||   |||    |||:::   ||||||::
Db         243 ----------------------------CTTCCGGCCGCCCACCAACCTGCGCAGCGT 272

Qy         106 eSerProTrpArgTyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAlaPh 126
               :|||||||||  ||||||:::     |||      |||||||||:::   |||
Db         273 GTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGGTACCCCAGGTACCTGCCTGA 332

Qy         126 eAlaGluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLe 146
               |||   ||||||||||||||||||:::          |||  |||
Db         333 AGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCGGCGAGGAGGACGTGCGCTT 392

Qy         146 uAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgProCysSerArgAs 166
               |||      :::          :::||||||||||||   |||
Db         393 CCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCGCCGCACCCCCGCCTGCGCCGG 452

Qy         166 pGlySerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIleHisValPr 186
               |||      :::   |||                          ::::::   :::||
Db         453 CGGCCGTTCCGTCTACACCGAGGCC--------------------TACGTCACCATCCC 491

Qy         186 oValGlyCysThrCysVal 192
               ||||||||||||||||||
Db         492 CGTGGGCTGCACCTGCGTC 510

RESULT 11
US-09-480-297A-17
; Sequence 17, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(507)
;   OTHER INFORMATION:
;   NAME/KEY: mat_peptide
;   LOCATION: (49)..()
;   OTHER INFORMATION:
US-09-480-297A-17

Alignment Scores:

Pred. No.:              2.9e-09     Length:          985
Score:                  193.00      Matches:         58
Percent Similarity:     40.1%       Conservative:    17
Best Local Similarity:  31.0%       Mismatches:      86
Query Match:            18.0%       Indels:          26
DB:                     3           Gaps:            6

US-09-854-280-3 (1-197) x US-09-480-297A-17 (1-985)

Qy          10 LeuThrTrpLeuHisThrCysLeuAlaHisHisAspProSerLeuArgGlyHisProHis 29
               :::  :::|||      :::      |||      |||||||||
Db          13 GTTGCATTCTTGGCAATGATCGTGGGAACCCACACCGTCAGCTTGCGGATCCAGGAGGGC 72

Qy          30 SerHisGlyThrProHisCysTyrSerAlaGluGluLeuProLeuGlyGlnAlaProPro 49
                        |||  |||      ::::::|||            |||   ||||||
Db          73 TGCAGTCACTTGCCCAGCTGCTGCCCCAGCAAAGAG------------CAAGAACCCCCG 120

Qy          50 HisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeuProValAlaLeuValSerSer 69
                                    |||||                 |||   ||||||
Db         121 GAG---------GAGTGGCTGAAGTGGAGCTCT-----------GCATCTGTGTCCCCC 159

Qy          70 LeuGluAlaAlaSerHisArgGlyArgHisGluArgProSerAlaThrThrGlnCysPro 89
               |||      ||||||          |||          |||:::          |||
Db         160 CCAGAGCCTCTGAGCCACACCCACCACGCAGAATCCTGCAGGGCCAGCAAGGATGGCCCC 219

Qy          90 ValLeuArgProGluGluValLeuGluAlaAspThrHisGlnArgSerIleSerProTrp 109
               :::                              :::   |||:::||||||||||||
Db         220 CTC-------------------------------AACAGCAGGGCCATCTCTCCTTGG 246

Qy         110 ArgTyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAlaPheAlaGluCys 129
                   |||   :::|||   |||   :::|||   ||||||   |||      |||   |||
Db         247 AGCTATGAGTTGGACAGGGACTTGAATCGGGTCCCCCAGGACCTGTACCACGCTCGATGC 306

Qy         130 LeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLeu---AsnSer 148
               ||||||     |||:::     :::||||||                |||   ||||||
Db         307 CTGTGCCCACACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCGCTGGGCAACTCC 366

Qy         149 ValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgProCysSerArgAspGlySer 168
               |||  |||      :::      |||      ||||||||||||      :::
Db         367 GTCCCACTTTACCACAACCAGACGGTCTTCTACCGGCGGCCATGCCATGGTGAGGAAGGT 426

Qy         169 GlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIleHisValProValGly 188
                     |||         :::                          |||   :::
Db         427 ---------ACCCATCGCCGCTACTGCTTGGAGCGCAGGCTCTACCGAGTCTCCTTGGCT 477

Qy         189 CysThrCysValLeuProArg 195
               |||   ||||||  ||||||
Db         478 TGTGTGTGTGTGCGGCCCCGG 498

RESULT 12
US-09-836-385-3
; Sequence 3, Application US/09836385
; Patent No. 6676939
; GENERAL INFORMATION:
;  APPLICANT: Hurst, Stephen D.
;  APPLICANT:  Zurawski, Sandra M.
;  APPLICANT:  Rennick, Donna M.
;  TITLE OF INVENTION: Cytokine Uses; Compositions; Methods
;  FILE REFERENCE: DX01088K
;  CURRENT APPLICATION NUMBER: US/09/836,385
;  CURRENT FILING DATE:  2001-04-17
;  PRIOR APPLICATION NUMBER: US 60/198,488
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: rodent
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(507)
;   NAME/KEY: mat_peptide
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;   LOCATION: (49)..(507)
US-09-836-385-3

Alignment Scores:
Pred. No.:              2.9e-09         Length:         985
Score:                  193.00          Matches:        58
Percent Similarity:     40.1%           Conservative:   17
Best Local Similarity:  31.0%           Mismatches:     86
Query Match:            18.0%           Indels:         26
DB:                     3               Gaps:           6

US-09-854-280-3 (1-197) x US-09-836-385-3 (1-985)

Qy         10 LeuThrTrpLeuHisThrCysLeuAlaHisHisAspProSerLeuArgGlyHisProHis 29
              :::   :::|||         :::       |||      |||||||||
Db         13 GTTGCATTCTTGGCAATGATCGTGGGAACCCACACCGTCAGCTTGCGGATCCAGGAGGGC 72

Qy         30 SerHisGlyThrProHisCysTyrSerAlaGluGluLeuProLeuGlyGlnAlaProPro 49
                     |||   |||      ::::::|||             |||   ||||||
Db         73 TGCAGTCACTTGCCCAGCTGCTGCCCCAGCAAAGAG-----------CAAGAACCCCCG 120

Qy         50 HisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeuProValAlaLeuValSerSer 69
                           ||||||                  |||   ||||||
Db        121 GAG---------GAGTGGCTGAAGTGGAGCTCT-----------GCATCTGTGTCCCCC 159

Qy         70 LeuGluAlaAlaSerHisArgGlyArgHisGluArgProSerAlaThrThrGlnCysPro 89
                 |||      ||||||          |||      |||:::          |||
Db        160 CCAGAGCCTCTGAGCCACACCCACCACGCAGAATCCTGCAGGGCCAGCAAGGATGGCCCC 219

Qy         90 ValLeuArgProGluGluValLeuGluAlaAspThrHisGlnArgSerIleSerProTrp 109
              :::                                 :::   |||:::||||||||||||
Db        220 CTC---------------------------------AACAGCAGGGCCATCTCTCCTTGG 246

Qy        110 ArgTyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAlaPheAlaGluCys 129
                 |||   :::|||   |||   :::|||   ||||||   |||      |||   |||
Db        247 AGCTATGAGTTGGACAGGGACTTGAATCGGGTCCCCCAGGACCTGTACCACGCTCGATGC 306

Qy        130 LeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLeu---AsnSer 148
              ||||||      |||:::      :::||||||                |||   ||||||
Db        307 CTGTGCCCACACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCGCTGGGCAACTCC 366

Qy        149 ValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgProCysSerArgAspGlySer 168
              |||   |||      :::      |||      ||||||||||      :::
Db        367 GTCCCACTTTACCACAACCAGACGGTCTTCTACCGGCGGCCATGCCATGGTGAGGAAGGT 426

Qy        169 GlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIleHisValProValGly 188
                       |||      :::                              |||   :::
Db        427 ---------ACCCATCGCCGCTACTGCTTGGAGCGCAGGCTCTACCGAGTCTCCTTGGCT 477

Qy        189 CysThrCysValLeuProArg 195
              |||   ||||||   ||||||
Db        478 TGTGTGTGTGTGCGGCCCCGG 498

RESULT 13
US-09-480-297A-11
; Sequence 11, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 1143
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(615)
;   OTHER INFORMATION:
;   NAME/KEY: mat_peptide
;   LOCATION: (73)..()
;   OTHER INFORMATION:
US-09-480-297A-11

Alignment Scores:
Pred. No.:              3.96e-09        Length:         1143
Score:                  192.50          Matches:        52
Percent Similarity:     45.5%           Conservative:   14
Best Local Similarity:  35.9%           Mismatches:     51
Query Match:            17.9%           Indels:         30
DB:                     3               Gaps:           4

US-09-854-280-3 (1-197) x US-09-480-297A-11 (1-1143)

Qy         48 ProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeuProValAlaLeuVal 67
              |||||||||      ||||||  |||::   |||   |||:::|||   |||
Db        183 CCACCACACGCTGCAGCTCGGGCCGCGCGAGCAGGCGC-GCAATGCCAGCTGCC------ 235

Qy         68 SerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArgProSerAlaThrThrGln 87
                                                  ||||||   |||
Db        236 ------------------------------------CGGCCGGGGGCAGGGCCGCCG 256

Qy         88 CysProValLeuArgProGluGluValLeuGluAlaAspThrHisGlnArgSerIleSer 107
                          ||||||                  |||:::   ||||||:::|||
Db        257 ACCGCCGC-TTCCGGCCA-----------------CCCACCAACCTGCGCAGCGTGTCG 297

Qy        108 ProTrpArgTyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAlaPheAla 127
              ||||||  ||||||:::      |||      |||:::|||:::   |||      |||
Db        298 CCCTGGGCGTACAGGATTTCCTACGACCCTGCTCGCTTTCCGAGGTACCTGCCCGAAGCC 357

Qy        128 GluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLeuAsn 147
                 ||||||||||||||||||:::      .      |||   |||
Db        358 TACTGCCTGTGCCGAGGCTGCCTGACCGGGCTCTACGGGGAGGAGGACTTCCGCTTTCGC 417

Qy        148 SerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgProCysSerArgAspGly 167
              |||      :::             :::||||||||||||                |||
Db        418 AGCACACCCGTCTTCTCTCCAGCCGTGGTGCTGCGGCGCACAGCGGCCTGCGCGGGCGGC 477

Qy        168 SerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIleHisValProVal 187
                    :::             :::|||   |||      :::|||   :::||||||
Db        478 CGCTCTGTG-------------TACGCCGAACAC------TACATCACCATCCCGGTG 516

Qy        188 GlyCysThrCysVal 192
              ||||||||||||||
Db        517 GGCTGCACCTGCGTG 531

RESULT 14
US-09-724-864-2
; Sequence 2, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
;  APPLICANT:  Watson, James D
;  APPLICANT:  Murison, James G.
;  TITLE OF INVENTION:  Polynucleotides, polypeptides expressed
;  TITLE OF INVENTION:  by the polynucleotides and methods for their use.
;  FILE REFERENCE:  11000.1050U1
;  CURRENT APPLICATION NUMBER: US/09/724,864
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER:  U.S. No. 6380362 60/171,678
;  PRIOR FILING DATE:  1999-12-23
;  NUMBER OF SEQ ID NOS:  72
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1258
;   TYPE: DNA
;   ORGANISM: Mouse
US-09-724-864-2
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Alignment Scores:
Pred. No.:                4.52e-09        Length:         1258
Score:                    192.50          Matches:        52
Percent Similarity:       45.5%           Conservative:   14
Best Local Similarity:    35.9%           Mismatches:     51
Query Match:              17.9%           Indels:         30
DB:                       3               Gaps:           4

US-09-854-280-3 (1-197) x US-09-724-864-2 (1-1258)

Qy          48 ProProHisLeuLeuAlaArgGlyAlaLysTrpGlyGlnAlaLeuProValAlaLeuVal 67
               ||||||||       ||||||  |||:::  |||  |||:::|||  |||
Db         275 CCACCACACGCTGCAGCTCGGGCCGCGCGAGCAGGCGC-GCAATGCCAGCTGCC------ 327

Qy          68 SerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArgProSerAlaThrThrGln 87
                                                    ||||||  |||
Db         328 ------------------------------------CGGCCGGGGGCAGGGCCGCCG 348

Qy          88 CysProValLeuArgProGluGluValLeuGluAlaAspThrHisGlnArgSerIleSer 107
                     ||||||                    |||:::  ||||||:::|||
Db         349 ACCGCCGC-TTCCGGCCA----------------CCCACCAACCTGCGCAGCGTGTCG 389

Qy         108 ProTrpArgTyrArgValAspThrAspGluAspArgTyrProGlnLysLeuAlaPheAla 127
               ||||||  ||||||:::     |||     |||:::|||:::  |||     |||
Db         390 CCCTGGGCGTACAGGATTTCCTACGACCCTGCTCGCTTTCCGAGGTACCTGCCCGAAGCC 449

Qy         128 GluCysLeuCysArgGlyCysIleAspAlaArgThrGlyArgGluThrAlaAlaLeuAsn 147
                ||||||||||||||||:::           |||   |||
Db         450 TACTGCCTGTGCCGAGGCTGCCTGACCGGGCTCTACGGGGAGGAGGACTTCCGCTTTCGC 509

Qy         148 SerValArgLeuLeuGlnSerLeuLeuValLeuArgArgArgProCysSerArgAspGly 167
               |||     :::           :::||||||||||||                 |||
Db         510 AGCACACCCGTCTTCTCTCCAGCCGTGGTGCTGCGGCGCACAGCGGCCTGCGCGGGCGGC 569

Qy         168 SerGlyLeuProThrProGlyAlaPheAlaPheHisThrGluPheIleHisValProVal 187
                   :::             :::|||  |||     :::|||  :::||||||
Db         570 CGCTCTGTG-------------TACGCCGAACAC-----TACATCACCATCCCGGTG 608

Qy         188 GlyCysThrCysVal 192
               ||||||||||||||
Db         609 GGCTGCACCTGCGTG 623

RESULT 15
US-09-480-297A-5
; Sequence 5, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 454
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(453)
;   OTHER INFORMATION:
US-09-480-297A-5

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Score:                    192.00          Matches:        45
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Best Local Similarity:    33.8%           Mismatches:     61
Query Match:              17.9%           Indels:         10
DB:                       3               Gaps:           4

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Qy          62 LeuProValAlaLeuValSerSerLeuGluAlaAlaSerHisArgGlyArgHisGluArg 81
               |||          ::::::|||:::                        |||      |||:::
Db          46 CTGGCGGCCGGCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAG 105

Qy          82 ProSerAlaThrThrGlnCysProVal---LeuArgPro---GluGluValLeuGluAla 99
                  :::             ||||||        ||||||   :::
Db         106 ---GCGCGCAACGCGAGCTGCCCGGCAGGGGGCAGGCCCGCCGACCGCCGCTTCCGGACG 162

Qy         100 AspThrHisGlnArgSerIleSerProTrpArgTyrArgValAspThrAspGluAspArg 119
                  |||:::  ||||||:::|||||||||  ||||||:::     |||      |||
Db         163 CCCACCAACCTGCGCAGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGG 222

Qy         120 TyrProGlnLysLeuAlaPheAlaGluCysLeuCysArgGlyCysIleAspAlaArgThr 139
               ||||||:::  |||      |||  |||||||||||||||||:::
Db         223 TACCCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTC 282

Qy         140 GlyArgGluThrAlaAlaLeuAsnSerValArgLeuLeuGlnSerLeuLeuValLeuArg 159
               |||  |||                |||     :::           :::|||||||||
Db         283 GGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCGC 342

Qy         160 ArgArgProCysSerArgAspGlySerGlyLeuProThrProGlyAlaPheAlaPheHis 179
               |||  |||          |||      :::  |||
Db         343 CGCACCCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCC-------------- 387

Qy         180 ThrGluPheIleHisValProValGlyCysThrCysVal 192
                     ::::::  :::||||||||||||||||||||
Db         388 ------TACGTCACCATCCCCGTGGGCTGCACCTGCGTC 420

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GenCore version 5.1.7
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Run on: April 30, 2006, 23:13:21 ; Search time 794 Seconds
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Perfect score: 1073
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1073	100.0	594	3	US-09-854-280-17	Sequence 17, Appl
2	1073	100.0	594	3	US-09-854-208-17	Sequence 17, Appl
3	1073	100.0	1047	3	US-09-854-280-4	Sequence 4, Appli
4	1073	100.0	1047	3	US-09-854-208-4	Sequence 4, Appli
5	1073	100.0	1047	3	US-09-874-503-3	Sequence 3, Appli
6	1073	100.0	1047	3	US-09-747-259-3	Sequence 3, Appli
8	1073	100.0	1047	3	US-09-908-827-3	Sequence 3, Appli
11	1073	100.0	1047	5	US-10-000-157-3	Sequence 3, Appli
170	1073	100.0	1047	5	US-10-036-160-10	Sequence 10, Appl
482	1073	100.0	1047	6	US-10-174-587-447	Sequence 447, App
517	1073	100.0	1047	6	US-10-410-927-3	Sequence 3, Appli
519	1073	100.0	1047	6	US-10-410-374-3	Sequence 3, Appli
520	1073	100.0	1047	6	US-10-410-552-3	Sequence 3, Appli
521	1073	100.0	1047	6	US-10-458-442-3	Sequence 3, Appli
539	1073	100.0	1047	7	US-10-408-385-3	Sequence 3, Appli
544	1073	100.0	1047	8	US-10-884-091-10	Sequence 10, Appl
545	1073	100.0	1047	9	US-10-491-997-21	Sequence 21, Appl
549	1073	100.0	1067	3	US-09-731-816-28	Sequence 28, Appl
550	1073	100.0	1067	3	US-09-320-713-28	Sequence 28, Appl
551	1073	100.0	1067	5	US-10-153-770-28	Sequence 28, Appl
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553	1073	100.0	1107	6	US-10-366-791-22	Sequence 22, Appl
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Job time : 812 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2006, 00:17:03 ; Search time 1990 Seconds
(without alignments)
402.045 Million cell updates/sec

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Searched: 9295968 seqs, 2030634719 residues

Total number of hits satisfying chosen parameters: 18591936

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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SUMMARIES

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		26	176	16.4	644	18	US-11-251-011-22	Sequence 22, Appl
		27	176	16.4	644	18	US-11-251-012-22	Sequence 22, Appl
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		31	173	16.1	535	18	US-11-103-195-159	Sequence 159, App
		32	173	16.1	692	17	US-11-157-049-11	Sequence 11, Appl
		33	173	16.1	923	17	US-11-150-533-15	Sequence 15, Appl
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		38	161	15.0	1874	17	US-11-150-533-13	Sequence 13, Appl
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		48	157.5	14.7	540	17	US-11-128-061-4373	Sequence 4373, Ap
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		57	135.5	12.6	497	17	US-11-157-049-13	Sequence 13, Appl
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		81	98	9.1	3252	10	US-10-955-054A-7	Sequence 7, Appli
c		82	98	9.1	61739	11	US-10-330-773-320	Sequence 320, App
c		83	97.5	9.1	1781	7	US-09-925-065A-669699	Sequence 669699,
c		84	97.5	9.1	2383	7	US-09-925-065A-700817	Sequence 700817,
c		85	97.5	9.1	2383	7	US-09-925-065A-700818	Sequence 700818,
c		86	97.5	9.1	2383	7	US-09-925-065A-700819	Sequence 700819,
		87	97	9.0	1958	18	US-11-096-568A-26982	Sequence 26982, A

	88	97	9.0	3048	11	US-10-501-035-100 Sequence 100, App
	89	96.5	9.0	1161	7	US-09-925-065A-279687 Sequence 279687,
c	90	96.5	9.0	6134	17	US-11-128-061-515 Sequence 515, App
c	91	96.5	9.0	6134	17	US-11-128-049-515 Sequence 515, App
c	92	96	8.9	1451	7	US-09-925-065A-25296 Sequence 25296, A
c	93	96	8.9	1451	11	US-10-301-480-126533 Sequence 126533,
c	94	96	8.9	1451	12	US-10-301-480-739942 Sequence 739942,
c	95	95.5	8.9	1374	18	US-11-096-568A-2065 Sequence 2065, Ap
	96	95.5	8.9	73930	11	US-10-330-773-554 Sequence 554, App
c	97	95	8.9	998	12	US-10-301-480-592707 Sequence 592707,
c	98	95	8.9	998	12	US-10-301-480-1206116 Sequence 1206116,
	99	95	8.9	3310	18	US-11-072-512-545 Sequence 545, App
c	100	95	8.9	4030	10	US-10-750-185-45743 Sequence 45743, A
c	101	95	8.9	4030	10	US-10-750-623-45743 Sequence 45743, A
	102	95	8.9	13650	10	US-10-995-561-155 Sequence 155, App
	103	95	8.9	13711	10	US-10-995-561-154 Sequence 154, App
	104	95	8.9	14194	10	US-10-995-561-153 Sequence 153, App
c	105	95	8.9	14619	17	US-11-128-061-745 Sequence 745, App
c	106	95	8.9	14619	17	US-11-128-049-745 Sequence 745, App
c	107	94.5	8.8	2005	18	US-11-072-512-288 Sequence 288, App
c	108	94	8.8	591	7	US-09-925-065A-934850 Sequence 934850,
	109	94	8.8	599	7	US-09-925-065A-921535 Sequence 921535,
c	110	94	8.8	600	7	US-09-925-065A-928031 Sequence 928031,
c	111	94	8.8	1608	10	US-10-750-185-50981 Sequence 50981, A
c	112	94	8.8	1608	10	US-10-750-623-50981 Sequence 50981, A
	113	93.5	8.7	628	7	US-09-925-065A-46958 Sequence 46958, A
	114	93.5	8.7	628	11	US-10-301-480-148196 Sequence 148196,
	115	93.5	8.7	628	12	US-10-301-480-761605 Sequence 761605,
c	116	93	8.7	1516	10	US-10-750-185-27476 Sequence 27476, A
c	117	93	8.7	1516	10	US-10-750-623-27476 Sequence 27476, A
	118	93	8.7	1669	18	US-11-072-512-1679 Sequence 1679, Ap
c	119	92.5	8.6	86361	10	US-10-995-561-13364 Sequence 13364, A
	120	92	8.6	1248	11	US-10-301-480-28137 Sequence 28137, A
	121	92	8.6	1248	12	US-10-301-480-641546 Sequence 641546,
	122	92	8.6	2295	10	US-10-750-185-30057 Sequence 30057, A
	123	92	8.6	2295	10	US-10-750-623-30057 Sequence 30057, A
	124	92	8.6	2860	18	US-11-072-512-951 Sequence 951, App
	125	92	8.6	86081	10	US-10-995-561-13246 Sequence 13246, A
	126	91.5	8.5	1314	10	US-10-750-185-37379 Sequence 37379, A
	127	91.5	8.5	1314	10	US-10-750-623-37379 Sequence 37379, A
	128	91.5	8.5	2046	17	US-11-136-527-3994 Sequence 3994, Ap
	129	91.5	8.5	13818	10	US-10-995-561-13505 Sequence 13505, A
	130	91.5	8.5	38449	10	US-10-995-561-13358 Sequence 13358, A
	131	91	8.5	725	10	US-10-750-185-43087 Sequence 43087, A
	132	91	8.5	725	10	US-10-750-623-43087 Sequence 43087, A
c	133	91	8.5	4729	13	US-10-204-639-100 Sequence 100, App
c	134	91	8.5	153376	17	US-11-121-086-5 Sequence 5, Appli
c	135	91	8.5	172543	17	US-11-121-086-6 Sequence 6, Appli
c	136	90.5	8.4	15231	18	US-11-036-196-1780 Sequence 1780, Ap
c	137	90.5	8.4	15234	17	US-11-136-527-306 Sequence 306, App
	138	90.5	8.4	191684	17	US-11-121-086-2 Sequence 2, Appli
c	139	90	8.4	707	11	US-10-301-480-91140 Sequence 91140, A
c	140	90	8.4	707	12	US-10-301-480-704549 Sequence 704549,
c	141	90	8.4	978	12	US-10-301-480-538151 Sequence 538151,
c	142	90	8.4	978	12	US-10-301-480-1151560 Sequence 1151560,
	143	90	8.4	1248	11	US-10-301-480-28135 Sequence 28135, A
	144	90	8.4	1248	11	US-10-301-480-28138 Sequence 28138, A
	145	90	8.4	1248	12	US-10-301-480-641544 Sequence 641544,
	146	90	8.4	1248	12	US-10-301-480-641547 Sequence 641547,
	147	90	8.4	1261	7	US-09-925-065A-72028 Sequence 72028, A
	148	90	8.4	1261	7	US-09-925-065A-72029 Sequence 72029, A
	149	90	8.4	1261	11	US-10-301-480-173267 Sequence 173267,
	150	90	8.4	1261	11	US-10-301-480-173268 Sequence 173268,
	151	90	8.4	1261	12	US-10-301-480-786676 Sequence 786676,
	152	90	8.4	1261	12	US-10-301-480-786677 Sequence 786677,
c	153	90	8.4	5543	11	US-10-330-773-393 Sequence 393, App
c	154	90	8.4	8083	11	US-10-330-773-391 Sequence 391, App
c	155	90	8.4	29454	11	US-10-330-773-951 Sequence 951, App
c	156	90	8.4	191331	17	US-11-112-908-20 Sequence 20, Appl
	157	89.5	8.3	702	12	US-10-301-480-569318 Sequence 569318,
	158	89.5	8.3	702	12	US-10-301-480-1182727 Sequence 1182727,
c	159	89.5	8.3	998	12	US-10-301-480-549700 Sequence 549700,
c	160	89.5	8.3	998	12	US-10-301-480-1163109 Sequence 1163109,
c	161	89.5	8.3	6377	17	US-11-069-834-57 Sequence 57, Appl
c	162	89.5	8.3	6442	17	US-11-069-834-55 Sequence 55, Appl
	163	89.5	8.3	8252	17	US-11-011-332A-150 Sequence 150, App
	164	89	8.3	1656	17	US-11-012-668-13 Sequence 13, Appl
	165	89	8.3	1944	10	US-10-995-561-476 Sequence 476, App
	166	89	8.3	2977	10	US-10-995-561-477 Sequence 477, App
	167	89	8.3	2986	10	US-10-995-561-478 Sequence 478, App
	168	89	8.3	3043	17	US-11-183-914-14 Sequence 14, Appl
	169	89	8.3	3106	10	US-10-995-561-479 Sequence 479, App
	170	89	8.3	3205	10	US-10-995-561-475 Sequence 475, App
c	171	89	8.3	110608	10	US-10-775-169-193 Sequence 193, App
	172	89	8.3	113193	13	US-10-478-943D-1 Sequence 1, Appli
c	173	88.5	8.2	893	10	US-10-453-372-1181 Sequence 1181, Ap
c	174	88.5	8.2	1278	11	US-10-978-927-21 Sequence 21, Appl
c	175	88.5	8.2	1278	11	US-10-978-927-22 Sequence 22, Appl
c	176	88.5	8.2	1278	11	US-10-978-927-26 Sequence 26, Appl
c	177	88.5	8.2	1278	11	US-10-978-927-38 Sequence 38, Appl
c	178	88.5	8.2	1278	11	US-10-507-692-4 Sequence 4, Appli
c	179	88.5	8.2	1295	11	US-10-978-927-25 Sequence 25, Appl
c	180	88.5	8.2	1345	11	US-10-978-927-40 Sequence 40, Appl
c	181	88.5	8.2	1692	10	US-10-750-185-26692 Sequence 26692, A
c	182	88.5	8.2	1692	10	US-10-750-623-26692 Sequence 26692, A
c	183	88.5	8.2	1729	11	US-10-978-927-23 Sequence 23, Appl
c	184	88.5	8.2	4778	17	US-11-082-154A-70 Sequence 70, Appl
c	185	88.5	8.2	5285	13	US-10-524-823-1 Sequence 1, Appli
c	186	88.5	8.2	5505	13	US-10-524-823-2 Sequence 2, Appli
c	187	88.5	8.2	5510	17	US-11-082-154A-71 Sequence 71, Appl
c	188	88.5	8.2	5855	10	US-10-161-408-27 Sequence 27, Appl
c	189	88.5	8.2	5855	17	US-11-082-154A-112 Sequence 112, App
c	190	88.5	8.2	5855	17	US-11-082-154A-127 Sequence 127, App
	191	88.5	8.2	6119	17	US-11-082-154A-126 Sequence 126, App
c	192	88.5	8.2	7600	17	US-11-082-154A-115 Sequence 115, App
c	193	88.5	8.2	7631	17	US-11-082-154A-116 Sequence 116, App
c	194	88.5	8.2	8521	17	US-11-082-154A-123 Sequence 123, App
c	195	88.5	8.2	8851	17	US-11-082-154A-124 Sequence 124, App
c	196	88.5	8.2	9080	17	US-11-082-154A-110 Sequence 110, App
c	197	88.5	8.2	10474	17	US-11-082-154A-125 Sequence 125, App
c	198	88.5	8.2	12263	11	US-10-978-927-19 Sequence 19, Appl
c	199	88.5	8.2	22855	17	US-11-124-368A-2908 Sequence 2908, Ap
	200	88	8.2	684	18	US-11-224-663-741 Sequence 741, App
	201	88	8.2	684	18	US-11-224-525-741 Sequence 741, App
c	202	88	8.2	1433	10	US-10-953-392-15 Sequence 15, Appl
c	203	88	8.2	1433	10	US-10-954-147-15 Sequence 15, Appl
c	204	88	8.2	1753	7	US-09-925-065A-88104 Sequence 88104, A
c	205	88	8.2	1753	11	US-10-301-480-189345 Sequence 189345,
c	206	88	8.2	1753	12	US-10-301-480-802754 Sequence 802754,
c	207	88	8.2	2079	11	US-10-301-480-39499 Sequence 39499, A
c	208	88	8.2	2079	11	US-10-301-480-39500 Sequence 39500, A
c	209	88	8.2	2079	11	US-10-301-480-39501 Sequence 39501, A
c	210	88	8.2	2079	12	US-10-301-480-652908 Sequence 652908,
c	211	88	8.2	2079	12	US-10-301-480-652909 Sequence 652909,
c	212	88	8.2	2079	12	US-10-301-480-652910 Sequence 652910,
c	213	88	8.2	2886	11	US-10-301-480-98063 Sequence 98063, A
c	214	88	8.2	2886	12	US-10-301-480-711472 Sequence 711472,
c	215	88	8.2	165911	18	US-11-114-798-52 Sequence 52, Appl
	216	88	8.2	168516	17	US-11-121-086-3 Sequence 3, Appli
c	217	88	8.2	181172	17	US-11-121-086-41 Sequence 41, Appl
	218	87.5	8.2	623	7	US-09-925-065A-653611 Sequence 653611,
c	219	87.5	8.2	636	7	US-09-925-065A-519027 Sequence 519027,
c	220	87.5	8.2	765	7	US-09-925-065A-25103 Sequence 25103, A
c	221	87.5	8.2	765	11	US-10-301-480-126340 Sequence 126340,
c	222	87.5	8.2	765	12	US-10-301-480-739749 Sequence 739749,
	223	87.5	8.2	1195	11	US-10-301-480-27999 Sequence 27999, A
	224	87.5	8.2	1195	12	US-10-301-480-641408 Sequence 641408,
	225	87.5	8.2	1273	11	US-10-301-480-28650 Sequence 28650, A
	226	87.5	8.2	1273	12	US-10-301-480-642059 Sequence 642059,
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	228	87.5	8.2	2089	18	US-11-072-512-1055 Sequence 1055, Ap
c	233	87.5	8.2	3680	18	US-11-090-729-1 Sequence 1, Appli
	234	87.5	8.2	34875	10	US-10-775-169-316 Sequence 316, App
	235	87.5	8.2	34875	11	US-10-501-035-71 Sequence 71, Appl
	236	87.5	8.2	67858	10	US-10-995-561-13484 Sequence 13484, A
c	237	87.5	8.2	90120	11	US-10-330-773-390 Sequence 390, App

c 238	87.5	8.2	159434	11	US-10-330-773-707	Sequence 707, App
239	87.5	8.2	164810	17	US-11-121-086-4	Sequence 4, Appli
c 240	87.5	8.2	168516	17	US-11-121-086-3	Sequence 3, Appli
241	87.5	8.2	172543	17	US-11-121-086-6	Sequence 6, Appli
c 242	87	8.1	600	10	US-10-750-185-1501	Sequence 1501, Ap
c 243	87	8.1	600	10	US-10-750-623-1501	Sequence 1501, Ap
244	87	8.1	619	7	US-09-925-065A-229486	Sequence 229486,
c 245	87	8.1	752	12	US-10-301-480-591644	Sequence 591644,
c 246	87	8.1	752	12	US-10-301-480-1205053	Sequence 1205053,
247	87	8.1	1104	10	US-10-750-185-62272	Sequence 62272, A
248	87	8.1	1104	10	US-10-750-623-62272	Sequence 62272, A
249	87	8.1	2240	18	US-11-072-512-2	Sequence 2, Appli
250	87	8.1	2804	13	US-10-455-772-195	Sequence 195, App
c 251	87	8.1	2817	18	US-11-051-720-17	Sequence 17, Appl
c 252	87	8.1	2817	18	US-11-043-806-45	Sequence 45, Appl
253	87	8.1	3400	13	US-10-455-772-205	Sequence 205, App
c 254	87	8.1	40987	10	US-10-995-561-13503	Sequence 13503, A
255	87	8.1	67088	10	US-10-995-561-13365	Sequence 13365, A
c 256	86.5	8.1	678	7	US-09-925-065A-519026	Sequence 519026,
257	86.5	8.1	995	12	US-10-301-480-565247	Sequence 565247,
258	86.5	8.1	995	12	US-10-301-480-1178656	Sequence 1178656,
259	86.5	8.1	1033	10	US-10-750-185-57550	Sequence 57550, A
260	86.5	8.1	1033	10	US-10-750-623-57550	Sequence 57550, A
c 261	86.5	8.1	1400	18	US-11-096-568A-15729	Sequence 15729, A
c 262	86.5	8.1	1542	18	US-11-096-568A-18558	Sequence 18558, A
c 263	86.5	8.1	2150	18	US-11-072-512-1786	Sequence 1786, Ap
264	86.5	8.1	2458	18	US-11-036-196-1451	Sequence 1451, Ap
265	86.5	8.1	3490	17	US-11-122-329-110	Sequence 110, App
266	86.5	8.1	4583	10	US-10-750-185-59929	Sequence 59929, A
267	86.5	8.1	4583	10	US-10-750-623-59929	Sequence 59929, A
c 268	86.5	8.1	7659	17	US-11-091-883-498	Sequence 498, App
269	86.5	8.1	7706	13	US-10-204-639-120	Sequence 120, App
270	86.5	8.1	7893	17	US-11-186-731-3	Sequence 3, Appli
271	86.5	8.1	8106	17	US-11-186-731-1	Sequence 1, Appli
c 272	86.5	8.1	9645	17	US-11-186-284-48	Sequence 48, Appl
c 273	86.5	8.1	9646	17	US-11-080-991-53	Sequence 53, Appl
274	86.5	8.1	23907	17	US-11-186-731-6	Sequence 6, Appli
275	86.5	8.1	24120	17	US-11-186-731-4	Sequence 4, Appli
276	86.5	8.1	73404	17	US-11-124-368A-2914	Sequence 2914, Ap
c 277	86.5	8.1	79544	11	US-10-330-773-741	Sequence 741, App
c 278	86.5	8.1	127722	11	US-10-330-773-278	Sequence 278, App
279	86	8.0	696	7	US-09-925-065A-9212	Sequence 9212, Ap
280	86	8.0	696	11	US-10-301-480-110449	Sequence 110449,
281	86	8.0	696	12	US-10-301-480-723858	Sequence 723858,
282	86	8.0	972	7	US-09-925-065A-77865	Sequence 77865, A
283	86	8.0	972	11	US-10-301-480-179104	Sequence 179104,
284	86	8.0	972	12	US-10-301-480-792513	Sequence 792513,
285	86	8.0	1184	18	US-11-096-568A-18371	Sequence 18371, A
286	86	8.0	1342	18	US-11-036-196-1961	Sequence 1961, Ap
287	86	8.0	1708	18	US-11-072-512-1901	Sequence 1901, Ap
c 288	86	8.0	1833	17	US-11-000-688-168	Sequence 168, App
289	86	8.0	2228	17	US-11-136-527-4091	Sequence 4091, Ap
290	86	8.0	2228	18	US-11-224-663-623	Sequence 623, App
291	86	8.0	2228	18	US-11-224-525-623	Sequence 623, App
292	86	8.0	2266	13	US-10-455-772-197	Sequence 197, App
c 293	86	8.0	2611	18	US-11-072-512-330	Sequence 330, App
294	86	8.0	37500	10	US-10-522-037-1	Sequence 1, Appli
c 295	86	8.0	150481	17	US-11-112-908-37	Sequence 37, Appl
c 296	86	8.0	171162	17	US-11-112-908-38	Sequence 38, Appl
c 297	85.5	8.0	610	7	US-09-925-065A-869021	Sequence 869021,
c 298	85.5	8.0	610	7	US-09-925-065A-869022	Sequence 869022,
299	85.5	8.0	1431	7	US-09-925-065A-728347	Sequence 728347,
300	85.5	8.0	1617	18	US-11-096-568A-19901	Sequence 19901, A
c 301	85.5	8.0	1943	18	US-11-072-512-1892	Sequence 1892, Ap
302	85.5	8.0	2147	10	US-10-055-877-104	Sequence 104, App
303	85.5	8.0	2162	10	US-10-055-877-112	Sequence 112, App
304	85.5	8.0	2215	7	US-09-925-065A-719943	Sequence 719943,
305	85.5	8.0	2215	7	US-09-925-065A-719944	Sequence 719944,
306	85.5	8.0	2215	7	US-09-925-065A-719945	Sequence 719945,
307	85.5	8.0	2215	7	US-09-925-065A-719946	Sequence 719946,
c 308	85.5	8.0	2230	10	US-10-750-185-60658	Sequence 60658, A
c 309	85.5	8.0	2230	10	US-10-750-623-60658	Sequence 60658, A
310	85.5	8.0	2278	10	US-10-055-877-108	Sequence 108, App
311	85.5	8.0	4663	11	US-10-912-971-1	Sequence 1, Appli
c 312	85.5	8.0	187745	17	US-11-121-086-83	Sequence 83, Appl
313	85.5	8.0	200628	17	US-11-121-086-62	Sequence 62, Appl
c 314	85	7.9	535	7	US-09-925-065A-45852	Sequence 45852, A
c 315	85	7.9	535	11	US-10-301-480-147090	Sequence 147090,
c 316	85	7.9	535	12	US-10-301-480-760499	Sequence 760499,
c 317	85	7.9	581	7	US-09-925-065A-348066	Sequence 348066,
c 318	85	7.9	581	7	US-09-925-065A-348067	Sequence 348067,
c 319	85	7.9	581	12	US-10-301-480-420237	Sequence 420237,
c 320	85	7.9	581	12	US-10-301-480-420238	Sequence 420238,
c 321	85	7.9	581	12	US-10-301-480-1033646	Sequence 1033646,
c 322	85	7.9	581	12	US-10-301-480-1033647	Sequence 1033647,
323	85	7.9	596	7	US-09-925-065A-653612	Sequence 653612,
c 324	85	7.9	605	7	US-09-925-065A-923968	Sequence 923968,
325	85	7.9	612	7	US-09-925-065A-811753	Sequence 811753,
c 326	85	7.9	620	7	US-09-925-065A-838090	Sequence 838090,
327	85	7.9	696	7	US-09-925-065A-9211	Sequence 9211, Ap
328	85	7.9	696	11	US-10-301-480-110448	Sequence 110448,
329	85	7.9	696	12	US-10-301-480-723857	Sequence 723857,
330	85	7.9	1055	10	US-10-750-185-51401	Sequence 51401, A
331	85	7.9	1055	10	US-10-750-623-51401	Sequence 51401, A
c 332	85	7.9	1450	17	US-11-124-368A-151	Sequence 151, App
c 333	85	7.9	1972	7	US-09-925-065A-728303	Sequence 728303,
c 334	85	7.9	1972	7	US-09-925-065A-728304	Sequence 728304,
c 335	85	7.9	1972	7	US-09-925-065A-728305	Sequence 728305,
c 336	85	7.9	1972	7	US-09-925-065A-728306	Sequence 728306,
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338	85	7.9	3239	18	US-11-137-807-17	Sequence 17, Appl
339	85	7.9	4299	11	US-10-912-971-9	Sequence 9, Appli
c 340	85	7.9	4835	10	US-10-055-877-53	Sequence 53, Appl
c 341	85	7.9	4835	10	US-10-453-372-881	Sequence 881, App
c 342	85	7.9	5000	10	US-10-453-372-865	Sequence 865, App
c 343	85	7.9	5000	10	US-10-453-372-883	Sequence 883, App
c 344	85	7.9	5005	10	US-10-453-372-867	Sequence 867, App
c 345	85	7.9	5005	10	US-10-453-372-885	Sequence 885, App
c 346	85	7.9	5172	10	US-10-453-372-859	Sequence 859, App
c 347	85	7.9	7319	10	US-10-055-877-45	Sequence 45, Appl
c 348	85	7.9	7319	10	US-10-453-372-871	Sequence 871, App
c 349	85	7.9	7334	10	US-10-055-877-51	Sequence 51, Appl
c 350	85	7.9	7334	10	US-10-453-372-877	Sequence 877, App
c 351	85	7.9	7337	10	US-10-055-877-43	Sequence 43, Appl
c 352	85	7.9	7337	10	US-10-453-372-869	Sequence 869, App
353	85	7.9	8250	10	US-10-453-372-769	Sequence 769, App
c 354	85	7.9	92969	11	US-10-330-773-178	Sequence 178, App
c 355	85	7.9	97081	11	US-10-330-773-957	Sequence 957, App
356	85	7.9	167891	17	US-11-121-086-14	Sequence 14, Appl
357	84.5	7.9	600	7	US-09-925-065A-487456	Sequence 487456,
358	84.5	7.9	634	7	US-09-925-065A-941437	Sequence 941437,
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362	84.5	7.9	982	12	US-10-301-480-531839	Sequence 531839,
363	84.5	7.9	982	12	US-10-301-480-1145248	Sequence 1145248,
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c 365	84.5	7.9	1464	18	US-11-096-568A-20325	Sequence 20325, A
c 366	84.5	7.9	1564	18	US-11-031-206-75	Sequence 75, Appl
c 367	84.5	7.9	2201	17	US-11-136-527-3268	Sequence 3268, Ap
c 368	84.5	7.9	2615	18	US-11-072-512-1280	Sequence 1280, Ap
c 369	84.5	7.9	3202	18	US-11-182-885-1	Sequence 1, Appli
370	84.5	7.9	4654	17	US-11-091-883-374	Sequence 374, App
371	84.5	7.9	6491	18	US-11-072-175-84	Sequence 84, Appl
c 372	84.5	7.9	81656	11	US-10-330-773-853	Sequence 853, App
373	84.5	7.9	165911	18	US-11-114-798-52	Sequence 52, Appl
374	84.5	7.9	181172	17	US-11-121-086-41	Sequence 41, Appl
375	84.5	7.9	268685	10	US-10-933-025-22	Sequence 22, Appl
376	84.5	7.9	268685	18	US-11-219-360-22	Sequence 22, Appl
c 377	84	7.8	535	7	US-09-925-065A-45851	Sequence 45851, A
c 378	84	7.8	535	11	US-10-301-480-147089	Sequence 147089,
c 379	84	7.8	535	12	US-10-301-480-760498	Sequence 760498,
c 380	84	7.8	543	7	US-09-925-065A-831150	Sequence 831150,
c 381	84	7.8	586	7	US-09-925-065A-745609	Sequence 745609,
c 382	84	7.8	593	7	US-09-925-065A-745608	Sequence 745608,
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	387	84	7.8	738	7	US-09-925-065A-942935 Sequence 942935,
	388	84	7.8	988	12	US-10-301-480-592141 Sequence 592141,
	389	84	7.8	988	12	US-10-301-480-1205550 Sequence 1205550,
	390	84	7.8	1094	17	US-11-214-199-9 Sequence 9, Appli
	391	84	7.8	1454	7	US-09-925-065A-551098 Sequence 551098,
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	393	84	7.8	1454	12	US-10-301-480-1142457 Sequence 1142457,
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	395	84	7.8	1460	10	US-10-750-623-32137 Sequence 32137, A
	396	84	7.8	1635	10	US-10-750-185-57079 Sequence 57079, A
	397	84	7.8	1635	10	US-10-750-623-57079 Sequence 57079, A
	398	84	7.8	2136	10	US-10-750-185-55747 Sequence 55747, A
	399	84	7.8	2136	10	US-10-750-623-55747 Sequence 55747, A
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c	401	84	7.8	3366	11	US-10-330-773-257 Sequence 257, App
c	402	84	7.8	4261	17	US-11-122-329-112 Sequence 112, App
c	403	84	7.8	5562	13	US-10-204-639-95 Sequence 95, Appl
c	404	84	7.8	6710	11	US-10-330-773-259 Sequence 259, App
	405	84	7.8	8689	17	US-11-136-527-2554 Sequence 2554, Ap
c	406	84	7.8	86149	11	US-10-330-773-254 Sequence 254, App
c	407	84	7.8	113193	13	US-10-478-943D-1 Sequence 1, Appli
c	408	84	7.8	415117	10	US-10-995-561-13274 Sequence 13274, A
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c	411	83.5	7.8	568	12	US-10-301-480-306099 Sequence 306099,
c	412	83.5	7.8	568	12	US-10-301-480-919508 Sequence 919508,
c	413	83.5	7.8	570	7	US-09-925-065A-220650 Sequence 220650,
c	414	83.5	7.8	586	7	US-09-925-065A-488094 Sequence 488094,
	415	83.5	7.8	600	7	US-09-925-065A-487457 Sequence 487457,
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c	417	83.5	7.8	624	7	US-09-925-065A-840332 Sequence 840332,
c	418	83.5	7.8	685	10	US-10-750-185-29906 Sequence 29906, A
c	419	83.5	7.8	685	10	US-10-750-623-29906 Sequence 29906, A
c	420	83.5	7.8	918	12	US-10-301-480-578630 Sequence 578630,
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	422	83.5	7.8	953	12	US-10-301-480-569649 Sequence 569649,
	423	83.5	7.8	953	12	US-10-301-480-1183058 Sequence 1183058,
	424	83.5	7.8	989	12	US-10-301-480-545223 Sequence 545223,
	425	83.5	7.8	989	12	US-10-301-480-1158632 Sequence 1158632,
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c	427	83.5	7.8	1506	12	US-10-301-480-704860 Sequence 704860,
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c	433	83.5	7.8	3018	10	US-10-750-185-43824 Sequence 43824, A
c	434	83.5	7.8	3018	10	US-10-750-623-43824 Sequence 43824, A
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c	436	83.5	7.8	4248	10	US-10-750-623-30707 Sequence 30707, A
c	437	83.5	7.8	6410	17	US-11-108-172-1094 Sequence 1094, Ap
c	438	83.5	7.8	10968	17	US-11-075-185-35 Sequence 35, Appl
c	439	83.5	7.8	34116	17	US-11-124-367A-5020 Sequence 5020, Ap
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	442	83.5	7.8	127340	17	US-11-112-908-35 Sequence 35, Appl
c	443	83.5	7.8	149419	17	US-11-112-908-49 Sequence 49, Appl
c	444	83.5	7.8	161726	17	US-11-112-908-48 Sequence 48, Appl
c	445	83.5	7.8	161726	17	US-11-112-908-52 Sequence 52, Appl
c	446	83.5	7.8	166111	17	US-11-112-908-47 Sequence 47, Appl
c	447	83.5	7.8	317876	10	US-10-995-561-13227 Sequence 13227, A
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	449	83	7.7	788	11	US-10-301-480-107875 Sequence 107875,
	450	83	7.7	788	12	US-10-301-480-721284 Sequence 721284,
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	453	83	7.7	908	12	US-10-301-480-739750 Sequence 739750,
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	456	83	7.7	1248	11	US-10-301-480-28136 Sequence 28136, A
	457	83	7.7	1248	12	US-10-301-480-641545 Sequence 641545,
	458	83	7.7	1375	7	US-09-925-065A-74206 Sequence 74206, A
	459	83	7.7	1375	11	US-10-301-480-175445 Sequence 175445,
	460	83	7.7	1375	12	US-10-301-480-788854 Sequence 788854,
	461	83	7.7	1388	18	US-11-096-568A-24202 Sequence 24202, A
	462	83	7.7	1404	17	US-11-037-243-4 Sequence 4, Appli
	463	83	7.7	1631	18	US-11-096-568A-21920 Sequence 21920, A
	465	83	7.7	1661	11	US-10-973-115B-223 Sequence 223, App
	468	83	7.7	1661	18	US-11-290-153-223 Sequence 223, App
c	469	83	7.7	1680	10	US-10-770-726-37 Sequence 37, Appl
	470	83	7.7	2099	18	US-11-072-512-1394 Sequence 1394, Ap
	472	83	7.7	2197	11	US-10-973-115B-313 Sequence 313, App
	475	83	7.7	2197	18	US-11-290-153-313 Sequence 313, App
	476	83	7.7	2454	10	US-10-750-185-34958 Sequence 34958, A
	477	83	7.7	2454	10	US-10-750-623-34958 Sequence 34958, A
	478	83	7.7	2786	18	US-11-036-196-1736 Sequence 1736, Ap
	479	83	7.7	5191	17	US-11-136-527-2993 Sequence 2993, Ap
	480	83	7.7	5191	18	US-11-036-196-1928 Sequence 1928, Ap
	481	83	7.7	12732	10	US-10-802-796-1 Sequence 1, Appli
	482	83	7.7	12732	18	US-11-221-284-1 Sequence 1, Appli
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	484	83	7.7	197781	17	US-11-112-908-34 Sequence 34, Appl
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	490	82.5	7.7	587	12	US-10-301-480-220723 Sequence 220723,
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	492	82.5	7.7	587	12	US-10-301-480-834132 Sequence 834132,
	493	82.5	7.7	629	7	US-09-925-065A-451567 Sequence 451567,
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	495	82.5	7.7	630	12	US-10-301-480-1123998 Sequence 1123998,
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	499	82.5	7.7	861	12	US-10-301-480-783445 Sequence 783445,
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c	501	82.5	7.7	991	12	US-10-301-480-599119 Sequence 599119,
c	502	82.5	7.7	991	12	US-10-301-480-1212528 Sequence 1212528,
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	504	82.5	7.7	997	12	US-10-301-480-1149729 Sequence 1149729,
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	506	82.5	7.7	1122	18	US-11-040-218-60 Sequence 60, Appl
	507	82.5	7.7	1164	18	US-11-040-218-62 Sequence 62, Appl
	508	82.5	7.7	1167	18	US-11-040-218-64 Sequence 64, Appl
	509	82.5	7.7	1209	18	US-11-040-218-66 Sequence 66, Appl
	510	82.5	7.7	1379	18	US-11-096-568A-11215 Sequence 11215, A
	511	82.5	7.7	1538	17	US-11-024-959-257 Sequence 257, App
	512	82.5	7.7	1606	13	US-10-455-772-1001 Sequence 1001, Ap
	513	82.5	7.7	1729	13	US-10-455-772-995 Sequence 995, App
	514	82.5	7.7	1781	13	US-10-455-772-1003 Sequence 1003, Ap
c	515	82.5	7.7	1894	13	US-10-782-413-72 Sequence 72, Appl
c	516	82.5	7.7	2240	18	US-11-072-512-2 Sequence 2, Appli
c	517	82.5	7.7	2599	7	US-09-925-065A-66002 Sequence 66002, A
c	518	82.5	7.7	2599	7	US-09-925-065A-66003 Sequence 66003, A
c	519	82.5	7.7	2599	7	US-09-925-065A-66004 Sequence 66004, A
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c	523	82.5	7.7	2599	12	US-10-301-480-780650 Sequence 780650,
c	524	82.5	7.7	2599	12	US-10-301-480-780651 Sequence 780651,
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c	528	82.5	7.7	3201	18	US-11-072-512-1526 Sequence 1526, Ap
c	529	82.5	7.7	3239	18	US-11-137-807-17 Sequence 17, Appl
c	530	82.5	7.7	4277	17	US-11-136-527-2527 Sequence 2527, Ap
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	532	82.5	7.7	9066	17	US-11-129-143-42 Sequence 42, Appl
	533	82.5	7.7	9066	17	US-11-129-143-44 Sequence 44, Appl
	534	82.5	7.7	9066	17	US-11-129-143-46 Sequence 46, Appl
	535	82.5	7.7	9066	17	US-11-129-143-48 Sequence 48, Appl

	536	82.5	7.7	9066	17	US-11-129-143-50	Sequence 50, Appl
	537	82.5	7.7	9066	17	US-11-129-143-52	Sequence 52, Appl
	538	82.5	7.7	27936	17	US-11-124-367A-5042	Sequence 5042, Ap
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c	540	82.5	7.7	268685	10	US-10-933-025-22	Sequence 22, Appl
c	541	82.5	7.7	268685	18	US-11-219-360-22	Sequence 22, Appl
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c	544	82	7.6	601	7	US-09-925-065A-627430	Sequence 627430,
c	545	82	7.6	993	12	US-10-301-480-612588	Sequence 612588,
c	546	82	7.6	993	12	US-10-301-480-1225997	Sequence 1225997,
c	547	82	7.6	1034	10	US-10-750-185-37054	Sequence 37054, A
c	548	82	7.6	1034	10	US-10-750-623-37054	Sequence 37054, A
	549	82	7.6	1649	18	US-11-096-568A-18343	Sequence 18343, A
	550	82	7.6	2123	18	US-11-096-568A-8708	Sequence 8708, Ap
	551	82	7.6	2263	10	US-10-750-185-28640	Sequence 28640, A
	552	82	7.6	2263	10	US-10-750-623-28640	Sequence 28640, A
c	553	82	7.6	2479	11	US-10-330-773-770	Sequence 770, App
	555	82	7.6	2623	11	US-10-973-115B-63	Sequence 63, Appl
	558	82	7.6	2623	18	US-11-290-153-63	Sequence 63, Appl
	559	82	7.6	2869	10	US-10-750-185-56548	Sequence 56548, A
	560	82	7.6	2869	10	US-10-750-623-56548	Sequence 56548, A
	561	82	7.6	3811	10	US-10-750-185-41708	Sequence 41708, A
	562	82	7.6	3811	10	US-10-750-623-41708	Sequence 41708, A
	563	82	7.6	6230	10	US-10-995-561-353	Sequence 353, App
	564	82	7.6	6379	10	US-10-995-561-352	Sequence 352, App
	565	82	7.6	6383	10	US-10-995-561-351	Sequence 351, App
	566	82	7.6	16382	17	US-11-108-172-1112	Sequence 1112, Ap
	567	82	7.6	16382	17	US-11-000-688-239	Sequence 239, App
c	568	82	7.6	16917	17	US-11-124-367A-5000	Sequence 5000, Ap
c	569	82	7.6	18138	10	US-10-995-561-13385	Sequence 13385, A
c	570	82	7.6	53916	11	US-10-330-773-65	Sequence 65, Appl
c	571	82	7.6	79731	11	US-10-330-773-617	Sequence 617, App
c	572	82	7.6	86574	10	US-10-775-169-173	Sequence 173, App
c	573	82	7.6	116856	17	US-11-143-980-1	Sequence 1, Appli
	574	82	7.6	142605	17	US-11-121-086-64	Sequence 64, Appl
	575	82	7.6	148935	10	US-10-995-561-13308	Sequence 13308, A
	576	82	7.6	159440	13	US-10-960-414-12	Sequence 12, Appl
c	577	82	7.6	188682	17	US-11-112-908-23	Sequence 23, Appl
	578	82	7.6	197241	18	US-11-114-798-47	Sequence 47, Appl
c	579	81.5	7.6	533	10	US-10-623-155-210	Sequence 210, App
c	580	81.5	7.6	561	17	US-11-128-061-3497	Sequence 3497, Ap
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c	582	81.5	7.6	561	17	US-11-128-049-3497	Sequence 3497, Ap
c	583	81.5	7.6	561	17	US-11-128-049-7139	Sequence 7139, Ap
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	587	81.5	7.6	588	12	US-10-301-480-664966	Sequence 664966,
	588	81.5	7.6	588	12	US-10-301-480-909645	Sequence 909645,
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c	594	81.5	7.6	618	7	US-09-925-065A-8144	Sequence 8144, Ap
c	595	81.5	7.6	618	11	US-10-301-480-109380	Sequence 109380,
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c	597	81.5	7.6	618	12	US-10-301-480-722789	Sequence 722789,
c	598	81.5	7.6	618	12	US-10-301-480-722790	Sequence 722790,
	599	81.5	7.6	861	7	US-09-925-065A-68796	Sequence 68796, A
	600	81.5	7.6	861	11	US-10-301-480-170035	Sequence 170035,
	601	81.5	7.6	861	12	US-10-301-480-783444	Sequence 783444,
	602	81.5	7.6	881	17	US-11-069-642-118	Sequence 118, App
	603	81.5	7.6	1056	10	US-10-750-185-33262	Sequence 33262, A
	604	81.5	7.6	1056	10	US-10-750-623-33262	Sequence 33262, A
	605	81.5	7.6	1369	17	US-11-015-546A-11	Sequence 11, Appl
	606	81.5	7.6	1375	17	US-11-015-546A-39	Sequence 39, Appl
	607	81.5	7.6	1400	17	US-11-136-527-8086	Sequence 8086, Ap
c	608	81.5	7.6	1426	18	US-11-096-568A-24687	Sequence 24687, A
c	609	81.5	7.6	1695	18	US-11-096-568A-12871	Sequence 12871, A
	610	81.5	7.6	1765	10	US-10-750-185-24870	Sequence 24870, A
	611	81.5	7.6	1765	10	US-10-750-623-24870	Sequence 24870, A
	612	81.5	7.6	2010	18	US-11-198-886-5	Sequence 5, Appli
	613	81.5	7.6	2080	17	US-11-140-625-2	Sequence 2, Appli
	614	81.5	7.6	2245	18	US-11-096-568A-24815	Sequence 24815, A
	615	81.5	7.6	2761	18	US-11-036-196-2003	Sequence 2003, Ap
	616	81.5	7.6	2814	17	US-11-136-527-3990	Sequence 3990, Ap
	617	81.5	7.6	3050	18	US-11-072-512-262	Sequence 262, App
	618	81.5	7.6	3089	18	US-11-072-512-914	Sequence 914, App
	619	81.5	7.6	3322	18	US-11-072-512-373	Sequence 373, App
	620	81.5	7.6	3743	18	US-11-072-512-273	Sequence 273, App
	621	81.5	7.6	5015	18	US-11-245-147-166	Sequence 166, App
c	622	81.5	7.6	7300	17	US-11-136-527-1989	Sequence 1989, Ap
c	623	81.5	7.6	40070	11	US-10-330-773-747	Sequence 747, App
c	624	81.5	7.6	70513	10	US-10-995-561-13368	Sequence 13368, A
	625	81.5	7.6	92969	11	US-10-330-773-178	Sequence 178, App
c	626	81.5	7.6	100000	17	US-11-124-367A-4999	Sequence 4999, Ap
c	627	81.5	7.6	138808	11	US-10-330-773-905	Sequence 905, App
c	628	81.5	7.6	175603	11	US-10-330-773-531	Sequence 531, App
c	629	81.5	7.6	197096	17	US-11-121-086-107	Sequence 107, App
c	630	81.5	7.6	200628	17	US-11-121-086-62	Sequence 62, Appl
	631	81.5	7.6	260209	10	US-10-933-025-23	Sequence 23, Appl
	632	81.5	7.6	260209	18	US-11-219-360-23	Sequence 23, Appl
	633	81	7.5	538	7	US-09-925-065A-526192	Sequence 526192,
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c	635	81	7.5	541	12	US-10-301-480-1119048	Sequence 1119048,
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	637	81	7.5	562	7	US-09-925-065A-113841	Sequence 113841,
c	638	81	7.5	582	11	US-10-301-480-65786	Sequence 65786, A
c	639	81	7.5	582	12	US-10-301-480-679195	Sequence 679195,
c	640	81	7.5	597	11	US-10-301-480-84603	Sequence 84603, A
c	641	81	7.5	597	12	US-10-301-480-698012	Sequence 698012,
c	642	81	7.5	629	7	US-09-925-065A-800782	Sequence 800782,
	643	81	7.5	646	7	US-09-925-065A-785564	Sequence 785564,
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c	645	81	7.5	706	12	US-10-301-480-1195024	Sequence 1195024,
c	646	81	7.5	764	13	US-10-986-405-122	Sequence 122, App
	647	81	7.5	799	7	US-09-925-065A-550693	Sequence 550693,
	648	81	7.5	799	7	US-09-925-065A-550694	Sequence 550694,
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	651	81	7.5	799	12	US-10-301-480-1142052	Sequence 1142052,
	652	81	7.5	799	12	US-10-301-480-1142053	Sequence 1142053,
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c	654	81	7.5	967	12	US-10-301-480-544793	Sequence 544793,
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c	656	81	7.5	967	12	US-10-301-480-1158202	Sequence 1158202,
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c	658	81	7.5	991	12	US-10-301-480-1189037	Sequence 1189037,
c	659	81	7.5	999	12	US-10-301-480-549888	Sequence 549888,
	660	81	7.5	999	12	US-10-301-480-557146	Sequence 557146,
c	661	81	7.5	999	12	US-10-301-480-1163297	Sequence 1163297,
	662	81	7.5	999	12	US-10-301-480-1170555	Sequence 1170555,
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c	664	81	7.5	1398	10	US-10-750-185-52982	Sequence 52982, A
c	665	81	7.5	1398	10	US-10-750-623-52982	Sequence 52982, A
c	666	81	7.5	1400	17	US-11-136-527-6802	Sequence 6802, Ap
	667	81	7.5	1400	17	US-11-136-527-6854	Sequence 6854, Ap
c	668	81	7.5	1507	17	US-11-055-637-73	Sequence 73, Appl
	669	81	7.5	1683	17	US-11-136-527-2758	Sequence 2758, Ap
	670	81	7.5	1701	10	US-10-750-185-47792	Sequence 47792, A
	671	81	7.5	1701	10	US-10-750-623-47792	Sequence 47792, A
c	672	81	7.5	1724	17	US-11-122-329-102	Sequence 102, App
	673	81	7.5	1854	18	US-11-096-568A-13341	Sequence 13341, A
c	674	81	7.5	1910	18	US-11-299-182-13	Sequence 13, Appl
	675	81	7.5	2323	17	US-11-076-427A-3	Sequence 3, Appli
	676	81	7.5	2366	10	US-10-750-185-53875	Sequence 53875, A
	677	81	7.5	2366	10	US-10-750-623-53875	Sequence 53875, A
	678	81	7.5	2446	10	US-10-523-588-6	Sequence 6, Appli
	679	81	7.5	2446	10	US-10-523-588-7	Sequence 7, Appli
	680	81	7.5	2712	10	US-10-971-560-6	Sequence 6, Appli
	681	81	7.5	2738	11	US-10-501-035-184	Sequence 184, App
	682	81	7.5	2738	17	US-11-122-329-66	Sequence 66, Appl
	683	81	7.5	2773	10	US-10-523-588-8	Sequence 8, Appli
c	684	81	7.5	2815	10	US-10-821-234-165	Sequence 165, App

	685	81	7.5	3028	13	US-10-455-772-111 Sequence 111, App
	686	81	7.5	3039	13	US-10-979-095-15 Sequence 15, Appl
c	687	81	7.5	3183	17	US-11-136-527-2706 Sequence 2706, Ap
	688	81	7.5	3438	18	US-11-072-512-521 Sequence 521, App
	689	81	7.5	3741	18	US-11-036-196-1703 Sequence 1703, Ap
	690	81	7.5	6021	10	US-10-971-560-5 Sequence 5, Appli
	691	81	7.5	8599	17	US-11-136-527-3033 Sequence 3033, Ap
	692	81	7.5	23597	10	US-10-995-561-13316 Sequence 13316, A
	693	81	7.5	37507	10	US-10-522-037-2 Sequence 2, Appli
c	694	81	7.5	48174	11	US-10-330-773-10 Sequence 10, Appl
c	695	81	7.5	57303	17	US-11-124-367A-5032 Sequence 5032, Ap
	696	81	7.5	95604	17	US-11-124-367A-5097 Sequence 5097, Ap
c	697	81	7.5	100000	17	US-11-124-367A-5091 Sequence 5091, Ap
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c	699	80.5	7.5	578	7	US-09-925-065A-74794 Sequence 74794, A
c	700	80.5	7.5	578	7	US-09-925-065A-74796 Sequence 74796, A
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c	702	80.5	7.5	578	11	US-10-301-480-176033 Sequence 176033,
c	703	80.5	7.5	578	11	US-10-301-480-176035 Sequence 176035,
c	704	80.5	7.5	578	12	US-10-301-480-789441 Sequence 789441,
c	705	80.5	7.5	578	12	US-10-301-480-789442 Sequence 789442,
c	706	80.5	7.5	578	12	US-10-301-480-789444 Sequence 789444,
c	707	80.5	7.5	579	7	US-09-925-065A-652895 Sequence 652895,
	708	80.5	7.5	588	11	US-10-301-480-51556 Sequence 51556, A
	709	80.5	7.5	588	12	US-10-301-480-664965 Sequence 664965,
	710	80.5	7.5	590	7	US-09-925-065A-499653 Sequence 499653,
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	712	80.5	7.5	629	7	US-09-925-065A-451566 Sequence 451566,
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	714	80.5	7.5	630	12	US-10-301-480-1123997 Sequence 1123997,
c	715	80.5	7.5	998	12	US-10-301-480-603650 Sequence 603650,
c	716	80.5	7.5	998	12	US-10-301-480-1217059 Sequence 1217059,
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c	718	80.5	7.5	1020	10	US-10-750-623-35739 Sequence 35739, A
c	719	80.5	7.5	1045	10	US-10-454-437-219 Sequence 219, App
c	720	80.5	7.5	1066	10	US-10-454-437-217 Sequence 217, App
c	721	80.5	7.5	1066	17	US-11-055-822-65 Sequence 65, Appl
c	722	80.5	7.5	1066	18	US-11-239-674-63 Sequence 63, Appl
	723	80.5	7.5	1192	7	US-09-925-065A-11377 Sequence 11377, A
	724	80.5	7.5	1192	11	US-10-301-480-112614 Sequence 112614,
	725	80.5	7.5	1192	12	US-10-301-480-726023 Sequence 726023,
	726	80.5	7.5	1422	18	US-11-096-568A-16195 Sequence 16195, A
c	727	80.5	7.5	1566	17	US-11-112-908-435 Sequence 435, App
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	729	80.5	7.5	1669	10	US-10-750-623-43418 Sequence 43418, A
	730	80.5	7.5	1804	18	US-11-096-568A-18014 Sequence 18014, A
	731	80.5	7.5	1878	18	US-11-096-568A-14729 Sequence 14729, A
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	733	80.5	7.5	1920	7	US-09-925-065A-81408 Sequence 81408, A
	734	80.5	7.5	1920	11	US-10-301-480-182647 Sequence 182647,
	735	80.5	7.5	1920	11	US-10-301-480-182648 Sequence 182648,
	736	80.5	7.5	1920	12	US-10-301-480-796056 Sequence 796056,
	737	80.5	7.5	1920	12	US-10-301-480-796057 Sequence 796057,
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	739	80.5	7.5	2285	11	US-10-330-773-821 Sequence 821, App
c	740	80.5	7.5	2329	7	US-09-925-065A-724064 Sequence 724064,
	741	80.5	7.5	2615	18	US-11-072-512-1280 Sequence 1280, Ap
c	742	80.5	7.5	2642	13	US-10-455-772-161 Sequence 161, App
	743	80.5	7.5	2651	7	US-09-925-065A-19554 Sequence 19554, A
	744	80.5	7.5	2651	7	US-09-925-065A-19555 Sequence 19555, A
	745	80.5	7.5	2651	7	US-09-925-065A-19556 Sequence 19556, A
	746	80.5	7.5	2651	7	US-09-925-065A-19557 Sequence 19557, A
	747	80.5	7.5	2651	11	US-10-301-480-120791 Sequence 120791,
	748	80.5	7.5	2651	11	US-10-301-480-120792 Sequence 120792,
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	752	80.5	7.5	2651	12	US-10-301-480-734201 Sequence 734201,
	753	80.5	7.5	2651	12	US-10-301-480-734202 Sequence 734202,
	754	80.5	7.5	2651	12	US-10-301-480-734203 Sequence 734203,
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c	756	80.5	7.5	2762	13	US-10-455-772-149 Sequence 149, App
	757	80.5	7.5	3018	17	US-11-186-284-212 Sequence 212, App
c	758	80.5	7.5	3030	10	US-10-821-234-216 Sequence 216, App
c	759	80.5	7.5	3351	13	US-10-455-772-153 Sequence 153, App
c	760	80.5	7.5	3397	13	US-10-455-772-151 Sequence 151, App
	761	80.5	7.5	3455	18	US-11-224-663-145 Sequence 145, App
	762	80.5	7.5	3455	18	US-11-224-525-145 Sequence 145, App
c	763	80.5	7.5	3468	13	US-10-455-772-163 Sequence 163, App
	768	80.5	7.5	4770	17	US-11-136-527-299 Sequence 299, App
c	769	80.5	7.5	5493	10	US-10-955-054A-64 Sequence 64, Appl
	770	80.5	7.5	6453	11	US-10-501-035-130 Sequence 130, App
	771	80.5	7.5	6453	18	US-11-219-264-5 Sequence 5, Appli
c	772	80.5	7.5	100000	17	US-11-124-367A-5048 Sequence 5048, Ap
c	773	80.5	7.5	155083	11	US-10-330-773-868 Sequence 868, App
c	774	80.5	7.5	177623	17	US-11-112-908-41 Sequence 41, Appl
	775	80.5	7.5	440684	11	US-10-330-773-114 Sequence 114, App
c	776	80.5	7.5	1694969	13	US-10-506-454-1690 Sequence 1690, Ap
c	777	80	7.5	462	11	US-10-932-182A-78410 Sequence 78410, A
c	778	80	7.5	462	11	US-10-932-182A-78410 Sequence 78410, A
	779	80	7.5	540	7	US-09-925-065A-299227 Sequence 299227,
c	780	80	7.5	542	7	US-09-925-065A-47655 Sequence 47655, A
c	781	80	7.5	542	11	US-10-301-480-148893 Sequence 148893,
c	782	80	7.5	542	12	US-10-301-480-762302 Sequence 762302,
	783	80	7.5	543	12	US-10-301-480-375837 Sequence 375837,
	784	80	7.5	543	12	US-10-301-480-989246 Sequence 989246,
	785	80	7.5	577	12	US-10-301-480-578086 Sequence 578086,
	786	80	7.5	577	12	US-10-301-480-1191495 Sequence 1191495,
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c	792	80	7.5	938	10	US-10-750-623-51323 Sequence 51323, A
	793	80	7.5	973	12	US-10-301-480-555162 Sequence 555162,
	794	80	7.5	973	12	US-10-301-480-1168571 Sequence 1168571,
	795	80	7.5	995	12	US-10-301-480-589978 Sequence 589978,
	796	80	7.5	995	12	US-10-301-480-1203387 Sequence 1203387,
	797	80	7.5	998	12	US-10-301-480-575681 Sequence 575681,
	798	80	7.5	998	12	US-10-301-480-1189090 Sequence 1189090,
	799	80	7.5	1056	10	US-10-972-587-21 Sequence 21, Appl
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	801	80	7.5	1314	17	US-11-043-889-56 Sequence 56, Appl
	802	80	7.5	1343	18	US-11-096-568A-22830 Sequence 22830, A
	803	80	7.5	1374	18	US-11-232-805-42 Sequence 42, Appl
c	804	80	7.5	1376	10	US-10-750-185-57786 Sequence 57786, A
c	805	80	7.5	1376	10	US-10-750-623-57786 Sequence 57786, A
	806	80	7.5	1399	7	US-09-925-065A-83309 Sequence 83309, A
	807	80	7.5	1399	11	US-10-301-480-184549 Sequence 184549,
	808	80	7.5	1399	12	US-10-301-480-797958 Sequence 797958,
c	809	80	7.5	1412	7	US-09-925-065A-71390 Sequence 71390, A
c	810	80	7.5	1412	11	US-10-301-480-172629 Sequence 172629,
c	811	80	7.5	1412	12	US-10-301-480-786038 Sequence 786038,
	812	80	7.5	1476	18	US-11-096-568A-15893 Sequence 15893, A
c	813	80	7.5	1482	16	US-11-012-762-11 Sequence 11, Appl
	814	80	7.5	1638	11	US-10-203-486-23 Sequence 23, Appl
	815	80	7.5	1760	10	US-10-750-185-63320 Sequence 63320, A
	816	80	7.5	1760	10	US-10-750-623-63320 Sequence 63320, A
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c	818	80	7.5	1762	10	US-10-750-623-54308 Sequence 54308, A
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	821	80	7.5	2336	18	US-11-072-512-1925 Sequence 1925, Ap
	822	80	7.5	2500	7	US-09-925-065A-57756 Sequence 57756, A
	823	80	7.5	2500	11	US-10-301-480-158994 Sequence 158994,
	824	80	7.5	2500	12	US-10-301-480-772403 Sequence 772403,
	825	80	7.5	2543	10	US-10-750-185-44882 Sequence 44882, A
	826	80	7.5	2543	10	US-10-750-623-44882 Sequence 44882, A
	827	80	7.5	2558	17	US-11-043-889-57 Sequence 57, Appl
	828	80	7.5	2565	17	US-11-043-889-54 Sequence 54, Appl
	829	80	7.5	3036	7	US-09-925-065A-718297 Sequence 718297,
	830	80	7.5	3036	7	US-09-925-065A-718298 Sequence 718298,
	831	80	7.5	3113	7	US-09-925-065A-52897 Sequence 52897, A
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	833	80	7.5	3113	11	US-10-301-480-100246 Sequence 100246,
	834	80	7.5	3113	11	US-10-301-480-154135 Sequence 154135,

	835	80	7.5	3113	12	US-10-301-480-713654 Sequence 713654,
	836	80	7.5	3113	12	US-10-301-480-713655 Sequence 713655,
	837	80	7.5	3113	12	US-10-301-480-767544 Sequence 767544,
c	838	80	7.5	3594	10	US-10-775-169-317 Sequence 317, App
c	839	80	7.5	4007	10	US-10-750-185-30908 Sequence 30908, A
c	840	80	7.5	4007	10	US-10-750-623-30908 Sequence 30908, A
c	841	80	7.5	4551	10	US-10-220-824-7 Sequence 7, Appli
	842	80	7.5	5247	10	US-10-750-185-64326 Sequence 64326, A
	843	80	7.5	5247	10	US-10-750-623-64326 Sequence 64326, A
	844	80	7.5	6244	18	US-11-036-196-1748 Sequence 1748, Ap
	845	80	7.5	6286	17	US-11-136-527-2567 Sequence 2567, Ap
c	846	80	7.5	13961	17	US-11-124-367A-5089 Sequence 5089, Ap
c	847	80	7.5	14131	10	US-10-775-169-333 Sequence 333, App
c	848	80	7.5	14131	17	US-11-122-329-84 Sequence 84, Appl
	849	80	7.5	14172	17	US-11-075-185-2 Sequence 2, Appli
	850	80	7.5	19573	17	US-11-124-367A-5052 Sequence 5052, Ap
	851	80	7.5	34794	17	US-11-165-697-44 Sequence 44, Appl
	852	80	7.5	35344	10	US-10-995-561-13307 Sequence 13307, A
c	853	80	7.5	36741	17	US-11-127-832-12 Sequence 12, Appl
	854	80	7.5	85980	18	US-11-114-798-46 Sequence 46, Appl
c	855	80	7.5	86081	10	US-10-995-561-13246 Sequence 13246, A
	856	80	7.5	88421	17	US-11-205-109-1 Sequence 1, Appli
c	857	80	7.5	100097	13	US-10-960-414-203 Sequence 203, App
	858	80	7.5	100387	17	US-11-121-086-94 Sequence 94, Appl
c	859	80	7.5	348101	11	US-10-330-773-122 Sequence 122, App
	860	79.5	7.4	497	7	US-09-925-065A-475025 Sequence 475025,
	861	79.5	7.4	501	7	US-09-925-065A-475024 Sequence 475024,
	862	79.5	7.4	560	7	US-09-925-065A-41078 Sequence 41078, A
	863	79.5	7.4	560	7	US-09-925-065A-41079 Sequence 41079, A
	864	79.5	7.4	560	11	US-10-301-480-142316 Sequence 142316,
	865	79.5	7.4	560	11	US-10-301-480-142317 Sequence 142317,
	866	79.5	7.4	560	12	US-10-301-480-755725 Sequence 755725,
	867	79.5	7.4	560	12	US-10-301-480-755726 Sequence 755726,
c	868	79.5	7.4	617	7	US-09-925-065A-8664 Sequence 8664, Ap
c	869	79.5	7.4	617	11	US-10-301-480-109901 Sequence 109901,
c	870	79.5	7.4	617	12	US-10-301-480-723310 Sequence 723310,
c	871	79.5	7.4	626	7	US-09-925-065A-186767 Sequence 186767,
c	872	79.5	7.4	626	7	US-09-925-065A-186768 Sequence 186768,
c	873	79.5	7.4	635	12	US-10-301-480-276876 Sequence 276876,
c	874	79.5	7.4	635	12	US-10-301-480-276877 Sequence 276877,
c	875	79.5	7.4	635	12	US-10-301-480-890285 Sequence 890285,
c	876	79.5	7.4	635	12	US-10-301-480-890286 Sequence 890286,
	877	79.5	7.4	640	7	US-09-925-065A-705141 Sequence 705141,
c	878	79.5	7.4	642	12	US-10-301-480-611128 Sequence 611128,
c	879	79.5	7.4	642	12	US-10-301-480-1224537 Sequence 1224537,
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	881	79.5	7.4	728	10	US-10-750-623-42456 Sequence 42456, A
	882	79.5	7.4	774	17	US-11-135-855-19 Sequence 19, Appl
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c	884	79.5	7.4	836	12	US-10-301-480-1217563 Sequence 1217563,
c	885	79.5	7.4	978	12	US-10-301-480-603255 Sequence 603255,
c	886	79.5	7.4	978	12	US-10-301-480-1216664 Sequence 1216664,
c	887	79.5	7.4	1059	11	US-10-301-480-97733 Sequence 97733, A
c	888	79.5	7.4	1059	12	US-10-301-480-711142 Sequence 711142,
	889	79.5	7.4	1072	10	US-10-750-185-36342 Sequence 36342, A
	890	79.5	7.4	1072	10	US-10-750-623-36342 Sequence 36342, A
	891	79.5	7.4	1109	10	US-10-955-054A-56 Sequence 56, Appl
	892	79.5	7.4	1109	13	US-10-784-004-594 Sequence 594, App
	893	79.5	7.4	1109	13	US-10-784-004-1022 Sequence 1022, Ap
	894	79.5	7.4	1191	10	US-10-750-185-45797 Sequence 45797, A
	895	79.5	7.4	1191	10	US-10-750-623-45797 Sequence 45797, A
c	896	79.5	7.4	1278	13	US-10-455-772-157 Sequence 157, App
	897	79.5	7.4	1400	17	US-11-136-527-6142 Sequence 6142, Ap
c	898	79.5	7.4	1669	18	US-11-096-568A-22888 Sequence 22888, A
	899	79.5	7.4	1790	13	US-10-455-772-997 Sequence 997, App
c	900	79.5	7.4	1880	13	US-10-455-772-65 Sequence 65, Appl
	901	79.5	7.4	2009	11	US-10-493-909-54 Sequence 54, Appl
	902	79.5	7.4	2009	18	US-11-185-436-1 Sequence 1, Appli
	903	79.5	7.4	2009	18	US-11-186-422-3 Sequence 3, Appli
	904	79.5	7.4	2039	11	US-10-893-483-67 Sequence 67, Appl
c	905	79.5	7.4	2188	18	US-11-096-568A-20060 Sequence 20060, A
	906	79.5	7.4	2260	11	US-10-893-483-68 Sequence 68, Appl
	907	79.5	7.4	2290	18	US-11-072-512-8 Sequence 8, Appli
	908	79.5	7.4	2407	17	US-11-136-527-2046 Sequence 2046, Ap
	909	79.5	7.4	2418	13	US-10-782-413-60 Sequence 60, Appl
c	910	79.5	7.4	2447	11	US-10-330-773-186 Sequence 186, App
	911	79.5	7.4	2453	11	US-10-893-483-30 Sequence 30, Appl
	912	79.5	7.4	2748	18	US-11-183-261-15 Sequence 15, Appl
	913	79.5	7.4	2767	10	US-10-821-234-43 Sequence 43, Appl
	914	79.5	7.4	3255	10	US-10-964-313-1 Sequence 1, Appli
	915	79.5	7.4	3282	13	US-10-469-469-92 Sequence 92, Appl
	916	79.5	7.4	4441	10	US-10-750-185-54843 Sequence 54843, A
	917	79.5	7.4	4441	10	US-10-750-623-54843 Sequence 54843, A
	918	79.5	7.4	8459	11	US-10-501-035-86 Sequence 86, Appl
	919	79.5	7.4	12301	11	US-10-893-483-69 Sequence 69, Appl
c	920	79.5	7.4	12649	18	US-11-225-354-20 Sequence 20, Appl
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	922	79.5	7.4	28553	10	US-10-995-561-13477 Sequence 13477, A
c	923	79.5	7.4	54767	10	US-10-995-561-13357 Sequence 13357, A
c	924	79.5	7.4	68820	11	US-10-330-773-908 Sequence 908, App
c	925	79.5	7.4	76427	17	US-11-124-367A-5041 Sequence 5041, Ap
	926	79.5	7.4	82746	13	US-10-496-351-56 Sequence 56, Appl
c	927	79.5	7.4	100000	17	US-11-124-367A-5024 Sequence 5024, Ap
c	928	79.5	7.4	100000	17	US-11-124-367A-5026 Sequence 5026, Ap
	929	79.5	7.4	126552	17	US-11-121-086-1 Sequence 1, Appli
	930	79.5	7.4	150481	17	US-11-112-908-37 Sequence 37, Appl
c	931	79.5	7.4	153752	11	US-10-330-773-508 Sequence 508, App
c	932	79.5	7.4	163162	17	US-11-121-086-66 Sequence 66, Appl
	933	79.5	7.4	171162	17	US-11-112-908-38 Sequence 38, Appl
c	934	79.5	7.4	189252	17	US-11-121-086-54 Sequence 54, Appl
c	935	79.5	7.4	191091	17	US-11-121-086-60 Sequence 60, Appl
c	936	79.5	7.4	191684	17	US-11-121-086-2 Sequence 2, Appli
	937	79.5	7.4	228006	11	US-10-330-773-119 Sequence 119, App
c	938	79	7.4	541	12	US-10-301-480-505638 Sequence 505638,
c	939	79	7.4	541	12	US-10-301-480-1119047 Sequence 1119047,
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c	941	79	7.4	542	11	US-10-301-480-148892 Sequence 148892,
c	942	79	7.4	542	12	US-10-301-480-762301 Sequence 762301,
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c	944	79	7.4	553	7	US-09-925-065A-445567 Sequence 445567,
c	945	79	7.4	553	7	US-09-925-065A-445568 Sequence 445568,
c	946	79	7.4	593	7	US-09-925-065A-458581 Sequence 458581,
c	947	79	7.4	593	7	US-09-925-065A-458582 Sequence 458582,
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	949	79	7.4	608	7	US-09-925-065A-682251 Sequence 682251,
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	952	79	7.4	811	7	US-09-925-065A-28354 Sequence 28354, A
	953	79	7.4	811	11	US-10-301-480-129591 Sequence 129591,
	954	79	7.4	811	12	US-10-301-480-743000 Sequence 743000,
	955	79	7.4	819	18	US-11-225-354-28 Sequence 28, Appl
	956	79	7.4	844	18	US-11-051-720-1490 Sequence 1490, Ap
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c	958	79	7.4	956	12	US-10-301-480-1195129 Sequence 1195129,
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	963	79	7.4	989	12	US-10-301-480-1194711 Sequence 1194711,
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c	969	79	7.4	1101	11	US-10-931-198-47 Sequence 47, Appl
c	970	79	7.4	1101	12	US-10-942-042-47 Sequence 47, Appl
c	971	79	7.4	1160	10	US-10-750-185-35276 Sequence 35276, A
c	972	79	7.4	1160	10	US-10-750-623-35276 Sequence 35276, A
c	973	79	7.4	1322	10	US-10-750-185-32206 Sequence 32206, A
c	974	79	7.4	1322	10	US-10-750-623-32206 Sequence 32206, A
c	975	79	7.4	1400	17	US-11-136-527-5713 Sequence 5713, Ap
c	976	79	7.4	1408	7	US-09-925-065A-90803 Sequence 90803, A
c	977	79	7.4	1408	11	US-10-301-480-192044 Sequence 192044,
c	978	79	7.4	1408	12	US-10-301-480-805453 Sequence 805453,
c	979	79	7.4	1433	7	US-09-925-065A-79527 Sequence 79527, A
c	980	79	7.4	1433	7	US-09-925-065A-79528 Sequence 79528, A

c 981	79	7.4	1433	11	US-10-301-480-180766	Sequence 180766,
c 982	79	7.4	1433	11	US-10-301-480-180767	Sequence 180767,
c 983	79	7.4	1433	12	US-10-301-480-794175	Sequence 794175,
c 984	79	7.4	1433	12	US-10-301-480-794176	Sequence 794176,
c 985	79	7.4	1486	17	US-11-136-527-505	Sequence 505, App
986	79	7.4	1544	18	US-11-096-568A-22900	Sequence 22900, A
987	79	7.4	1626	10	US-10-750-185-36339	Sequence 36339, A
988	79	7.4	1626	10	US-10-750-623-36339	Sequence 36339, A
c 989	79	7.4	1629	10	US-10-750-185-63932	Sequence 63932, A
c 990	79	7.4	1629	10	US-10-750-623-63932	Sequence 63932, A
991	79	7.4	1647	17	US-11-137-465-14	Sequence 14, Appl
c 992	79	7.4	1777	17	US-11-136-527-2619	Sequence 2619, Ap
993	79	7.4	1936	11	US-10-501-035-127	Sequence 127, App
994	79	7.4	2035	18	US-11-072-512-1442	Sequence 1442, Ap
c 995	79	7.4	2384	13	US-10-960-414-457	Sequence 457, App
c 996	79	7.4	2475	17	US-11-136-527-1617	Sequence 1617, Ap
997	79	7.4	2837	18	US-11-096-568A-14760	Sequence 14760, A
998	79	7.4	3404	18	US-11-072-512-363	Sequence 363, App
c 999	79	7.4	4697	10	US-10-453-372-1185	Sequence 1185, Ap
c1000	79	7.4	4760	10	US-10-453-372-1179	Sequence 1179, Ap
1001	79	7.4	5312	17	US-11-075-046-39	Sequence 39, Appl
1002	79	7.4	5312	17	US-11-075-046-41	Sequence 41, Appl
1003	79	7.4	5312	17	US-11-075-046-43	Sequence 43, Appl
1004	79	7.4	5312	17	US-11-075-046-45	Sequence 45, Appl
c1005	79	7.4	5688	10	US-10-453-372-1189	Sequence 1189, Ap
c1006	79	7.4	6224	10	US-10-453-372-1173	Sequence 1173, Ap
c1007	79	7.4	6494	10	US-10-453-372-1187	Sequence 1187, Ap
1008	79	7.4	11807	11	US-10-893-483-103	Sequence 103, App
1009	79	7.4	16658	11	US-10-893-483-104	Sequence 104, App
1010	79	7.4	16668	11	US-10-893-483-100	Sequence 100, App
1011	79	7.4	24770	11	US-10-893-483-96	Sequence 96, Appl
c1012	79	7.4	52705	17	US-11-124-367A-5059	Sequence 5059, Ap
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1015	79	7.4	159660	17	US-11-112-908-43	Sequence 43, Appl
1016	79	7.4	169495	17	US-11-121-086-61	Sequence 61, Appl
c1017	79	7.4	170995	17	US-11-121-086-35	Sequence 35, Appl
c1018	79	7.4	175100	17	US-11-121-086-21	Sequence 21, Appl
1019	79	7.4	177623	17	US-11-112-908-41	Sequence 41, Appl
1020	79	7.4	191091	17	US-11-121-086-60	Sequence 60, Appl
1021	79	7.4	191350	10	US-10-857-780-4	Sequence 4, Appli
c1022	78.5	7.3	517	11	US-10-301-480-91867	Sequence 91867, A
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c1024	78.5	7.3	517	12	US-10-301-480-705276	Sequence 705276,
c1025	78.5	7.3	517	12	US-10-301-480-705277	Sequence 705277,
1026	78.5	7.3	541	12	US-10-301-480-545358	Sequence 545358,
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1029	78.5	7.3	581	7	US-09-925-065A-122666	Sequence 122666,
1030	78.5	7.3	587	12	US-10-301-480-220721	Sequence 220721,
1031	78.5	7.3	587	12	US-10-301-480-834130	Sequence 834130,
1032	78.5	7.3	590	7	US-09-925-065A-499652	Sequence 499652,
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c1034	78.5	7.3	602	7	US-09-925-065A-733323	Sequence 733323,
1035	78.5	7.3	611	12	US-10-301-480-419766	Sequence 419766,
1036	78.5	7.3	611	12	US-10-301-480-1033175	Sequence 1033175,
c1037	78.5	7.3	620	7	US-09-925-065A-755760	Sequence 755760,
c1038	78.5	7.3	640	7	US-09-925-065A-918437	Sequence 918437,
c1039	78.5	7.3	726	13	US-10-915-002-132	Sequence 132, App
c1040	78.5	7.3	929	7	US-09-925-065A-703903	Sequence 703903,
c1041	78.5	7.3	929	7	US-09-925-065A-703904	Sequence 703904,
c1042	78.5	7.3	948	17	US-11-119-351-5	Sequence 5, Appli
1043	78.5	7.3	969	12	US-10-301-480-549321	Sequence 549321,
1044	78.5	7.3	969	12	US-10-301-480-1162730	Sequence 1162730,
1045	78.5	7.3	971	12	US-10-301-480-549322	Sequence 549322,
1046	78.5	7.3	971	12	US-10-301-480-1162731	Sequence 1162731,
1047	78.5	7.3	998	18	US-11-238-549-3	Sequence 3, Appli
1048	78.5	7.3	1116	11	US-10-501-035-42	Sequence 42, Appl
c1049	78.5	7.3	1117	18	US-11-096-568A-9297	Sequence 9297, Ap
c1050	78.5	7.3	1147	18	US-11-096-568A-12674	Sequence 12674, A
c1051	78.5	7.3	1297	10	US-10-750-185-43439	Sequence 43439, A
c1052	78.5	7.3	1297	10	US-10-750-623-43439	Sequence 43439, A
1053	78.5	7.3	1307	11	US-10-301-480-35206	Sequence 35206, A
1054	78.5	7.3	1307	11	US-10-301-480-35207	Sequence 35207, A
1055	78.5	7.3	1307	12	US-10-301-480-648615	Sequence 648615,
1056	78.5	7.3	1307	12	US-10-301-480-648616	Sequence 648616,
c1057	78.5	7.3	1464	18	US-11-248-383-2	Sequence 2, Appli
1058	78.5	7.3	1540	17	US-11-112-908-436	Sequence 436, App
1059	78.5	7.3	1577	18	US-11-096-568A-10586	Sequence 10586, A
c1060	78.5	7.3	1614	18	US-11-096-568A-23017	Sequence 23017, A
1061	78.5	7.3	1639	18	US-11-096-568A-23401	Sequence 23401, A
1062	78.5	7.3	1688	18	US-11-072-512-820	Sequence 820, App
c1063	78.5	7.3	1705	7	US-09-925-065A-724994	Sequence 724994,
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1066	78.5	7.3	1782	10	US-10-467-657-3951	Sequence 3951, Ap
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1068	78.5	7.3	1912	11	US-10-301-480-180769	Sequence 180769,
1069	78.5	7.3	1912	12	US-10-301-480-794178	Sequence 794178,
c1070	78.5	7.3	1939	12	US-10-644-807-145	Sequence 145, App
1071	78.5	7.3	2073	18	US-11-096-568A-3063	Sequence 3063, Ap
1072	78.5	7.3	2149	10	US-10-750-185-49490	Sequence 49490, A
1073	78.5	7.3	2149	10	US-10-750-623-49490	Sequence 49490, A
c1074	78.5	7.3	2193	11	US-10-301-480-94195	Sequence 94195, A
c1075	78.5	7.3	2193	11	US-10-301-480-94196	Sequence 94196, A
c1076	78.5	7.3	2193	11	US-10-301-480-94197	Sequence 94197, A
c1077	78.5	7.3	2193	12	US-10-301-480-707604	Sequence 707604,
c1078	78.5	7.3	2193	12	US-10-301-480-707605	Sequence 707605,
c1079	78.5	7.3	2193	12	US-10-301-480-707606	Sequence 707606,
c1080	78.5	7.3	2281	18	US-11-072-512-1140	Sequence 1140, Ap
c1081	78.5	7.3	2443	10	US-10-995-561-114	Sequence 114, App
c1082	78.5	7.3	2488	10	US-10-995-561-105	Sequence 105, App
c1083	78.5	7.3	2767	10	US-10-821-234-43	Sequence 43, Appl
c1084	78.5	7.3	2835	18	US-11-072-512-1501	Sequence 1501, Ap
c1085	78.5	7.3	2933	10	US-10-750-185-26639	Sequence 26639, A
c1086	78.5	7.3	2933	10	US-10-750-623-26639	Sequence 26639, A
c1087	78.5	7.3	2967	10	US-10-750-185-29827	Sequence 29827, A
c1088	78.5	7.3	2967	10	US-10-750-623-29827	Sequence 29827, A
c1093	78.5	7.3	2980	11	US-10-511-538-228	Sequence 228, App
c1094	78.5	7.3	3282	7	US-09-925-065A-676622	Sequence 676622,
c1095	78.5	7.3	3282	7	US-09-925-065A-705414	Sequence 705414,
1096	78.5	7.3	3326	11	US-10-330-773-66	Sequence 66, Appl
c1097	78.5	7.3	3338	10	US-10-750-185-32296	Sequence 32296, A
c1098	78.5	7.3	3338	10	US-10-750-623-32296	Sequence 32296, A
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1100	78.5	7.3	3949	18	US-11-072-175-2	Sequence 2, Appli
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1103	78.5	7.3	4282	17	US-11-183-624-3	Sequence 3, Appli
1104	78.5	7.3	4711	17	US-11-000-688-440	Sequence 440, App
1105	78.5	7.3	4711	17	US-11-169-041-28	Sequence 28, Appl
1106	78.5	7.3	4816	13	US-10-204-639-94	Sequence 94, Appl
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c1112	78.5	7.3	6510	10	US-10-995-561-112	Sequence 112, App
c1113	78.5	7.3	6873	13	US-10-965-103-11	Sequence 11, Appl
c1114	78.5	7.3	7823	10	US-10-995-561-117	Sequence 117, App
c1115	78.5	7.3	7848	10	US-10-995-561-111	Sequence 111, App
c1116	78.5	7.3	7935	10	US-10-995-561-113	Sequence 113, App
c1117	78.5	7.3	7959	10	US-10-995-561-108	Sequence 108, App
c1118	78.5	7.3	8013	10	US-10-995-561-104	Sequence 104, App
c1119	78.5	7.3	8155	10	US-10-995-561-116	Sequence 116, App
c1120	78.5	7.3	8226	10	US-10-995-561-107	Sequence 107, App
c1121	78.5	7.3	8278	10	US-10-995-561-106	Sequence 106, App
c1122	78.5	7.3	8332	10	US-10-995-561-110	Sequence 110, App
c1123	78.5	7.3	8371	10	US-10-995-561-109	Sequence 109, App
c1124	78.5	7.3	9975	13	US-10-496-351-4	Sequence 4, Appli
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c1163	78	7.3	1191	18	US-11-143-947A-36	Sequence 36, Appl
c1164	78	7.3	1191	18	US-11-143-966A-36	Sequence 36, Appl
1165	78	7.3	1275	13	US-10-548-748-43	Sequence 43, Appl
c1166	78	7.3	1344	18	US-11-143-943A-37	Sequence 37, Appl
c1167	78	7.3	1344	18	US-11-143-947A-37	Sequence 37, Appl
c1168	78	7.3	1344	18	US-11-143-966A-37	Sequence 37, Appl
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c1185	78	7.3	1675	18	US-11-290-153-135	Sequence 135, App
1186	78	7.3	1823	7	US-09-925-065A-681281	Sequence 681281,
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c1194	78	7.3	3213	10	US-10-467-657-1653	Sequence 1653, Ap
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c1196	78	7.3	4051	10	US-10-775-169-315	Sequence 315, App
c1197	78	7.3	4064	17	US-11-195-197-8	Sequence 8, Appli
1198	78	7.3	4400	17	US-11-136-527-1982	Sequence 1982, Ap
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1203	78	7.3	50484	11	US-10-893-483-63	Sequence 63, Appl
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1208	78	7.3	92861	11	US-10-330-773-820	Sequence 820, App
1209	78	7.3	96256	10	US-10-775-169-352	Sequence 352, App
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1213	78	7.3	110608	10	US-10-775-169-193	Sequence 193, App
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1216	78	7.3	143947	17	US-11-193-771-37	Sequence 37, Appl
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1218	78	7.3	143947	17	US-11-193-806-37	Sequence 37, Appl
1219	78	7.3	143947	17	US-11-193-857-37	Sequence 37, Appl
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1223	77.5	7.2	501	7	US-09-925-065A-762359	Sequence 762359,
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c1233	77.5	7.2	702	10	US-10-750-623-63729	Sequence 63729, A
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c1242	77.5	7.2	986	12	US-10-301-480-1202208	Sequence 1202208,
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1276	77.5	7.2	2467	13	US-10-784-004-620	Sequence 620, App
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c1283	77.5	7.2	3266	10	US-10-750-623-30229	Sequence 30229, A
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c1286	77.5	7.2	15409	17	US-11-124-367A-5013	Sequence 5013, Ap
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1292	77.5	7.2	191150	13	US-10-517-905-19	Sequence 19, Appl
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c1311	77	7.2	598	12	US-10-301-480-761409	Sequence 761409,
c1312	77	7.2	598	12	US-10-301-480-761410	Sequence 761410,
c1313	77	7.2	598	12	US-10-301-480-761411	Sequence 761411,
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1316	77	7.2	658	7	US-09-925-065A-785222	Sequence 785222,
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c1319	77	7.2	677	10	US-10-750-623-31576	Sequence 31576, A
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1323	77	7.2	788	12	US-10-301-480-721285	Sequence 721285,
c1324	77	7.2	809	12	US-10-301-480-592893	Sequence 592893,
c1325	77	7.2	809	12	US-10-301-480-1206302	Sequence 1206302,
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c1330	77	7.2	971	12	US-10-301-480-1145785	Sequence 1145785,
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c1332	77	7.2	990	12	US-10-301-480-1159069	Sequence 1159069,
c1333	77	7.2	999	12	US-10-301-480-586104	Sequence 586104,
c1334	77	7.2	999	12	US-10-301-480-1199513	Sequence 1199513,
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c1342	77	7.2	1172	12	US-10-301-480-703308	Sequence 703308,
c1343	77	7.2	1211	18	US-11-096-568A-26986	Sequence 26986, A
1344	77	7.2	1230	18	US-11-096-568A-19162	Sequence 19162, A
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c1350	77	7.2	1387	10	US-10-750-623-64260	Sequence 64260, A
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1357	77	7.2	1775	18	US-11-096-568A-15110	Sequence 15110, A
1359	77	7.2	1841	11	US-10-973-115B-457	Sequence 457, App
1366	77	7.2	1841	18	US-11-290-153-457	Sequence 457, App
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c1370	77	7.2	2434	11	US-10-491-468-52	Sequence 52, Appl
1371	77	7.2	2522	18	US-11-253-151-5	Sequence 5, Appli
c1372	77	7.2	2560	18	US-11-072-512-1284	Sequence 1284, Ap
1373	77	7.2	2561	17	US-11-127-877-26	Sequence 26, Appl
c1374	77	7.2	2743	18	US-11-072-512-391	Sequence 391, App
1375	77	7.2	2818	18	US-11-072-512-625	Sequence 625, App
1376	77	7.2	3032	18	US-11-167-838-1	Sequence 1, Appli
1377	77	7.2	3032	18	US-11-167-838-2	Sequence 2, Appli
1378	77	7.2	3032	18	US-11-167-838-3	Sequence 3, Appli
1379	77	7.2	3032	18	US-11-167-838-4	Sequence 4, Appli
c1380	77	7.2	3067	13	US-10-508-440-12	Sequence 12, Appl
1381	77	7.2	3298	17	US-11-136-527-3261	Sequence 3261, Ap
1382	77	7.2	3726	18	US-11-036-196-1716	Sequence 1716, Ap
1383	77	7.2	3726	18	US-11-224-663-531	Sequence 531, App
1384	77	7.2	3726	18	US-11-224-525-531	Sequence 531, App
1385	77	7.2	3753	17	US-11-136-527-2483	Sequence 2483, Ap
1386	77	7.2	5398	11	US-10-724-598-1	Sequence 1, Appli
1387	77	7.2	6177	17	US-11-094-917-7	Sequence 7, Appli
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c1389	77	7.2	6453	18	US-11-219-264-5	Sequence 5, Appli
1390	77	7.2	6622	11	US-10-933-746-42	Sequence 42, Appl
1391	77	7.2	7996	11	US-10-330-773-388	Sequence 388, App
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1393	77	7.2	9630	17	US-11-124-367A-102	Sequence 102, App
1394	77	7.2	15231	18	US-11-036-196-1780	Sequence 1780, Ap
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c1410	77	7.2	162537	17	US-11-121-086-59	Sequence 59, Appl
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1438	76.5	7.1	744	18	US-11-103-195-67	Sequence 67, Appl
c1439	76.5	7.1	773	7	US-09-925-065A-553612	Sequence 553612,
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1464	76.5	7.1	1608	18	US-11-096-568A-10150	Sequence 10150, A
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1466	76.5	7.1	1637	18	US-11-096-568A-22155	Sequence 22155, A
1467	76.5	7.1	1680	18	US-11-173-893-3	Sequence 3, Appli
1468	76.5	7.1	1707	10	US-10-750-185-40786	Sequence 40786, A
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c1485	76.5	7.1	1863	12	US-10-301-480-809207	Sequence 809207,
c1486	76.5	7.1	1863	12	US-10-301-480-809208	Sequence 809208,
1487	76.5	7.1	2180	17	US-11-150-533-23	Sequence 23, Appl
1488	76.5	7.1	2228	17	US-11-136-527-1840	Sequence 1840, Ap
1489	76.5	7.1	2255	17	US-11-150-533-1	Sequence 1, Appli
1490	76.5	7.1	2387	18	US-11-173-893-11	Sequence 11, Appl
1491	76.5	7.1	2841	18	US-11-200-296B-11	Sequence 11, Appl
1492	76.5	7.1	3111	18	US-11-173-893-1	Sequence 1, Appli
1493	76.5	7.1	3151	17	US-11-000-688-931	Sequence 931, App
c1494	76.5	7.1	3409	18	US-11-072-512-895	Sequence 895, App
1495	76.5	7.1	3410	17	US-11-234-786-110	Sequence 110, App
c1496	76.5	7.1	3431	18	US-11-245-147-174	Sequence 174, App
c1497	76.5	7.1	3438	18	US-11-072-512-521	Sequence 521, App
c1498	76.5	7.1	4010	18	US-11-245-147-217	Sequence 217, App
1499	76.5	7.1	4305	17	US-11-080-991-67	Sequence 67, Appl
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(without alignments)
9838.537 Million cell updates/sec

Title: US-09-854-280-4
Perfect score: 1047
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	637.4	60.9	1027	4	BC069410	BC069410 Homo sapi
	2	588	56.2	588	11	DQ030711	DQ030711 Homo sapi
	3	521	49.8	586	11	DQ030712	DQ030712 Pan trogl
	4	462	44.1	466	5	BX281422	BX281422 BX281422
c	5	377	36.0	669	10	AG139411	AG139411 Pan trogl
c	6	244.8	23.4	264	2	BE551188	BE551188 7b55g03.x
c	7	66	6.3	1203	10	CNS015Y4	AL106054 Drosophil
	8	61.4	5.9	2656	10	CL505520	CL505520 SAIL_751_
c	9	61.2	5.8	535	10	CE738486	CE738486 tigr-gss-
	10	60.8	5.8	1454	10	AG290167	AG290167 Mus muscu
c	11	59.4	5.7	1177	10	AG441911	AG441911 Mus muscu
c	12	58.6	5.6	873	10	AG043471	AG043471 Pan trogl
	13	58	5.5	1452	10	AG032979	AG032979 Pan trogl
	14	57.6	5.5	1331	7	CK404476	CK404476 AUF_IfHdk
	15	57.6	5.5	1785	9	CC219595	CC219595 CH261-62D
	16	56.8	5.4	441	1	AI275406	AI275406 ql63c10.x
	17	56.8	5.4	836	3	BI828970	BI828970 603074846
	18	56.4	5.4	1520	10	AG057334	AG057334 Pan trogl
c	19	55.8	5.3	932	10	CNS0072Q	AL066742 Drosophil
c	20	55.6	5.3	925	10	CNS0091P	AL053013 Drosophil
c	21	55.4	5.3	699	8	DN407935	DN407935 LIB4007-0
	22	55.2	5.3	524	1	AI430337	AI430337 mf68b10.y
	23	55.2	5.3	526	5	BX517868	BX517868 BX517868
	24	55.2	5.3	718	3	BI561289	BI561289 603256441
	25	55	5.3	1151	7	CK210749	CK210749 FGAS02257
c	26	54.8	5.2	1137	2	BG809979	BG809979 mgct002xd
	27	54.8	5.2	1402	3	BM809524	BM809524 AGENCOURT
	28	54.6	5.2	925	10	CNS0091P	AL053013 Drosophil
c	29	54.6	5.2	1239	10	AG435545	AG435545 Mus muscu
c	30	54.4	5.2	862	10	AG036151	AG036151 Pan trogl
	31	54.4	5.2	1311	3	BM544820	BM544820 AGENCOURT
	32	54.2	5.2	664	8	DN989597	DN989597 TC108206
	33	53.8	5.1	534	11	DQ036975	DQ036975 Homo sapi
c	34	53.6	5.1	1628	10	CG757066	CG757066 P052-2-A0
	35	53.2	5.1	1288	5	BQ678719	BQ678719 AGENCOURT
	36	53	5.1	989	10	CL466911	CL466911 SAIL_1263
	37	52.8	5.0	1185	3	BQ072237	BQ072237 AGENCOURT
c	38	52.6	5.0	435	2	BG579143	BG579143 df23f12.y
	39	52.6	5.0	844	10	CNS0052P	AL056652 Drosophil
c	40	52.6	5.0	873	7	CV663458	CV663458 LCPE04EX0
	41	52.6	5.0	1610	9	BZ569386	BZ569386 pacs2-164
	42	52.2	5.0	534	11	DQ036976	DQ036976 Pan trogl
c	43	52.2	5.0	903	3	BM985915	BM985915 6_H01_T3
	44	52.2	5.0	1025	11	CNS03LNW	AL249701 Tetraodon
	45	52.2	5.0	1897	10	CL468169	CL468169 SAIL_1282
c	46	51.8	4.9	943	5	BQ897301	BQ897301 AGENCOURT
c	47	51.8	4.9	1182	10	CL080907	CL080907 CH216-160
	48	51.6	4.9	1203	10	CNS015Y4	AL106054 Drosophil
	49	51.6	4.9	1300	8	DN679241	DN679241 CGX04-H11
	50	51.6	4.9	1713	10	AG435689	AG435689 Mus muscu
c	51	51.4	4.9	935	10	CNS006XK	AL066051 Drosophil
	52	51.4	4.9	961	10	AG592904	AG592904 Mus muscu
	53	51.4	4.9	1100	5	BU850190	BU850190 AGENCOURT
	54	51.4	4.9	1374	10	AG435756	AG435756 Mus muscu
	55	51.4	4.9	1694	10	CL509291	CL509291 SAIL_811_
	56	51.2	4.9	910	10	AG032931	AG032931 Pan trogl
c	57	51.2	4.9	1116	9	BZ569478	BZ569478 pacs2-164
c	58	51.2	4.9	1210	10	AG448374	AG448374 Mus muscu
c	59	51.2	4.9	1506	10	AG442117	AG442117 Mus muscu
	60	51	4.9	1032	5	BQ649800	BQ649800 AGENCOURT
c	61	51	4.9	1081	5	BX428685	BX428685 BX428685
	62	51	4.9	1830	10	CL078620	CL078620 CH216-151
c	63	51	4.9	1956	10	CG754548	CG754548 P050-1-A1
c	64	50.8	4.9	832	10	AG132251	AG132251 Pan trogl
c	65	50.8	4.9	989	10	AG030675	AG030675 Pan trogl
c	66	50.8	4.9	1086	1	AJ927520	AJ927520 AJ927520
c	67	50.8	4.9	1177	10	AG448271	AG448271 Mus muscu
	68	50.8	4.9	1212	3	BQ069498	BQ069498 AGENCOURT
	69	50.8	4.9	2420	10	CL509247	CL509247 SAIL_811_
	70	50.6	4.8	1038	10	CL478560	CL478560 SAIL_292_
	71	50.6	4.8	1081	1	AW727480	AW727480 GA__Ea001
	72	50.6	4.8	1132	10	CL510069	CL510069 SAIL_823_
c	73	50.6	4.8	1286	3	BM908603	BM908603 AGENCOURT
	74	50.4	4.8	819	1	AJ924594	AJ924594 AJ924594
	75	50.4	4.8	940	10	CL482784	CL482784 SAIL_367_
	76	50.4	4.8	1101	10	CNS00397	AL063912 Drosophil
	77	50.4	4.8	1115	8	DN680558	DN680558 CGX11-F10
c	78	50.4	4.8	1286	10	AG448422	AG448422 Mus muscu
	79	50.4	4.8	1381	10	AG396965	AG396965 Mus muscu
	80	50.4	4.8	1392	10	AG390642	AG390642 Mus muscu
c	81	50.2	4.8	957	3	BM416095	BM416095 OP21179 M
c	82	50.2	4.8	1077	10	CNS0156Q	AL105068 Drosophil
c	83	50.2	4.8	1081	5	BU170411	BU170411 AGENCOURT
	84	50.2	4.8	1093	5	BQ719863	BQ719863 AGENCOURT
c	85	50.2	4.8	1134	10	CW953401	CW953401 TcB39.2_H
c	86	50.2	4.8	1169	10	AG290036	AG290036 Mus muscu
	87	50.2	4.8	1244	3	BQ050866	BQ050866 AGENCOURT
c	88	50.2	4.8	1548	10	AG435551	AG435551 Mus muscu
c	89	50	4.8	844	10	CNS0052P	AL056652 Drosophil
c	90	50	4.8	876	10	CW940373	CW940373 TcB21.2_B
c	91	50	4.8	1163	10	AG441711	AG441711 Mus muscu
c	92	50	4.8	1224	10	AG448370	AG448370 Mus muscu
c	93	50	4.8	1231	10	AG430715	AG430715 Mus muscu
c	94	50	4.8	1675	10	AG360980	AG360980 Mus muscu
c	95	49.8	4.8	1703	10	CL078618	CL078618 CH216-151

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	97	49.6	4.7	907	7	CF868868 CF868868 tric016xl
c	98	49.6	4.7	912	10	CW941005 CW941005 TcB22.1_D
	99	49.6	4.7	1142	10	CL461680 CL461680 SAIL_1150
c	100	49.6	4.7	1166	6	CD509197 CD509197 CDA95-A05
	101	49.6	4.7	1449	10	AG360973 AG360973 Mus muscu
	102	49.6	4.7	1626	1	AJ928957 AJ928957 AJ928957
	103	49.4	4.7	420	8	W88186 W88186 mf68b10.r1
c	104	49.4	4.7	848	10	CW949803 CW949803 TcB34.4_B
	105	49.4	4.7	1153	3	BM804596 BM804596 AGENCOURT
c	106	49.4	4.7	1190	8	DN724708 DN724708 CNB20-G01
c	107	49.4	4.7	1216	10	AG441574 AG441574 Mus muscu
c	108	49.4	4.7	1328	10	AG441962 AG441962 Mus muscu
c	109	49.4	4.7	1450	10	AG429738 AG429738 Mus muscu
c	110	49.2	4.7	916	10	CW938719 CW938719 TcB18.4_E
c	111	49.2	4.7	953	10	AG391885 AG391885 Mus muscu
c	112	49.2	4.7	957	10	CL494117 CL494117 SAIL_58_C
c	113	49.2	4.7	1124	10	AG041123 AG041123 Pan trogl
c	114	49.2	4.7	1148	1	AJ926816 AJ926816 AJ926816
	115	49.2	4.7	1195	6	CA488491 CA488491 AGENCOURT
c	116	49.2	4.7	1360	10	CL469817 CL469817 SAIL_133_
c	117	49	4.7	664	9	BH140755 BH140755 ZMMBB0000
c	118	49	4.7	718	10	CZ179533 CZ179533 69146Orao
	119	49	4.7	839	10	CNS004NB AL054280 Drosophil
	120	49	4.7	840	9	B19033 B19033 T28M6-Sp6 T
	121	49	4.7	848	10	AG060231 AG060231 Pan trogl
	122	49	4.7	993	10	AG090948 AG090948 Pan trogl
	123	49	4.7	1017	6	CA977001 CA977001 AGENCOURT
c	124	49	4.7	1030	10	AG077951 AG077951 Pan trogl
	125	49	4.7	1188	10	AG435194 AG435194 Mus muscu
	126	49	4.7	1674	10	CL078342 CL078342 CH216-149
	127	48.8	4.7	562	8	DR799876 DR799876 ZM_BFb002
	128	48.8	4.7	724	10	AG171201 AG171201 Pan trogl
c	129	48.8	4.7	781	10	CW951290 CW951290 TcB36.3_H
	130	48.8	4.7	869	10	AG162064 AG162064 Pan trogl
c	131	48.8	4.7	917	5	BU183626 BU183626 AGENCOURT
	132	48.8	4.7	952	11	CNS0766T AL431019 T7 end of
	133	48.8	4.7	959	10	AG450311 AG450311 Mus muscu
c	134	48.8	4.7	1110	10	CL072693 CL072693 CH216-126
	135	48.8	4.7	1159	9	CC210735 CC210735 CH261-185
	136	48.6	4.6	388	2	BG909378 BG909378 TaLrl102C
	137	48.6	4.6	421	9	BH254057 BH254057 SALK_0159
	138	48.6	4.6	907	10	CL122680 CL122680 ISBI-82I1
	139	48.6	4.6	944	9	BZ051100 BZ051100 jnr62d07.
c	140	48.6	4.6	1184	10	AG371418 AG371418 Mus muscu
c	141	48.6	4.6	1210	7	CR553327 CR553327 CR553327
	142	48.4	4.6	744	10	CNS017ZK AL108698 Drosophil
	143	48.4	4.6	761	10	AG535575 AG535575 Mus muscu
c	144	48.4	4.6	802	10	CNS02R43 AL210108 Tetraodon
	145	48.4	4.6	925	10	CL468483 CL468483 SAIL_1287
	146	48.4	4.6	935	10	CNS006XK AL066051 Drosophil
c	147	48.4	4.6	1002	10	AG046242 AG046242 Pan trogl
c	148	48.4	4.6	1035	10	CNS017KO AL108162 Drosophil
	149	48.4	4.6	1121	10	AG062320 AG062320 Pan trogl
	150	48.4	4.6	1161	9	CC298228 CC298228 CH261-2F1
c	151	48.4	4.6	1196	8	DN707211 DN707211 CLJ70-B08
	152	48.4	4.6	1341	10	AG435660 AG435660 Mus muscu
c	153	48.2	4.6	876	3	BI951917 BI951917 HVSMEm000
	154	48.2	4.6	1043	5	BU510935 BU510935 AGENCOURT
c	155	48.2	4.6	1056	10	AG126159 AG126159 Pan trogl
c	156	48.2	4.6	1057	5	BX442979 BX442979 BX442979
	157	48.2	4.6	1086	10	CL979895 CL979895 OsIFCC045
	158	48.2	4.6	1097	6	CB206205 CB206205 AGENCOURT
c	159	48.2	4.6	1330	10	CL063297 CL063297 CH216-99P
	160	48.2	4.6	1340	10	AG430438 AG430438 Mus muscu
c	161	48.2	4.6	1538	10	CL031113 CL031113 CH216-32A
c	162	48.2	4.6	1656	10	AG448497 AG448497 Mus muscu
	163	48	4.6	940	10	CL479759 CL479759 SAIL_311_
	164	48	4.6	971	10	CL467520 CL467520 SAIL_1271
	165	48	4.6	990	10	CL500250 CL500250 SAIL_67_C
c	166	48	4.6	1063	10	CL498639 CL498639 SAIL_657_
	167	48	4.6	1100	10	CNS016KD AL106855 Drosophil
	168	48	4.6	1147	9	BZ051981 BZ051981 jnr56f09.
	169	48	4.6	1168	3	BM809732 BM809732 AGENCOURT
	170	48	4.6	1199	6	CA460903 CA460903 AGENCOURT
	171	48	4.6	1268	3	BI752215 BI752215 603022405
c	172	48	4.6	1370	10	AG340828 AG340828 Mus muscu
c	173	47.8	4.6	243	10	CE446061 CE446061 tigr-gss-
	174	47.8	4.6	955	1	AL536505 AL536505 AL536505
	175	47.8	4.6	978	10	AG030617 AG030617 Pan trogl
	176	47.8	4.6	1031	5	BU167290 BU167290 AGENCOURT
	177	47.8	4.6	1066	10	CL497282 CL497282 SAIL_639_
	178	47.8	4.6	1168	3	BM468388 BM468388 AGENCOURT
c	179	47.8	4.6	1625	10	AG043477 AG043477 Pan trogl
	180	47.8	4.6	1628	10	CL496050 CL496050 SAIL_619_
c	181	47.8	4.6	1751	10	AG435105 AG435105 Mus muscu
c	182	47.6	4.5	829	3	BI958040 BI958040 HVSMEn001
c	183	47.6	4.5	857	10	CW941243 CW941243 TcB22.2_F
	184	47.6	4.5	896	10	CL467806 CL467806 SAIL_1276
	185	47.6	4.5	910	10	CNS006ON AL065629 Drosophil
	186	47.6	4.5	927	5	BU179467 BU179467 AGENCOURT
c	187	47.6	4.5	945	10	AG450090 AG450090 Mus muscu
	188	47.6	4.5	962	10	CL468509 CL468509 SAIL_1287
	189	47.6	4.5	969	10	CL479087 CL479087 SAIL_301_
c	190	47.6	4.5	981	10	CW937110 CW937110 TcB16.1_B
	191	47.6	4.5	991	10	CL462942 CL462942 SAIL_1173
c	192	47.6	4.5	1093	6	CB905750 CB905750 tric075xp
c	193	47.6	4.5	1093	7	CF877401 CF877401 tric075xp
c	194	47.6	4.5	1097	5	BQ711431 BQ711431 AGENCOURT
	195	47.6	4.5	1209	10	CL505488 CL505488 SAIL_751_
	196	47.6	4.5	1215	10	AG387898 AG387898 Mus muscu
c	197	47.6	4.5	1692	10	AG396765 AG396765 Mus muscu
c	198	47.4	4.5	814	10	CW941256 CW941256 TcB22.2_F
	199	47.4	4.5	875	9	BZ051621 BZ051621 jnr59f12.
c	200	47.4	4.5	948	10	AG161418 AG161418 Pan trogl
	201	47.4	4.5	990	5	BU944153 BU944153 AGENCOURT
c	202	47.4	4.5	1013	10	AG080087 AG080087 Pan trogl
	203	47.4	4.5	1051	10	CL478891 CL478891 SAIL_299_
	204	47.4	4.5	1069	10	CL486078 CL486078 SAIL_427_
c	205	47.4	4.5	1100	10	CNS016KD AL106855 Drosophil
c	206	47.4	4.5	1110	1	AJ926050 AJ926050 AJ926050
c	207	47.4	4.5	1139	3	BM914614 BM914614 AGENCOURT
c	208	47.4	4.5	1188	5	BQ652269 BQ652269 AGENCOURT
c	209	47.4	4.5	1392	8	DN716556 DN716556 CNB113-E0
c	210	47.4	4.5	1690	10	AG435238 AG435238 Mus muscu
c	211	47.4	4.5	1961	10	AG435522 AG435522 Mus muscu
c	212	47.2	4.5	663	10	AG080425 AG080425 Pan trogl
c	213	47.2	4.5	1007	10	CW938543 CW938543 TcB18.3_E
	214	47.2	4.5	1059	6	CA453794 CA453794 AGENCOURT
	215	47.2	4.5	1101	10	CNS001T4 AL061330 Drosophil
c	216	47.2	4.5	1147	1	AJ928063 AJ928063 AJ928063
	217	47.2	4.5	1199	3	BQ073023 BQ073023 AGENCOURT
c	218	47.2	4.5	1434	8	DN477736 DN477736 altr002xl
	219	47.2	4.5	1509	2	BE910279 BE910279 601503624
	220	47.2	4.5	1518	10	CL469805 CL469805 SAIL_133_
c	221	47.2	4.5	1556	10	AG390838 AG390838 Mus muscu
c	222	47.2	4.5	1619	10	AG435648 AG435648 Mus muscu
c	223	47.2	4.5	1691	10	AG341104 AG341104 Mus muscu
	224	47	4.5	694	2	BG772779 BG772779 602720952
	225	47	4.5	866	8	CV774922 CV774922 FGAS06932
c	226	47	4.5	867	6	CB898580 CB898580 tric015xd
	227	47	4.5	880	9	CC912175 CC912175 t070h10ba
	228	47	4.5	950	10	CL478344 CL478344 SAIL_288_
	229	47	4.5	975	5	BU171307 BU171307 AGENCOURT
	230	47	4.5	1053	6	CA456946 CA456946 AGENCOURT
	231	47	4.5	1068	5	BU857460 BU857460 AGENCOURT
	232	47	4.5	1141	10	CL082639 CL082639 CH216-168
	233	47	4.5	1254	10	AG365445 AG365445 Mus muscu
	234	47	4.5	1448	9	CC194731 CC194731 CH261-183
	235	47	4.5	1505	8	DN663125 DN663125 CFW12-A10
c	236	47	4.5	1648	10	AG390465 AG390465 Mus muscu
	237	47	4.5	1691	10	CL078603 CL078603 CH216-151
	238	46.8	4.5	630	8	DR807650 DR807650 ZM_BFb003
	239	46.8	4.5	641	8	DR784904 DR784904 ZM_BFb000
	240	46.8	4.5	645	8	DR816378 DR816378 ZM_BFb004
	241	46.8	4.5	657	7	CO521874 CO521874 3530_1_14

	242	46.8	4.5	672	10	AG133158 AG133158 Pan trogl
	243	46.8	4.5	678	8	DR820780 DR820780 ZM_BFb005
c	244	46.8	4.5	683	5	BX333887 BX333887 BX333887
	245	46.8	4.5	696	2	BF718604 BF718604 KEST75 no
	246	46.8	4.5	700	8	DR786453 DR786453 ZM_BFb000
	247	46.8	4.5	717	9	BZ049776 BZ049776 jnr48h03.
c	248	46.8	4.5	757	3	BI959198 BI959198 HVSMEn001
	249	46.8	4.5	762	10	AG527521 AG527521 Mus muscu
	250	46.8	4.5	827	8	DR819122 DR819122 ZM_BFb005
c	251	46.8	4.5	827	9	AZ198560 AZ198560 SP_1037_B
	252	46.8	4.5	835	8	DR814688 DR814688 ZM_BFb004
c	253	46.8	4.5	856	10	CG327014 CG327014 OG0GN57TV
	254	46.8	4.5	920	5	BU929799 BU929799 AGENCOURT
	255	46.8	4.5	996	5	BU531181 BU531181 AGENCOURT
c	256	46.8	4.5	1016	10	AG365375 AG365375 Mus muscu
	257	46.8	4.5	1065	5	BQ681076 BQ681076 AGENCOURT
	258	46.8	4.5	1068	10	CL490461 CL490461 SAIL_539_
c	259	46.8	4.5	1071	10	AG060609 AG060609 Pan trogl
c	260	46.8	4.5	1101	10	CNS00DAT AL067109 Drosophil
c	261	46.8	4.5	1177	10	AG441817 AG441817 Mus muscu
c	262	46.8	4.5	1193	8	DN721663 DN721663 CNB14-F07
c	263	46.8	4.5	1222	10	CL119200 CL119200 ISB1-76D1
c	264	46.8	4.5	1289	10	CL147104 CL147104 ISB1-156E
	265	46.8	4.5	1344	10	AG435591 AG435591 Mus muscu
c	266	46.8	4.5	1542	10	AG032943 AG032943 Pan trogl
c	267	46.6	4.5	420	5	BU947016 BU947016 rf16e08.y
c	268	46.6	4.5	739	10	AG080613 AG080613 Pan trogl
	269	46.6	4.5	749	9	BH838502 BH838502 LMCR10001
	270	46.6	4.5	787	9	B21310 B21310 T3J8-T7 TAM
c	271	46.6	4.5	798	6	CB646141 CB646141 OSJNEb08G
	272	46.6	4.5	948	10	CL472234 CL472234 SAIL_173b
	273	46.6	4.5	974	10	AG043196 AG043196 Pan trogl
c	274	46.6	4.5	975	10	AG095351 AG095351 Pan trogl
	275	46.6	4.5	996	5	BQ708087 BQ708087 AGENCOURT
	276	46.6	4.5	1003	10	CL468493 CL468493 SAIL_1287
c	277	46.6	4.5	1008	10	AG063088 AG063088 Pan trogl
	278	46.6	4.5	1029	10	CL465666 CL465666 SAIL_1243
	279	46.6	4.5	1062	8	DN654975 DN654975 CEC14-C12
	280	46.6	4.5	1082	3	BM552391 BM552391 AGENCOURT
	281	46.6	4.5	1101	10	CNS001JM AL061089 Drosophil
	282	46.6	4.5	1101	10	CNS0153F AL104949 Drosophil
c	283	46.6	4.5	1136	1	AJ927171 AJ927171 AJ927171
	284	46.6	4.5	1153	9	CC252982 CC252982 CH261-187
	285	46.6	4.5	1181	1	AJ927566 AJ927566 AJ927566
c	286	46.6	4.5	1206	8	DN662030 DN662030 CFW06-E02
c	287	46.6	4.5	1212	10	CL641164 CL641164 CH213-6I0
	288	46.6	4.5	1337	10	AG393286 AG393286 Mus muscu
c	289	46.6	4.5	1548	10	CL043588 CL043588 CH216-58E
	290	46.6	4.5	2052	10	CL947063 CL947063 OsIFSB002
	291	46.4	4.4	309	10	CNS0037S AL064467 Drosophil
	292	46.4	4.4	428	6	CB050776 CB050776 NISC_gj19
	293	46.4	4.4	522	6	CB650491 CB650491 OSJNEb14P
c	294	46.4	4.4	599	8	DN417930 DN417930 LIB4215-0
c	295	46.4	4.4	653	2	BB622918 BB622918 BB622918
c	296	46.4	4.4	686	9	BZ000240 BZ000240 oeg78e03.
	297	46.4	4.4	704	10	AG060135 AG060135 Pan trogl
c	298	46.4	4.4	859	10	AG282470 AG282470 Mus muscu
c	299	46.4	4.4	860	6	CB905481 CB905481 tric074xm
c	300	46.4	4.4	860	7	CF876988 CF876988 tric074xm
	301	46.4	4.4	906	3	BI416574 BI416574 hasp001xg
c	302	46.4	4.4	937	10	AG377591 AG377591 Mus muscu
	303	46.4	4.4	993	9	CC302019 CC302019 CH261-91B
	304	46.4	4.4	998	5	BQ951828 BQ951828 AGENCOURT
c	305	46.4	4.4	1009	6	CB906568 CB906568 tric079xh
c	306	46.4	4.4	1009	7	CF878880 CF878880 tric079xh
	307	46.4	4.4	1057	11	CNS046BO AL276477 Tetraodon
	308	46.4	4.4	1142	10	CL468510 CL468510 SAIL_1287
	309	46.4	4.4	1150	5	BQ892481 BQ892481 AGENCOURT
c	310	46.4	4.4	1166	8	DN729534 DN729534 CNB47-G06
c	311	46.4	4.4	1178	10	AG333907 AG333907 Mus muscu
c	312	46.4	4.4	1277	10	CG753585 CG753585 P048-3-H1
	313	46.4	4.4	1280	2	BF973268 BF973268 602242177
	314	46.4	4.4	1360	3	BM463178 BM463178 AGENCOURT
	315	46.4	4.4	1405	5	BQ798843 BQ798843 EST 1012
c	316	46.4	4.4	1592	1	AJ924688 AJ924688 AJ924688
c	317	46.4	4.4	2287	10	AG341484 AG341484 Mus muscu
	318	46.4	4.4	2313	7	CK423624 CK423624 AUF_IpSpn
	319	46.2	4.4	657	8	DN432946 DN432946 LIB4217-0
c	320	46.2	4.4	827	9	AZ183795 AZ183795 SP_1002_A
c	321	46.2	4.4	843	10	CNS00CS1 AL059666 Drosophil
c	322	46.2	4.4	909	2	BE215391 BE215391 HV_CEb000
c	323	46.2	4.4	910	10	CNS006ON AL065629 Drosophil
c	324	46.2	4.4	975	10	CNS02KBD AL201298 Tetraodon
	325	46.2	4.4	989	10	CL468473 CL468473 SAIL_1287
	326	46.2	4.4	1006	10	CL476315 CL476315 SAIL_252b
c	327	46.2	4.4	1026	5	BU112476 BU112476 603129751
	328	46.2	4.4	1051	6	CB206210 CB206210 AGENCOURT
c	329	46.2	4.4	1063	11	CNS040FA AL268831 Tetraodon
	330	46.2	4.4	1085	10	CL466781 CL466781 SAIL_1261
c	331	46.2	4.4	1114	11	CR030904 CR030904 Reverse s
	332	46.2	4.4	1122	9	CC231036 CC231036 CH261-27F
c	333	46.2	4.4	1122	10	AG441585 AG441585 Mus muscu
	334	46.2	4.4	1152	10	AG076818 AG076818 Pan trogl
c	335	46.2	4.4	1167	10	AG360800 AG360800 Mus muscu
	336	46.2	4.4	1198	9	CC190008 CC190008 CH261-138
	337	46.2	4.4	1247	8	DN732757 DN732757 CNB66-B05
c	338	46.2	4.4	1287	8	DN677526 DN677526 CGX13-G01
c	339	46.2	4.4	1400	10	AG429585 AG429585 Mus muscu
	340	46	4.4	316	1	AJ936784 AJ936784 AJ936784
c	341	46	4.4	516	3	BI996737 BI996737 1031041E0
c	342	46	4.4	649	9	AQ853740 AQ853740 nbxb0032E
c	343	46	4.4	693	5	BQ819374 BQ819374 1030077C1
	344	46	4.4	721	9	BZ051506 BZ051506 jnr59a07.
	345	46	4.4	806	10	AG427940 AG427940 Mus muscu
c	346	46	4.4	862	10	AG381195 AG381195 Mus muscu
c	347	46	4.4	867	3	BI957861 BI957861 HVSMEn001
	348	46	4.4	867	5	BX440431 BX440431 BX440431
	349	46	4.4	870	9	CC905689 CC905689 t025a07ba
c	350	46	4.4	898	5	BQ430549 BQ430549 AGENCOURT
c	351	46	4.4	901	10	AG043735 AG043735 Pan trogl
c	352	46	4.4	915	10	CNS02FE6 AL194919 Tetraodon
c	353	46	4.4	965	10	CW951353 CW951353 TcB36.4_C
	354	46	4.4	977	10	CL484601 CL484601 SAIL_39_F
c	355	46	4.4	997	5	BQ670959 BQ670959 AGENCOURT
c	356	46	4.4	1004	6	CB562855 CB562855 AGENCOURT
	357	46	4.4	1037	5	BU153985 BU153985 AGENCOURT
	358	46	4.4	1043	10	CL474886 CL474886 SAIL_228_
	359	46	4.4	1051	5	BQ435546 BQ435546 AGENCOURT
c	360	46	4.4	1069	8	DN682995 DN682995 CGX27-D07
	361	46	4.4	1144	7	CR944200 CR944200 CR944200
c	362	46	4.4	1385	8	DN677991 DN677991 CFW96-E09
	363	46	4.4	1403	9	CC290252 CC290252 CH261-172
	364	45.8	4.4	715	10	AG139589 AG139589 Pan trogl
c	365	45.8	4.4	788	6	CB647911 CB647911 OSJNEb11A
c	366	45.8	4.4	792	10	AG449674 AG449674 Mus muscu
c	367	45.8	4.4	809	10	CW951428 CW951428 TcB36.4_F
	368	45.8	4.4	817	9	BZ051647 BZ051647 jnr58a11.
	369	45.8	4.4	826	10	AG856072 AG856072 Oryza sat
	370	45.8	4.4	854	5	BU960187 BU960187 AGENCOURT
	371	45.8	4.4	854	9	B18900 B18900 T20D17-Sp6
c	372	45.8	4.4	861	10	AG043892 AG043892 Pan trogl
c	373	45.8	4.4	862	10	CW953289 CW953289 TcB39.2_D
c	374	45.8	4.4	864	10	AG060559 AG060559 Pan trogl
c	375	45.8	4.4	881	5	BX427015 BX427015 BX427015
c	376	45.8	4.4	918	5	BX365380 BX365380 BX365380
	377	45.8	4.4	951	5	BU940544 BU940544 AGENCOURT
	378	45.8	4.4	961	10	CL468503 CL468503 SAIL_1287
c	379	45.8	4.4	971	10	CW938757 CW938757 TcB18.4_F
	380	45.8	4.4	1009	10	CNS010EW AL098882 Drosophil
c	381	45.8	4.4	1013	10	AG421540 AG421540 Mus muscu
	382	45.8	4.4	1052	10	CL462216 CL462216 SAIL_115_
	383	45.8	4.4	1071	10	CL513489 CL513489 SAIL_876_
	384	45.8	4.4	1093	3	BM803558 BM803558 AGENCOURT
c	385	45.8	4.4	1101	10	CNS00ELH AL069342 Drosophil
	386	45.8	4.4	1121	10	CL496797 CL496797 SAIL_631_
c	387	45.8	4.4	1176	8	DN729455 DN729455 CNB47-C12

c 388	45.8	4.4	1178	8	DN807812	DN807812 76885715
389	45.8	4.4	1192	3	BM556419	BM556419 AGENCOURT
c 390	45.8	4.4	1210	10	AG448190	AG448190 Mus muscu
391	45.8	4.4	1214	10	AG365333	AG365333 Mus muscu
392	45.8	4.4	1430	3	BM458823	BM458823 AGENCOURT
c 393	45.8	4.4	1552	10	AG430101	AG430101 Mus muscu
c 394	45.8	4.4	1822	10	AG435170	AG435170 Mus muscu
395	45.6	4.4	555	10	AG136825	AG136825 Pan trogl
c 396	45.6	4.4	657	7	CV664205	CV664205 LCPE04EX0
c 397	45.6	4.4	681	6	CA076145	CA076145 SCMCAM109
398	45.6	4.4	771	10	AG076969	AG076969 Pan trogl
c 399	45.6	4.4	774	2	BE040676	BE040676 OF04H04 O
c 400	45.6	4.4	807	2	BF629796	BF629796 HVSMEb001
401	45.6	4.4	818	10	AG080404	AG080404 Pan trogl
c 402	45.6	4.4	840	7	CK203176	CK203176 FGAS01170
403	45.6	4.4	847	10	AG853751	AG853751 Oryza sat
c 404	45.6	4.4	873	10	AG132025	AG132025 Pan trogl
c 405	45.6	4.4	918	2	BG809598	BG809598 mgct001xb
406	45.6	4.4	941	11	CNS03ZIW	AL267665 Tetraodon
c 407	45.6	4.4	960	10	AG126398	AG126398 Pan trogl
c 408	45.6	4.4	965	10	CW941304	CW941304 TcB22.2_H
409	45.6	4.4	965	10	CL514241	CL514241 SAIL_886_
c 410	45.6	4.4	969	5	BX462529	BX462529 BX462529
411	45.6	4.4	993	10	CL500348	CL500348 SAIL_680_
c 412	45.6	4.4	1007	5	BQ689807	BQ689807 AGENCOURT
c 413	45.6	4.4	1026	5	BX418913	BX418913 BX418913
c 414	45.6	4.4	1064	10	CNS016P9	AL107031 Drosophil
c 415	45.6	4.4	1072	10	CL503204	CL503204 SAIL_720_
c 416	45.6	4.4	1088	8	W15897	W15897 mb56b09.r1
417	45.6	4.4	1091	9	CC192677	CC192677 CH261-161
c 418	45.6	4.4	1092	8	DN666894	DN666894 CFW34-H02
c 419	45.6	4.4	1101	10	CNS00G33	AL071575 Drosophil
c 420	45.6	4.4	1107	6	CB905729	CB905729 tric075xn
c 421	45.6	4.4	1107	7	CF877385	CF877385 tric075xn
422	45.6	4.4	1114	5	BQ894501	BQ894501 AGENCOURT
c 423	45.6	4.4	1150	10	AG397013	AG397013 Mus muscu
424	45.6	4.4	1197	3	BM461131	BM461131 AGENCOURT
425	45.6	4.4	1218	10	AG435362	AG435362 Mus muscu
c 426	45.6	4.4	1225	10	AG430009	AG430009 Mus muscu
427	45.6	4.4	1253	9	CC300023	CC300023 CH261-107
428	45.6	4.4	1254	9	CC211081	CC211081 CH261-53A
c 429	45.6	4.4	1436	10	AG435568	AG435568 Mus muscu
c 430	45.6	4.4	1909	10	CL078604	CL078604 CH216-151
431	45.4	4.3	298	11	CNS04M2X	AL296898 Tetraodon
c 432	45.4	4.3	308	11	CR095827	CR095827 Forward s
c 433	45.4	4.3	609	10	CL617930	CL617930 OR_BBa001
c 434	45.4	4.3	670	10	AG126228	AG126228 Pan trogl
c 435	45.4	4.3	695	10	CL753698	CL753698 OR_BBa012
c 436	45.4	4.3	702	7	CV663748	CV663748 LCPE04EX0
c 437	45.4	4.3	704	3	BI954809	BI954809 HVSMEm001
c 438	45.4	4.3	705	10	AG385413	AG385413 Mus muscu
439	45.4	4.3	731	1	AI690712	AI690712 tx88d08.x
440	45.4	4.3	767	10	AG076679	AG076679 Pan trogl
c 441	45.4	4.3	777	10	CL614431	CL614431 OR_BBa000
442	45.4	4.3	780	10	AG524918	AG524918 Mus muscu
443	45.4	4.3	793	3	BI892334	BI892334 ZF637-3-0
c 444	45.4	4.3	798	3	BI416695	BI416695 hasp001xo
445	45.4	4.3	799	11	CNS03ZJK	AL267689 Tetraodon
c 446	45.4	4.3	815	10	AG608347	AG608347 Mus muscu
447	45.4	4.3	838	9	B19873	B19873 T18C3-Sp6 T
448	45.4	4.3	854	9	BZ051848	BZ051848 jnr57h03.
c 449	45.4	4.3	870	10	AG613032	AG613032 Mus muscu
450	45.4	4.3	888	10	AG030591	AG030591 Pan trogl
451	45.4	4.3	897	10	AG046101	AG046101 Pan trogl
452	45.4	4.3	905	10	CL497469	CL497469 SAIL_641_
453	45.4	4.3	912	10	CNS006N3	AL065775 Drosophil
454	45.4	4.3	920	10	CL471911	CL471911 SAIL_16_F
455	45.4	4.3	925	2	BG441241	BG441241 GA__Ea001
456	45.4	4.3	939	10	CL481697	CL481697 SAIL_346_
c 457	45.4	4.3	960	10	CNS0048W	AL051640 Drosophil
458	45.4	4.3	971	7	CF934397	CF934397 TrEST-B41
c 459	45.4	4.3	973	10	AG433979	AG433979 Mus muscu
460	45.4	4.3	1013	6	CA461083	CA461083 AGENCOURT
461	45.4	4.3	1102	3	BM465853	BM465853 AGENCOURT
462	45.4	4.3	1104	3	BM927784	BM927784 AGENCOURT
c 463	45.4	4.3	1116	10	AG429769	AG429769 Mus muscu
464	45.4	4.3	1120	3	BM914531	BM914531 AGENCOURT
465	45.4	4.3	1175	10	AG448201	AG448201 Mus muscu
466	45.4	4.3	1218	5	BQ876717	BQ876717 AGENCOURT
c 467	45.4	4.3	1275	10	AG442214	AG442214 Mus muscu
c 468	45.4	4.3	1381	10	AG396965	AG396965 Mus muscu
469	45.4	4.3	1389	3	BM019473	BM019473 603647660
c 470	45.4	4.3	1393	10	CL043635	CL043635 CH216-58H
c 471	45.4	4.3	1489	10	AG448218	AG448218 Mus muscu
c 472	45.4	4.3	1503	10	CL118256	CL118256 ISB1-70G1
c 473	45.4	4.3	1598	10	AG346280	AG346280 Mus muscu
474	45.4	4.3	1661	10	AG435089	AG435089 Mus muscu
c 475	45.4	4.3	1839	10	CG747711	CG747711 P041-2-E0
c 476	45.2	4.3	338	11	CR160509	CR160509 Forward s
477	45.2	4.3	423	9	BH755092	BH755092 SALK_0484
478	45.2	4.3	538	9	BH752140	BH752140 SALK_0518
479	45.2	4.3	583	3	BP319331	BP319331 BP319331
480	45.2	4.3	591	10	AG124266	AG124266 Pan trogl
c 481	45.2	4.3	611	10	AG081174	AG081174 Pan trogl
482	45.2	4.3	631	10	CW942930	CW942930 TcB24.3_D
483	45.2	4.3	637	8	DR792054	DR792054 ZM_BFb001
484	45.2	4.3	691	10	AG139567	AG139567 Pan trogl
485	45.2	4.3	707	10	CL477317	CL477317 SAIL_26_H
486	45.2	4.3	720	10	AG491023	AG491023 Mus muscu
487	45.2	4.3	721	7	CV521441	CV521441 0089P0060
c 488	45.2	4.3	744	10	AG153752	AG153752 Pan trogl
c 489	45.2	4.3	765	10	AG423333	AG423333 Mus muscu
490	45.2	4.3	766	10	CG113832	CG113832 PUFVV69TD
491	45.2	4.3	773	10	AG848502	AG848502 Oryza sat
492	45.2	4.3	821	9	CC604222	CC604222 OGUJK19TV
493	45.2	4.3	838	9	BZ051816	BZ051816 jnr57d05.
494	45.2	4.3	839	10	CNS00ZUP	AL098155 Drosophil
c 495	45.2	4.3	844	10	CW940150	CW940150 TcB20.4_H
496	45.2	4.3	863	6	CA465722	CA465722 AGENCOURT
c 497	45.2	4.3	870	5	BQ680926	BQ680926 AGENCOURT
c 498	45.2	4.3	881	10	CG317748	CG317748 OG1CW73TH
c 499	45.2	4.3	883	10	AG425045	AG425045 Mus muscu
c 500	45.2	4.3	899	10	AG135251	AG135251 Pan trogl
501	45.2	4.3	900	10	CG317757	CG317757 OG1CW73TV
502	45.2	4.3	902	5	BW973552	BW973552 BW973552
503	45.2	4.3	921	10	CL489959	CL489959 SAIL_531_
c 504	45.2	4.3	922	9	CC671530	CC671530 OGVBI82TV
505	45.2	4.3	927	10	CL487026	CL487026 SAIL_445_
c 506	45.2	4.3	928	2	BI258705	BI258705 602969866
c 507	45.2	4.3	932	10	AG442281	AG442281 Mus muscu
508	45.2	4.3	947	10	CL464979	CL464979 SAIL_1231
509	45.2	4.3	954	10	CL512388	CL512388 SAIL_85_C
c 510	45.2	4.3	984	10	CL513555	CL513555 SAIL_877_
c 511	45.2	4.3	987	9	CC639568	CC639568 OGUDQI9TV
c 512	45.2	4.3	1009	10	CNS017JA	AL108112 Drosophil
c 513	45.2	4.3	1059	8	DN807899	DN807899 74327355
514	45.2	4.3	1078	6	CA134568	CA134568 SCJFRT106
c 515	45.2	4.3	1088	2	BF256580	BF256580 HVSMEf001
c 516	45.2	4.3	1115	10	AG395467	AG395467 Mus muscu
c 517	45.2	4.3	1156	10	AG126610	AG126610 Pan trogl
c 518	45.2	4.3	1168	3	BM809732	BM809732 AGENCOURT
519	45.2	4.3	1181	3	BI869996	BI869996 603394150
c 520	45.2	4.3	1191	5	BQ410366	BQ410366 GA__Ed003
521	45.2	4.3	1198	3	BQ051422	BQ051422 AGENCOURT
522	45.2	4.3	1214	10	AG324452	AG324452 Mus muscu
523	45.2	4.3	1235	10	CL081604	CL081604 CH216-163
c 524	45.2	4.3	1242	7	CR552616	CR552616 CR552616
c 525	45.2	4.3	1253	8	DN430435	DN430435 LIB4217-0
526	45.2	4.3	1269	3	BM909678	BM909678 AGENCOURT
527	45.2	4.3	1278	10	AG060116	AG060116 Pan trogl
c 528	45.2	4.3	1279	8	DN657180	DN657180 CEC27-D06
529	45.2	4.3	1292	3	BQ070431	BQ070431 AGENCOURT
530	45.2	4.3	1294	9	CC279571	CC279571 CH261-151
c 531	45.2	4.3	1328	10	CL644395	CL644395 CH213-72E
532	45.2	4.3	1412	10	CL505072	CL505072 SAIL_744_
533	45.2	4.3	1578	9	CC303267	CC303267 CH261-29J

	534	45.2	4.3	1598	10	CL078355 CL078355 CH216-149
c	535	45.2	4.3	1641	2	BG860632 BG860632 1024071H1
	536	45.2	4.3	1798	10	AG171124 AG171124 Pan trogl
	537	45	4.3	253	11	CNS04521 AL274834 Tetraodon
	538	45	4.3	352	11	CR074561 CR074561 Reverse s
c	539	45	4.3	412	6	CB177724 CB177724 in95b02.x
	540	45	4.3	439	3	BI885650 BI885650 fn09h03.y
	541	45	4.3	453	2	BE623746 BE623746 ut20g06.y
c	542	45	4.3	787	10	AG367010 AG367010 Mus muscu
	543	45	4.3	845	9	BZ051746 BZ051746 jnr58d12.
c	544	45	4.3	877	10	AG136839 AG136839 Pan trogl
c	545	45	4.3	887	10	CW944323 CW944323 TcB26.2_F
c	546	45	4.3	888	2	BG809572 BG809572 mgct001xa
c	547	45	4.3	888	9	AQ746768 AQ746768 HS_2276_A
c	548	45	4.3	916	10	AG415574 AG415574 Mus muscu
c	549	45	4.3	918	10	AG137554 AG137554 Pan trogl
	550	45	4.3	921	10	CL465012 CL465012 SAIL_1232
	551	45	4.3	934	10	AG512337 AG512337 Mus muscu
	552	45	4.3	939	5	BQ670318 BQ670318 AGENCOURT
c	553	45	4.3	954	5	BX379428 BX379428 BX379428
c	554	45	4.3	955	8	DN808254 DN808254 74134026
c	555	45	4.3	976	3	BQ218020 BQ218020 AGENCOURT
	556	45	4.3	981	10	CL487097 CL487097 SAIL_447_
	557	45	4.3	1001	8	DR738746 DR738746 FGAS08396_
c	558	45	4.3	1002	10	AG060379 AG060379 Pan trogl
	559	45	4.3	1006	2	BG330306 BG330306 602430333
c	560	45	4.3	1009	10	CNS010EW AL098882 Drosophil
c	561	45	4.3	1013	5	BQ917686 BQ917686 AGENCOURT
c	562	45	4.3	1015	3	BI416650 BI416650 hasp001xm
	563	45	4.3	1026	5	BU900073 BU900073 AGENCOURT
c	564	45	4.3	1039	5	BQ889895 BQ889895 AGENCOURT
	565	45	4.3	1062	5	BQ673680 BQ673680 AGENCOURT
	566	45	4.3	1070	10	CL468494 CL468494 SAIL_1287
	567	45	4.3	1101	10	CNS01523 AL104901 Drosophil
	568	45	4.3	1130	10	CL077291 CL077291 CH216-144
	569	45	4.3	1152	10	CL471102 CL471102 SAIL_155_
	570	45	4.3	1155	10	AG130227 AG130227 Pan trogl
c	571	45	4.3	1166	8	DN693027 DN693027 CGX85-E11
	572	45	4.3	1171	9	B10823 B10823 T11E7-T7 TA
	573	45	4.3	1213	9	CC262299 CC262299 CH261-42H
	574	45	4.3	1222	10	AG435399 AG435399 Mus muscu
	575	45	4.3	1233	10	AG341388 AG341388 Mus muscu
	576	45	4.3	1252	10	CL082583 CL082583 CH216-168
c	577	45	4.3	1253	8	DN671759 DN671759 CFW64-F01
	578	45	4.3	1372	10	AG289910 AG289910 Mus muscu
	579	45	4.3	1548	10	AG435551 AG435551 Mus muscu
c	580	45	4.3	1793	10	CG754612 CG754612 P050-1-D0
c	581	45	4.3	1862	10	AG442225 AG442225 Mus muscu
c	582	45	4.3	2088	10	AG430027 AG430027 Mus muscu
	583	44.8	4.3	349	11	CNS03B0Q AL235907 Tetraodon
c	584	44.8	4.3	409	11	CNS04N71 AL298342 Tetraodon
	585	44.8	4.3	415	2	BE019715 BE019715 bb29d11.y
c	586	44.8	4.3	464	11	CNS04FCC AL288165 Tetraodon
	587	44.8	4.3	546	10	CNS02OMZ AL206900 Tetraodon
	588	44.8	4.3	638	11	CNS046XY AL277279 Tetraodon
c	589	44.8	4.3	688	2	BG786340 BG786340 SEAUMC006
	590	44.8	4.3	688	8	DR955049 DR955049 ZM_BFb004
c	591	44.8	4.3	747	10	CL512522 CL512522 SAIL_861_
c	592	44.8	4.3	788	10	CW938888 CW938888 TcB19.1_D
c	593	44.8	4.3	811	3	BI888042 BI888042 ZF637-1-0
c	594	44.8	4.3	834	3	BI416657 BI416657 hasp001xm
c	595	44.8	4.3	887	7	CV662609 CV662609 LCPE04EX0
c	596	44.8	4.3	898	10	AG128981 AG128981 Pan trogl
	597	44.8	4.3	906	10	CL459906 CL459906 SAIL_104_
c	598	44.8	4.3	913	10	CW945531 CW945531 TcB27.4_H
	599	44.8	4.3	919	9	BZ051714 BZ051714 jnr58a10.
	600	44.8	4.3	935	10	CL509703 CL509703 SAIL_815_
	601	44.8	4.3	941	11	CNS06LR7 AL404537 T3 end of
	602	44.8	4.3	945	10	CL492375 CL492375 SAIL_565_
	603	44.8	4.3	950	10	CL515190 CL515190 SAIL_898_
	604	44.8	4.3	968	6	CA471634 CA471634 AGENCOURT
	605	44.8	4.3	971	10	CL471629 CL471629 SAIL_163_
c	606	44.8	4.3	974	10	CW951455 CW951455 TcB36.4_G
	607	44.8	4.3	990	9	BZ051799 BZ051799 jnr57b04.
	608	44.8	4.3	992	5	BX426799 BX426799 BX426799
c	609	44.8	4.3	1011	8	DR735585 DR735585 FGAS08124
c	610	44.8	4.3	1042	10	CL505528 CL505528 SAIL_751_
	611	44.8	4.3	1052	5	BQ951911 BQ951911 AGENCOURT
	612	44.8	4.3	1069	5	BQ675554 BQ675554 AGENCOURT
	613	44.8	4.3	1101	10	CNS017RT AL108419 Drosophil
	614	44.8	4.3	1120	9	CC300085 CC300085 CH261-34P
	615	44.8	4.3	1142	10	CL505075 CL505075 SAIL_744_
	616	44.8	4.3	1196	6	CD505402 CD505402 CDA73-E04
	617	44.8	4.3	1199	5	BQ706827 BQ706827 AGENCOURT
c	618	44.8	4.3	1223	8	DN703034 DN703034 CLJ45-B07
c	619	44.8	4.3	1278	8	DN663203 DN663203 CFW12-E05
	620	44.8	4.3	1282	10	AG430149 AG430149 Mus muscu
c	621	44.8	4.3	1366	2	BF256667 BF256667 HVSMEf001
	622	44.8	4.3	1406	7	CK408425 CK408425 AUF_IfLvr
c	623	44.8	4.3	1423	10	AJ858038 AJ858038 Brassica
	624	44.8	4.3	1446	10	CL082756 CL082756 CH216-170
c	625	44.8	4.3	1453	8	DN806685 DN806685 76982446
	626	44.8	4.3	1571	10	CL082695 CL082695 CH216-169
	627	44.6	4.3	363	8	DN337677 DN337677 LIB3187-0
	628	44.6	4.3	600	9	CC623964 CC623964 OGVAL58TH
	629	44.6	4.3	638	10	AG046300 AG046300 Pan trogl
c	630	44.6	4.3	643	11	CR097781 CR097781 Reverse s
	631	44.6	4.3	717	10	AG076660 AG076660 Pan trogl
	632	44.6	4.3	761	3	BI887964 BI887964 ZF637-1-0
c	633	44.6	4.3	764	10	AG420371 AG420371 Mus muscu
	634	44.6	4.3	766	10	AG041031 AG041031 Pan trogl
c	635	44.6	4.3	768	10	AG138112 AG138112 Pan trogl
	636	44.6	4.3	772	8	DR972067 DR972067 ZM_BFb009
	637	44.6	4.3	787	9	CC918454 CC918454 t006i02ba
	638	44.6	4.3	794	9	AZ185894 AZ185894 SP_1005_B
c	639	44.6	4.3	796	10	CW943208 CW943208 TcB24.4_H
	640	44.6	4.3	801	10	AG473849 AG473849 Mus muscu
	641	44.6	4.3	806	10	AG458107 AG458107 Mus muscu
	642	44.6	4.3	824	9	B18410 B18410 T7K7-Sp6 TA
	643	44.6	4.3	827	10	AG446750 AG446750 Mus muscu
c	644	44.6	4.3	837	10	AG392429 AG392429 Mus muscu
c	645	44.6	4.3	875	10	CL477137 CL477137 SAIL_267b
c	646	44.6	4.3	878	2	BG786339 BG786339 SEAUMC006
	647	44.6	4.3	884	5	BU960957 BU960957 AGENCOURT
	648	44.6	4.3	897	10	CL472504 CL472504 SAIL_180_
c	649	44.6	4.3	915	10	AG081194 AG081194 Pan trogl
c	650	44.6	4.3	915	10	AG129036 AG129036 Pan trogl
c	651	44.6	4.3	919	7	CK160763 CK160763 FGAS04239
	652	44.6	4.3	928	7	CK402134 CK402134 AUF_IfInt
	653	44.6	4.3	935	10	CL490797 CL490797 SAIL_546_
	654	44.6	4.3	941	10	CL505315 CL505315 SAIL_749_
	655	44.6	4.3	944	5	BU854443 BU854443 AGENCOURT
c	656	44.6	4.3	954	10	AG387669 AG387669 Mus muscu
c	657	44.6	4.3	964	10	CNS003WG AL065254 Drosophil
c	658	44.6	4.3	965	5	BQ961201 BQ961201 AGENCOURT
	659	44.6	4.3	967	10	CNS00IYE AL075395 Drosophil
	660	44.6	4.3	981	10	CL493910 CL493910 SAIL_588_
	661	44.6	4.3	983	10	CL469439 CL469439 SAIL_1303
	662	44.6	4.3	986	10	AG534089 AG534089 Mus muscu
	663	44.6	4.3	989	10	CL041117 CL041117 CH216-51N
c	664	44.6	4.3	994	8	DN807908 DN807908 76895295
	665	44.6	4.3	995	10	CL478690 CL478690 SAIL_294_
	666	44.6	4.3	1001	10	CNS0155H AL105023 Drosophil
c	667	44.6	4.3	1004	10	AG134371 AG134371 Pan trogl
	668	44.6	4.3	1028	10	CL495801 CL495801 SAIL_615_
	669	44.6	4.3	1044	10	CL507089 CL507089 SAIL_777_
	670	44.6	4.3	1059	6	CA982844 CA982844 AGENCOURT
	671	44.6	4.3	1095	10	CL512412 CL512412 SAIL_85_H
c	672	44.6	4.3	1101	10	CNS00K66 AL077274 Drosophil
	673	44.6	4.3	1101	10	CNS0181I AL108768 Drosophil
c	674	44.6	4.3	1129	10	CW945472 CW945472 TcB27.4_F
c	675	44.6	4.3	1129	10	AG448563 AG448563 Mus muscu
	676	44.6	4.3	1136	9	CC292742 CC292742 CH261-185
c	677	44.6	4.3	1138	3	BQ070284 BQ070284 AGENCOURT
	678	44.6	4.3	1157	9	CC219063 CC219063 CH261-165
c	679	44.6	4.3	1169	10	AG032383 AG032383 Pan trogl

	680	44.6	4.3	1181	3	BM910708 BM910708 AGENCOURT
	681	44.6	4.3	1252	10	CG752943 CG752943 P047-4-D1
	682	44.6	4.3	1268	3	BM551006 BM551006 AGENCOURT
	683	44.6	4.3	1272	10	AG365674 AG365674 Mus muscu
c	684	44.6	4.3	1277	2	BG447302 GA__Eb004
c	685	44.6	4.3	1289	1	AJ929090 AJ929090
c	686	44.6	4.3	1300	8	DN723891 DN723891 CNB16-B05
c	687	44.6	4.3	1320	10	CL118071 CL118071 ISB1-69O2
	688	44.6	4.3	1427	10	AG333458 AG333458 Mus muscu
c	689	44.6	4.3	1552	10	CL646265 CL646265 CH213-111
c	690	44.4	4.2	362	11	CR139019 CR139019 Forward s
c	691	44.4	4.2	384	11	CNS035G7 AL228688 Tetraodon
	692	44.4	4.2	449	2	BE223458 BE223458 kp80a10.y
	693	44.4	4.2	506	3	BM036509 BM036509 fu78c12.y
	694	44.4	4.2	531	5	BQ479673 BQ479673 faa71e12.
c	695	44.4	4.2	564	2	BG786324 BG786324 SEAUMC006
	696	44.4	4.2	586	10	CNS01UD1 AL167662 Tetraodon
	697	44.4	4.2	597	8	DN411628 DN411628 LIB4215-0
	698	44.4	4.2	622	8	DN356641 DN356641 LIB3626-0
	699	44.4	4.2	652	8	DN415086 DN415086 LIB4215-0
	700	44.4	4.2	702	8	DN373236 DN373236 LIB3733-0
	701	44.4	4.2	714	10	AG477247 AG477247 Mus muscu
	702	44.4	4.2	755	9	BZ051544 BZ051544 jnr59e08.
	703	44.4	4.2	781	8	DN425693 DN425693 LIB4216-0
	704	44.4	4.2	782	3	BI887370 BI887370 ZF637-1-0
	705	44.4	4.2	795	9	AZ188474 AZ188474 SP_1012_A
c	706	44.4	4.2	800	10	AG063966 AG063966 Pan trogl
c	707	44.4	4.2	811	10	CNS011SC AL100662 Drosophil
c	708	44.4	4.2	822	10	CW950354 CW950354 TcB35.3_A
	709	44.4	4.2	823	5	BU532459 BU532459 AGENCOURT
	710	44.4	4.2	824	9	AZ185676 AZ185676 SP_1005_B
c	711	44.4	4.2	824	11	CR801785 CR801785 GR0AAA20D
	712	44.4	4.2	826	10	AG500195 AG500195 Mus muscu
	713	44.4	4.2	833	10	AG870119 AG870119 Oryza sat
c	714	44.4	4.2	844	10	CW953234 CW953234 TcB39.2_A
c	715	44.4	4.2	844	10	CZ620595 CZ620595 OM__Ba015
c	716	44.4	4.2	846	10	CNS010RJ AL099337 Drosophil
c	717	44.4	4.2	851	10	CL467101 CL467101 SAIL_1266
	718	44.4	4.2	855	10	AG133107 AG133107 Pan trogl
	719	44.4	4.2	864	10	AG543704 AG543704 Mus muscu
	720	44.4	4.2	882	10	CL516020 CL516020 SAIL_910_
	721	44.4	4.2	890	10	CL463891 CL463891 SAIL_120_
c	722	44.4	4.2	896	10	CW951337 CW951337 TcB36.4_B
	723	44.4	4.2	899	10	CL469647 CL469647 SAIL_130_
	724	44.4	4.2	903	9	BZ051933 BZ051933 jnr56a04.
c	725	44.4	4.2	909	10	AG125251 AG125251 Pan trogl
c	726	44.4	4.2	916	7	CV662670 CV662670 LCPE04EX0
	727	44.4	4.2	932	10	CL473519 CL473519 SAIL_201_
	728	44.4	4.2	935	5	BQ951972 BQ951972 AGENCOURT
	729	44.4	4.2	936	9	CC921440 CC921440 t051j04ba
	730	44.4	4.2	952	2	BG441341 BG441341 GA__Ea001
c	731	44.4	4.2	967	10	CL462989 CL462989 SAIL_1173
	732	44.4	4.2	978	10	CL468763 CL468763 SAIL_1290
	733	44.4	4.2	981	9	B07995 B07995 F27K24-T7.1
	734	44.4	4.2	983	6	CA975737 CA975737 AGENCOURT
	735	44.4	4.2	997	5	BU507274 BU507274 AGENCOURT
c	736	44.4	4.2	1000	5	BQ928954 BQ928954 AGENCOURT
	737	44.4	4.2	1004	6	CD051228 CD051228 AGENCOURT
	738	44.4	4.2	1007	6	CA477389 CA477389 AGENCOURT
c	739	44.4	4.2	1008	10	AG395157 AG395157 Mus muscu
	740	44.4	4.2	1028	7	CK424049 CK424049 AUF_IpSto
c	741	44.4	4.2	1032	10	CW950024 CW950024 TcB35.1_D
	742	44.4	4.2	1038	6	CA978241 CA978241 AGENCOURT
c	743	44.4	4.2	1039	10	AG562654 AG562654 Mus muscu
	744	44.4	4.2	1039	10	CL466017 CL466017 SAIL_1250
c	745	44.4	4.2	1073	3	BQ062089 BQ062089 AGENCOURT
	746	44.4	4.2	1101	10	CNS00M0E AL078978 Drosophil
	747	44.4	4.2	1109	3	BM543244 BM543244 AGENCOURT
c	748	44.4	4.2	1112	6	CA477644 CA477644 AGENCOURT
	749	44.4	4.2	1139	5	BQ643654 BQ643654 AGENCOURT
	750	44.4	4.2	1192	10	AG063968 AG063968 Pan trogl
c	751	44.4	4.2	1193	8	DN667445 DN667445 CFW38-B07
c	752	44.4	4.2	1196	10	AG382042 AG382042 Mus muscu
	753	44.4	4.2	1214	10	AG435068 AG435068 Mus muscu
	754	44.4	4.2	1218	10	CL081011 CL081011 CH216-160
c	755	44.4	4.2	1235	10	AG320749 AG320749 Mus muscu
c	756	44.4	4.2	1267	10	AG396118 AG396118 Mus muscu
c	757	44.4	4.2	1280	10	CL470317 CL470317 SAIL_140_
c	758	44.4	4.2	1302	10	AG448240 AG448240 Mus muscu
	759	44.4	4.2	1353	8	DN656623 DN656623 CEC24-B08
c	760	44.4	4.2	1387	8	DN737674 DN737674 CNB94-B06
c	761	44.4	4.2	1406	10	AG441598 AG441598 Mus muscu
c	762	44.4	4.2	1665	10	AG390972 AG390972 Mus muscu
c	763	44.4	4.2	1689	10	AG390487 AG390487 Mus muscu
c	764	44.4	4.2	1790	10	AG396847 AG396847 Mus muscu
c	765	44.4	4.2	1798	10	AG171124 AG171124 Pan trogl
	766	44.4	4.2	2280	2	BG962421 BG962421 602827251
c	767	44.2	4.2	369	10	BX990750 BX990750 Reverse s
c	768	44.2	4.2	433	11	CR093851 CR093851 Reverse s
c	769	44.2	4.2	455	5	CA033415 CA033415 pw52f03.y
	770	44.2	4.2	554	9	AZ045735 AZ045735 nbeb0087G
c	771	44.2	4.2	636	11	CR079344 CR079344 Reverse s
	772	44.2	4.2	705	9	BZ051762 BZ051762 jnr58f09.
	773	44.2	4.2	729	3	BI891823 BI891823 ZF637-3-0
c	774	44.2	4.2	729	11	CNS03JVQ AL247391 Tetraodon
	775	44.2	4.2	749	10	AG375372 AG375372 Mus muscu
	776	44.2	4.2	758	10	AG073529 AG073529 Pan trogl
	777	44.2	4.2	760	9	BZ051971 BZ051971 jnr56e08.
c	778	44.2	4.2	775	10	AG392495 AG392495 Mus muscu
c	779	44.2	4.2	785	9	BH930477 BH930477 odh69b01.
c	780	44.2	4.2	788	7	CV664679 CV664679 LCPE04EX0
c	781	44.2	4.2	792	7	CN048751 CN048751 v2_p2_D13
c	782	44.2	4.2	800	10	AG061542 AG061542 Pan trogl
c	783	44.2	4.2	807	10	CW943100 CW943100 TcB24.4_C
c	784	44.2	4.2	821	6	CB905416 CB905416 tric074xf
c	785	44.2	4.2	821	7	CF876936 CF876936 tric074xf
c	786	44.2	4.2	821	9	AQ893474 AQ893474 HS_4832_A
c	787	44.2	4.2	823	5	BQ411414 BQ411414 GA__Ed003
c	788	44.2	4.2	828	3	BI952479 BI952479 HVSMEm000
c	789	44.2	4.2	848	10	CW940993 CW940993 TcB22.1_C
	790	44.2	4.2	857	10	AG527242 AG527242 Mus muscu
c	791	44.2	4.2	863	10	CW941451 CW941451 TcB22.3_F
c	792	44.2	4.2	866	3	BQ221622 BQ221622 AGENCOURT
c	793	44.2	4.2	866	10	AG851473 AG851473 Oryza sat
c	794	44.2	4.2	875	9	AZ211145 AZ211145 SP_0159_B
c	795	44.2	4.2	879	10	CW949894 CW949894 TcB34.4_F
	796	44.2	4.2	893	10	CW941690 CW941690 TcB22.4_H
c	797	44.2	4.2	901	10	AG131311 AG131311 Pan trogl
c	798	44.2	4.2	905	10	AG416475 AG416475 Mus muscu
c	799	44.2	4.2	913	10	CW953543 CW953543 TcB39.3_F
	800	44.2	4.2	920	10	CL482127 CL482127 SAIL_355_
	801	44.2	4.2	921	10	CL096095 CL096095 ISB1-27H2
	802	44.2	4.2	921	10	CL465044 CL465044 SAIL_1233
c	803	44.2	4.2	923	10	CW953542 CW953542 TcB39.3_F
	804	44.2	4.2	932	10	CNS0072Q AL066742 Drosophil
	805	44.2	4.2	936	10	CNS01608 AL106130 Drosophil
c	806	44.2	4.2	945	10	AG117065 AG117065 Pan trogl
	807	44.2	4.2	950	8	DN578613 DN578613 92230850
	808	44.2	4.2	950	10	CL479739 CL479739 SAIL_311_
	809	44.2	4.2	952	10	CL469839 CL469839 SAIL_134_
	810	44.2	4.2	952	10	CL481610 CL481610 SAIL_344_
c	811	44.2	4.2	965	7	CR453454 CR453454
	812	44.2	4.2	971	10	CL474879 CL474879 SAIL_228_
c	813	44.2	4.2	974	10	CL029592 CL029592 CH216-29C
c	814	44.2	4.2	986	10	CL466885 CL466885 SAIL_1263
	815	44.2	4.2	993	10	CL468466 CL468466 SAIL_1287
c	816	44.2	4.2	997	6	CB905724 CB905724 tric075xn
c	817	44.2	4.2	997	7	CF877382 CF877382 tric075xn
	818	44.2	4.2	1004	10	CL485750 CL485750 SAIL_421_
c	819	44.2	4.2	1062	10	AG392619 AG392619 Mus muscu
c	820	44.2	4.2	1066	6	CB905393 CB905393 tric074xd
c	821	44.2	4.2	1066	7	CF876920 CF876920 tric074xd
c	822	44.2	4.2	1083	7	CV520573 CV520573 0089P0047
c	823	44.2	4.2	1100	6	CB905637 CB905637 tric075xh
c	824	44.2	4.2	1100	7	CF877318 CF877318 tric075xh
	825	44.2	4.2	1101	10	CNS00FXN AL071379 Drosophil

c 826	44.2	4.2	1105	10	CW952937	CW952937 TcB38.4_E
c 827	44.2	4.2	1113	8	DN808141	DN808141 76864687
828	44.2	4.2	1116	9	BZ557923	BZ557923 pacs1-60_
829	44.2	4.2	1126	9	CC245922	CC245922 CH261-180
830	44.2	4.2	1132	5	BQ672163	BQ672163 AGENCOURT
c 831	44.2	4.2	1152	10	AG469284	AG469284 Mus muscu
c 832	44.2	4.2	1194	10	AG448166	AG448166 Mus muscu
833	44.2	4.2	1198	8	DN673948	DN673948 CFW77-D08
834	44.2	4.2	1213	9	CC228523	CC228523 CH261-157
c 835	44.2	4.2	1230	3	BM809538	BM809538 AGENCOURT
c 836	44.2	4.2	1237	8	DN690375	DN690375 CGX70-B04
c 837	44.2	4.2	1243	10	CL643628	CL643628 CH213-53A
c 838	44.2	4.2	1276	8	DN675946	DN675946 CFW89-E02
839	44.2	4.2	1281	2	BG852363	BG852363 1024034A0
840	44.2	4.2	1284	10	CL082747	CL082747 CH216-170
841	44.2	4.2	1294	3	BM462443	BM462443 AGENCOURT
c 842	44.2	4.2	1318	7	CF874345	CF874345 tric006xn
c 843	44.2	4.2	1321	10	AG365665	AG365665 Mus muscu
c 844	44.2	4.2	1350	2	BE455228	BE455228 HVSMEh009
845	44.2	4.2	1362	3	BM556092	BM556092 AGENCOURT
846	44.2	4.2	1509	10	CL476587	CL476587 SAIL_258_
847	44.2	4.2	1556	10	AG390838	AG390838 Mus muscu
c 848	44.2	4.2	1642	10	CG754720	CG754720 P050-2-A0
849	44	4.2	375	1	AW733153	AW733153 bb04d12.x
c 850	44	4.2	415	9	BH613804	BH613804 SALK_0349
851	44	4.2	418	2	BF107743	BF107743 601823731
c 852	44	4.2	429	5	BU966261	BU966261 kk80d11.y
853	44	4.2	528	8	CX104445	CX104445 BI101N04
854	44	4.2	529	7	CK063008	CK063008 63626rsic
c 855	44	4.2	530	10	AG080585	AG080585 Pan trogl
c 856	44	4.2	539	7	CN300695	CN300695 170006000
857	44	4.2	564	3	BP240784	BP240784 BP240784
c 858	44	4.2	598	3	BM793875	BM793875 K-EST0074
859	44	4.2	622	5	BU620276	BU620276 UI-H-FH1-
860	44	4.2	623	8	DN483081	DN483081 root3_j11
c 861	44	4.2	643	3	BM791848	BM791848 K-EST0071
c 862	44	4.2	644	7	CN300707	CN300707 170006001
c 863	44	4.2	680	6	CD496837	CD496837 CDA24-E06
864	44	4.2	686	9	BZ029575	BZ029575 oei80d03.
c 865	44	4.2	701	2	BE514600	BE514600 601316946
c 866	44	4.2	714	9	BH920103	BH920103 odh75e02.
867	44	4.2	724	6	CA423463	CA423463 UI-H-FE1-
c 868	44	4.2	741	9	AZ194927	AZ194927 SP_1029_A
869	44	4.2	760	9	AZ187640	AZ187640 SP_1009_B
870	44	4.2	765	9	BZ051508	BZ051508 jnr59a10.
c 871	44	4.2	779	2	BE379093	BE379093 601237733
c 872	44	4.2	783	2	BE746427	BE746427 601579556
c 873	44	4.2	788	8	DN433460	DN433460 LIB4217-0
c 874	44	4.2	789	11	CNS03FOD	AL241942 Tetraodon
875	44	4.2	797	1	AW726060	AW726060 GA__Ea002
c 876	44	4.2	804	10	CW951542	CW951542 TcB37.1_C
c 877	44	4.2	809	9	AQ744538	AQ744538 HS_5508_A
878	44	4.2	812	9	BZ051575	BZ051575 jnr59a11.
c 879	44	4.2	823	7	CV660980	CV660980 LCPE04EX0
c 880	44	4.2	845	10	CW941218	CW941218 TcB22.2_E
881	44	4.2	848	10	CNS0118A	AL099940 Drosophil
c 882	44	4.2	850	5	BQ642989	BQ642989 AGENCOURT
883	44	4.2	871	9	AZ184410	AZ184410 SP_1002_B
c 884	44	4.2	897	3	BI416517	BI416517 hasp001xd
885	44	4.2	904	5	BU186354	BU186354 AGENCOURT
886	44	4.2	917	10	CL461236	CL461236 SAIL_1143
887	44	4.2	918	10	CL500872	CL500872 SAIL_68_E
c 888	44	4.2	927	2	BG786316	BG786316 SEAUMC006
c 889	44	4.2	930	2	BE746375	BE746375 601579684
c 890	44	4.2	933	10	CNS006XG	AL066047 Drosophil
c 891	44	4.2	939	10	CL513341	CL513341 SAIL_874_
892	44	4.2	942	6	CA460778	CA460778 AGENCOURT
c 893	44	4.2	949	6	CB905551	CB905551 tric075xb
894	44	4.2	957	10	CL501482	CL501482 SAIL_699_
c 895	44	4.2	961	10	CNS01087	AL098641 Drosophil
896	44	4.2	969	10	CL511545	CL511545 SAIL_84_A
897	44	4.2	977	10	CNS00JX7	AL076850 Drosophil
898	44	4.2	985	10	CNS02R29	AL210042 Tetraodon
c 899	44	4.2	990	10	CW945632	CW945632 TcB28.1_E
900	44	4.2	990	11	CNS03CU0	AL238257 Tetraodon
c 901	44	4.2	993	10	CL493309	CL493309 SAIL_576_
902	44	4.2	994	5	BU931446	BU931446 AGENCOURT
c 903	44	4.2	998	10	AG391635	AG391635 Mus muscu
904	44	4.2	1001	6	CA793045	CA793045 AGENCOURT
905	44	4.2	1008	10	AG426501	AG426501 Mus muscu
906	44	4.2	1018	10	CW924085	CW924085 EDCB241TF
907	44	4.2	1029	9	BZ569266	BZ569266 pacs2-164
908	44	4.2	1046	5	BQ682356	BQ682356 AGENCOURT
c 909	44	4.2	1061	2	BE795961	BE795961 601591128
c 910	44	4.2	1067	3	BQ057737	BQ057737 AGENCOURT
c 911	44	4.2	1090	10	CG749024	CG749024 P043-1-E0
c 912	44	4.2	1095	3	BQ278833	BQ278833 AGENCOURT
913	44	4.2	1099	8	DR735693	DR735693 FGAS08132
914	44	4.2	1101	10	CNS008J6	AL052144 Drosophil
915	44	4.2	1101	10	CNS014PA	AL104440 Drosophil
c 916	44	4.2	1111	10	AG394843	AG394843 Mus muscu
c 917	44	4.2	1156	1	AJ926994	AJ926994 AJ926994
918	44	4.2	1184	3	BQ054959	BQ054959 AGENCOURT
919	44	4.2	1242	3	BM911414	BM911414 AGENCOURT
c 920	44	4.2	1324	10	AG448157	AG448157 Mus muscu
c 921	44	4.2	1355	10	AG320565	AG320565 Mus muscu
c 922	44	4.2	1425	10	AG441757	AG441757 Mus muscu
c 923	44	4.2	1448	9	CC220110	CC220110 CH261-92F
924	44	4.2	1453	3	BM913150	BM913150 AGENCOURT
c 925	44	4.2	1463	10	CL515327	CL515327 SAIL_89_C
c 926	44	4.2	1531	10	AG430426	AG430426 Mus muscu
927	44	4.2	1686	9	CC286638	CC286638 CH261-16N
c 928	44	4.2	1700	10	AJ860850	AJ860850 Brassica
c 929	44	4.2	1908	8	DN807344	DN807344 76961740
c 930	44	4.2	2243	10	AG381986	AG381986 Mus muscu
c 931	44	4.2	2762	4	HSM800100	AL050019 Homo sapi
c 932	43.8	4.2	269	8	DN405673	DN405673 LIB4006-0
933	43.8	4.2	348	1	AL664001	AL664001 AL664001
934	43.8	4.2	384	2	BE223706	BE223706 kp87e07.y
c 935	43.8	4.2	388	5	BU781363	BU781363 kb17h05.y
c 936	43.8	4.2	393	2	BG657655	BG657655 TgESTzya3
c 937	43.8	4.2	510	11	CNS03J3I	AL246375 Tetraodon
938	43.8	4.2	520	3	BM096987	BM096987 EBpi07_SQ
c 939	43.8	4.2	580	3	BM278153	BM278153 As_tgz_53
c 940	43.8	4.2	584	3	BP339804	BP339804 BP339804
c 941	43.8	4.2	588	11	DR102A24T	AL985900 Danio rer
942	43.8	4.2	629	7	CV062034	CV062034 BNEL75f11
c 943	43.8	4.2	635	1	AI525004	AI525004 promrna-4
c 944	43.8	4.2	645	10	CNS012I3	AL101589 Drosophil
c 945	43.8	4.2	712	9	AZ197796	AZ197796 SP_1036_B
c 946	43.8	4.2	719	10	CW938245	CW938245 TcB18.1_A
c 947	43.8	4.2	724	9	AZ197686	AZ197686 SP_1035_B
948	43.8	4.2	730	10	AG351253	AG351253 Mus muscu
949	43.8	4.2	751	9	BZ051673	BZ051673 jnr58d12.
950	43.8	4.2	768	8	DR827260	DR827260 ZM_BFb007
c 951	43.8	4.2	774	9	CC612323	CC612323 OGPAI57TV
952	43.8	4.2	775	10	AG080464	AG080464 Pan trogl
953	43.8	4.2	776	10	CNS010RY	AL099352 Drosophil
954	43.8	4.2	778	8	DR822559	DR822559 ZM_BFb006
955	43.8	4.2	779	9	B21811	B21811 P8K18-Sp6 I
956	43.8	4.2	784	9	B21592	B21592 T5K4-Sp6 TA
957	43.8	4.2	784	9	BZ052004	BZ052004 jnr56a04.
958	43.8	4.2	790	10	AG480150	AG480150 Mus muscu
c 959	43.8	4.2	801	9	BZ531189	BZ531189 OGAKH92TM
c 960	43.8	4.2	810	10	AG127829	AG127829 Pan trogl
c 961	43.8	4.2	827	10	CNS0137T	AL102515 Drosophil
962	43.8	4.2	830	9	BH966848	BH966848 odh13d06.
c 963	43.8	4.2	831	1	AL665753	AL665753 AL665753
c 964	43.8	4.2	832	10	AG108460	AG108460 Pan trogl
c 965	43.8	4.2	838	9	AZ185657	AZ185657 SP_1005_B
966	43.8	4.2	848	10	CNS02YYE	AL220271 Tetraodon
c 967	43.8	4.2	849	10	CW947823	CW947823 TcB31.1_H
968	43.8	4.2	856	10	AG883445	AG883445 Oryza sat
c 969	43.8	4.2	863	6	CB238220	CB238220 AGENCOURT
970	43.8	4.2	868	10	AG514956	AG514956 Mus muscu
c 971	43.8	4.2	877	10	CW938478	CW938478 TcB18.3_C

972	43.8	4.2	884	7	CK446454	CK446454 pncs909aD
973	43.8	4.2	902	5	BU940869	BU940869 AGENCOURT
c 974	43.8	4.2	904	10	AG424774	AG424774 Mus muscu
c 975	43.8	4.2	916	3	BI953358	BI953358 HVSMEm001
976	43.8	4.2	918	10	CL467574	CL467574 SAIL_1272
977	43.8	4.2	922	10	CL482527	CL482527 SAIL_361_
978	43.8	4.2	926	10	CL486783	CL486783 SAIL_442_
c 979	43.8	4.2	926	11	CNS03C4D	AL237334 Tetraodon
980	43.8	4.2	935	10	CNS00G40	AL071406 Drosophil
c 981	43.8	4.2	942	10	AG120142	AG120142 Pan trogl
982	43.8	4.2	952	10	CL468590	CL468590 SAIL_1289
983	43.8	4.2	968	10	CL504373	CL504373 SAIL_736_
984	43.8	4.2	973	1	AJ924584	AJ924584 AJ924584
985	43.8	4.2	973	10	CL464664	CL464664 SAIL_1223
986	43.8	4.2	974	10	CG358932	CG358932 OG3AO33TV
c 987	43.8	4.2	994	6	CB907117	CB907117 tric081xg
c 988	43.8	4.2	994	7	CF880301	CF880301 tric081xg
c 989	43.8	4.2	1007	10	AG134493	AG134493 Pan trogl
c 990	43.8	4.2	1008	10	CW939128	CW939128 TcB19.2_F
c 991	43.8	4.2	1017	10	CL504849	CL504849 SAIL_743_
c 992	43.8	4.2	1065	10	CL044198	CL044198 CH216-60G
c 993	43.8	4.2	1069	8	DR739591	DR739591 FGAS08480
c 994	43.8	4.2	1080	3	BI416623	BI416623 hasp001xk
995	43.8	4.2	1081	10	CL464716	CL464716 SAIL_1225
996	43.8	4.2	1092	3	BQ051264	BQ051264 AGENCOURT
c 997	43.8	4.2	1092	10	CL508799	CL508799 SAIL_802_
998	43.8	4.2	1100	9	CC201131	CC201131 CH261-77E
c 999	43.8	4.2	1101	10	CNS00H18	AL072804 Drosophil
1000	43.8	4.2	1101	10	CNS017SY	AL108460 Drosophil
1001	43.8	4.2	1130	5	BU855749	BU855749 AGENCOURT
c1002	43.8	4.2	1142	6	CB905439	CB905439 tric074xh
c1003	43.8	4.2	1142	7	CF876953	CF876953 tric074xh
c1004	43.8	4.2	1145	3	BM551318	BM551318 AGENCOURT
c1005	43.8	4.2	1164	10	AG136790	AG136790 Pan trogl
c1006	43.8	4.2	1173	6	CB207639	CB207639 AGENCOURT
1007	43.8	4.2	1190	3	BM556881	BM556881 AGENCOURT
1008	43.8	4.2	1202	6	CA789347	CA789347 AGENCOURT
1009	43.8	4.2	1227	10	AG435127	AG435127 Mus muscu
c1010	43.8	4.2	1230	10	AG390693	AG390693 Mus muscu
c1011	43.8	4.2	1249	6	CB905420	CB905420 tric074xf
c1012	43.8	4.2	1249	7	CF876940	CF876940 tric074xf
c1013	43.8	4.2	1267	8	DN721737	DN721737 CNB140-A1
1014	43.8	4.2	1283	10	AG435406	AG435406 Mus muscu
c1015	43.8	4.2	1284	10	AG435071	AG435071 Mus muscu
1016	43.8	4.2	1341	3	BM546035	BM546035 AGENCOURT
1017	43.8	4.2	1369	10	AG081191	AG081191 Pan trogl
1018	43.8	4.2	1395	8	DN671039	DN671039 CFW60-D06
c1019	43.8	4.2	1442	10	CL476644	CL476644 SAIL_258_
1020	43.8	4.2	1446	7	CK408416	CK408416 AUF_IfLvr
c1021	43.8	4.2	1486	10	CL469802	CL469802 SAIL_133_
c1022	43.8	4.2	1511	10	CL508778	CL508778 SAIL_802_
c1023	43.8	4.2	1530	10	AG396191	AG396191 Mus muscu
c1024	43.8	4.2	1532	8	DN809779	DN809779 76969081
c1025	43.8	4.2	1549	8	DN807031	DN807031 76961690
1026	43.8	4.2	1695	9	CC290874	CC290874 CH261-172
c1027	43.8	4.2	1713	10	AG381912	AG381912 Mus muscu
c1028	43.8	4.2	1738	10	CG750956	CG750956 P045-2-H0
c1029	43.8	4.2	1870	10	AG382259	AG382259 Mus muscu
c1030	43.6	4.2	241	10	CW437615	CW437615 fsbb001f1
c1031	43.6	4.2	283	11	CR011723	CR011723 Reverse s
c1032	43.6	4.2	319	3	BI490033	BI490033 603031822
1033	43.6	4.2	327	11	CNS037PM	AL231619 Tetraodon
c1034	43.6	4.2	408	7	CR559733	CR559733 DKFZp459I
1035	43.6	4.2	421	4	CNS08X1R	BX032251 Single re
c1036	43.6	4.2	423	9	BH617923	BH617923 SALK_0381
1037	43.6	4.2	447	2	BE348478	BE348478 ht69e07.x
c1038	43.6	4.2	481	10	CNS016IP	AL106795 Drosophil
c1039	43.6	4.2	508	11	CR006110	CR006110 Reverse s
c1040	43.6	4.2	512	2	BG579102	BG579102 df23b05.y
c1041	43.6	4.2	564	9	BZ562495	BZ562495 pacs2-164
c1042	43.6	4.2	566	11	CNS03JN0	AL247077 Tetraodon
1043	43.6	4.2	572	9	BZ050840	BZ050840 jnr64d12.
c1044	43.6	4.2	585	10	CW870847	CW870847 she2h96-3
c1045	43.6	4.2	602	10	CNS010R6	AL099324 Drosophil
c1046	43.6	4.2	651	10	CG770015	CG770015 TcB52.3_C
c1047	43.6	4.2	671	3	BI960019	BI960019 HVSMEn002
c1048	43.6	4.2	676	10	AG165647	AG165647 Pan trogl
1049	43.6	4.2	684	9	BZ579729	BZ579729 msh2_744.
1050	43.6	4.2	684	10	AG602107	AG602107 Mus muscu
1051	43.6	4.2	689	10	AG133159	AG133159 Pan trogl
c1052	43.6	4.2	705	10	AG392596	AG392596 Mus muscu
1053	43.6	4.2	718	9	BZ051759	BZ051759 jnr58f06.
c1054	43.6	4.2	743	10	CW951338	CW951338 TcB36.4_B
1055	43.6	4.2	758	10	AG133039	AG133039 Pan trogl
c1056	43.6	4.2	763	6	CB905486	CB905486 tric074xm
c1057	43.6	4.2	763	7	CF876992	CF876992 tric074xm
1058	43.6	4.2	768	10	AG553166	AG553166 Mus muscu
1059	43.6	4.2	797	10	AG560282	AG560282 Mus muscu
c1060	43.6	4.2	806	10	CW950165	CW950165 TcB35.2_B
1061	43.6	4.2	813	10	AG462678	AG462678 Mus muscu
c1062	43.6	4.2	814	11	CR138760	CR138760 Reverse s
c1063	43.6	4.2	823	5	BU532459	BU532459 AGENCOURT
c1064	43.6	4.2	826	6	CF753703	CF753703 EST-77-2-
c1065	43.6	4.2	844	10	AG080590	AG080590 Pan trogl
c1066	43.6	4.2	848	3	BI956729	BI956729 HVSMEn000
1067	43.6	4.2	863	10	AG840337	AG840337 Oryza sat
c1068	43.6	4.2	872	7	CV662461	CV662461 LCPE04EX0
c1069	43.6	4.2	880	10	CW938439	CW938439 TcB18.3_A
c1070	43.6	4.2	882	2	BG299652	BG299652 HVSMEa002
c1071	43.6	4.2	885	10	AG123875	AG123875 Pan trogl
c1072	43.6	4.2	890	10	AG388286	AG388286 Mus muscu
1073	43.6	4.2	898	10	AG130335	AG130335 Pan trogl
1074	43.6	4.2	900	10	CL517041	CL517041 SAIL_99_C
c1075	43.6	4.2	906	10	AG444148	AG444148 Mus muscu
1076	43.6	4.2	906	10	CL506564	CL506564 SAIL_769_
c1077	43.6	4.2	907	11	CR117058	CR117058 Forward s
c1078	43.6	4.2	908	9	AZ191473	AZ191473 SP_1019_B
c1079	43.6	4.2	923	8	DR733189	DR733189 FGAS07895
1080	43.6	4.2	923	10	CL465225	CL465225 SAIL_1236
c1081	43.6	4.2	924	2	BE455162	BE455162 HVSMEh009
c1082	43.6	4.2	925	3	BI958094	BI958094 HVSMEn001
c1083	43.6	4.2	935	3	BI958090	BI958090 HVSMEn001
1084	43.6	4.2	939	10	CL460909	CL460909 SAIL_111_
c1085	43.6	4.2	940	10	AG417910	AG417910 Mus muscu
1086	43.6	4.2	942	10	AG062236	AG062236 Pan trogl
c1087	43.6	4.2	943	3	BM415351	BM415351 OP20425 M
c1088	43.6	4.2	966	5	BQ672441	BQ672441 AGENCOURT
c1089	43.6	4.2	966	10	AG138060	AG138060 Pan trogl
1090	43.6	4.2	968	5	BQ878901	BQ878901 AGENCOURT
c1091	43.6	4.2	970	11	CNS06DHW	AL393834 T7 end of
1092	43.6	4.2	974	10	AG071677	AG071677 Pan trogl
c1093	43.6	4.2	976	8	DN808520	DN808520 74134100
1094	43.6	4.2	979	10	CL470915	CL470915 SAIL_150_
1095	43.6	4.2	981	10	CL479467	CL479467 SAIL_307_
1096	43.6	4.2	981	10	CL485304	CL485304 SAIL_413_
c1097	43.6	4.2	984	10	CL511328	CL511328 SAIL_846_
c1098	43.6	4.2	985	5	BQ672571	BQ672571 AGENCOURT
1099	43.6	4.2	985	7	CK401878	CK401878 AUF_IfInt
c1100	43.6	4.2	992	10	AG276718	AG276718 Mus muscu
1101	43.6	4.2	994	5	BQ668824	BQ668824 AGENCOURT
c1102	43.6	4.2	994	10	AG076814	AG076814 Pan trogl
1103	43.6	4.2	996	9	CC921441	CC921441 t051k04ba
1104	43.6	4.2	1010	5	BQ709361	BQ709361 AGENCOURT
c1105	43.6	4.2	1012	8	DN807738	DN807738 76885732
c1106	43.6	4.2	1016	5	BQ947798	BQ947798 AGENCOURT
1107	43.6	4.2	1019	5	BQ674007	BQ674007 AGENCOURT
1108	43.6	4.2	1030	7	CF933334	CF933334 TrEST-B41
c1109	43.6	4.2	1038	5	BQ650630	BQ650630 AGENCOURT
c1110	43.6	4.2	1042	3	BI416535	BI416535 hasp001xe
c1111	43.6	4.2	1043	10	CW943045	CW943045 TcB24.4_A
1112	43.6	4.2	1050	10	CL508543	CL508543 SAIL_79_A
c1113	43.6	4.2	1059	8	DN809206	DN809206 74115277
c1114	43.6	4.2	1060	10	AG125637	AG125637 Pan trogl
c1115	43.6	4.2	1070	6	CA987146	CA987146 AGENCOURT
1116	43.6	4.2	1078	7	CK402011	CK402011 AUF_IfInt
1117	43.6	4.2	1081	10	AG545516	AG545516 Mus muscu

1118	43.6	4.2	1083	9	BZ050839	BZ050839 jnr64d11.
c1119	43.6	4.2	1087	10	AG050197	AG050197 Pan trogl
c1120	43.6	4.2	1092	10	AG395657	AG395657 Mus muscu
c1121	43.6	4.2	1101	10	CNS012PK	AL101858 Drosophil
1122	43.6	4.2	1101	10	CNS016MU	AL106944 Drosophil
1123	43.6	4.2	1108	8	DR735711	DR735711 FGAS08134
c1124	43.6	4.2	1115	10	CW950568	CW950568 TcB35.4_B
1125	43.6	4.2	1129	5	BQ707740	BQ707740 AGENCOURT
1126	43.6	4.2	1134	9	CC245095	CC245095 CH261-13G
c1127	43.6	4.2	1151	6	CB905418	CB905418 tric074xf
c1128	43.6	4.2	1151	7	CF876938	CF876938 tric074xf
c1129	43.6	4.2	1161	2	BF256588	BF256588 HVSMEf001
c1130	43.6	4.2	1162	8	W42215	W42215 mc69h10.r1
1131	43.6	4.2	1162	10	CL081029	CL081029 CH216-160
c1132	43.6	4.2	1177	7	CK402661	CK402661 AUF_IfInt
1133	43.6	4.2	1177	9	CC193928	CC193928 CH261-95J
c1134	43.6	4.2	1183	8	DN710897	DN710897 CLJ92-A06
c1135	43.6	4.2	1197	3	BI416470	BI416470 hasp001xa
c1136	43.6	4.2	1206	3	BM458888	BM458888 AGENCOURT
c1137	43.6	4.2	1222	9	BH146899	BH146899 ENTQM47TF
1138	43.6	4.2	1231	10	AG363910	AG363910 Mus muscu
c1139	43.6	4.2	1238	10	CW941071	CW941071 TcB22.1_G
1140	43.6	4.2	1239	9	CC319211	CC319211 TAM32-32P
1141	43.6	4.2	1247	1	AJ928042	AJ928042 AJ928042
1142	43.6	4.2	1282	10	CL081061	CL081061 CH216-160
1143	43.6	4.2	1282	10	CL081590	CL081590 CH216-163
1144	43.6	4.2	1286	8	DN701391	DN701391 CLJ35-D06
1145	43.6	4.2	1289	5	BQ884996	BQ884996 AGENCOURT
c1146	43.6	4.2	1319	9	CC243775	CC243775 CH261-20P
1147	43.6	4.2	1321	1	AJ924051	AJ924051 AJ924051
1148	43.6	4.2	1356	3	BM922223	BM922223 AGENCOURT
c1149	43.6	4.2	1358	8	DN726567	DN726567 CNB31-A02
c1150	43.6	4.2	1427	10	CG755119	CG755119 P050-4-B0
1151	43.6	4.2	1435	3	BM456591	BM456591 AGENCOURT
1152	43.6	4.2	1440	10	AG332984	AG332984 Mus muscu
c1153	43.6	4.2	1523	2	BF782985	BF782985 602109072
1154	43.6	4.2	1700	9	CC298790	CC298790 CH261-106
c1155	43.6	4.2	1709	8	DN808503	DN808503 76954993
c1156	43.6	4.2	1736	10	CL104572	CL104572 ISB1-43D1
c1157	43.6	4.2	1761	10	AG396417	AG396417 Mus muscu
1158	43.6	4.2	2244	9	CC255272	CC255272 CH261-42A
1159	43.4	4.1	354	1	AW651803	AW651803 ba28f11.y
c1160	43.4	4.1	424	11	CR075019	CR075019 Reverse s
c1161	43.4	4.1	447	9	BH169279	BH169279 SALK_0009
1162	43.4	4.1	528	10	AG590960	AG590960 Mus muscu
c1163	43.4	4.1	535	10	BX127198	BX127198 Danio rer
c1164	43.4	4.1	538	10	CL495879	CL495879 SAIL_616_
1165	43.4	4.1	569	1	AW078876	AW078876 xb19b06.x
c1166	43.4	4.1	584	9	AQ896366	AQ896366 HS_3117_A
1167	43.4	4.1	591	10	AG070598	AG070598 Pan trogl
1168	43.4	4.1	595	7	CO534846	CO534846 3530_1_23
c1169	43.4	4.1	596	10	CW946261	CW946261 TcB28.4_G
1170	43.4	4.1	601	7	CO521720	CO521720 3530_1_14
1171	43.4	4.1	629	7	CV670133	CV670133 LCPE04EX0
c1172	43.4	4.1	637	11	CNS04M1I	AL296847 Tetraodon
1173	43.4	4.1	642	8	DR810268	DR810268 ZM_BFb003
1174	43.4	4.1	653	9	BZ051862	BZ051862 jnr57a11.
c1175	43.4	4.1	671	10	CW938495	CW938495 TcB18.3_C
c1176	43.4	4.1	675	10	CW941089	CW941089 TcB22.1_G
c1177	43.4	4.1	676	10	AG169546	AG169546 Pan trogl
1178	43.4	4.1	698	9	BZ051779	BZ051779 jnr58h03.
c1179	43.4	4.1	701	3	BI955659	BI955659 HVSMEm002
c1180	43.4	4.1	706	3	BI859530	BI859530 603385385
1181	43.4	4.1	723	8	DR830825	DR830825 ZM_BFb007
1182	43.4	4.1	723	9	BZ051826	BZ051826 jnr57e09.
c1183	43.4	4.1	736	10	CW950666	CW950666 TcB35.4_F
1184	43.4	4.1	753	11	CNS077R7	AL433049 T7 end of
c1185	43.4	4.1	760	3	BM359742	BM359742 GA__Ea002
1186	43.4	4.1	760	8	DR972155	DR972155 ZM_BFb009
c1187	43.4	4.1	776	10	AG060484	AG060484 Pan trogl
1188	43.4	4.1	801	8	DR793529	DR793529 ZM_BFb001
1189	43.4	4.1	802	9	BZ051935	BZ051935 jnr56a07.
c1190	43.4	4.1	807	6	CF149720	CF149720 AGENCOURT
c1191	43.4	4.1	810	10	AG369753	AG369753 Mus muscu
1192	43.4	4.1	810	10	CNS0117K	AL099914 Drosophil
1193	43.4	4.1	818	8	DR796361	DR796361 ZM_BFb001
1194	43.4	4.1	820	8	DR785176	DR785176 ZM_BFb000
1195	43.4	4.1	821	11	CNS049PN	AL280868 Tetraodon
1196	43.4	4.1	836	9	AZ185303	AZ185303 SP_1005_A
1197	43.4	4.1	837	8	DR824882	DR824882 ZM_BFb006
1198	43.4	4.1	845	8	DN578226	DN578226 92284045
c1199	43.4	4.1	851	10	CW952868	CW952868 TcB38.4_B
c1200	43.4	4.1	855	7	CK425869	CK425869 AUF_IpTes
1201	43.4	4.1	856	6	CB908218	CB908218 tric084xl
1202	43.4	4.1	862	8	DR827942	DR827942 ZM_BFb007
c1203	43.4	4.1	865	6	CB816956	CB816956 d1g17pz.r
c1204	43.4	4.1	875	10	AG047588	AG047588 Pan trogl
1205	43.4	4.1	895	9	CC907113	CC907113 t032f06ba
1206	43.4	4.1	897	9	AZ186654	AZ186654 SP_1007_B
c1207	43.4	4.1	898	6	CB905663	CB905663 tric075xj
c1208	43.4	4.1	898	7	CF877337	CF877337 tric075xj
1209	43.4	4.1	900	10	CL508550	CL508550 SAIL_79_C
1210	43.4	4.1	914	10	CL492001	CL492001 SAIL_563_
1211	43.4	4.1	915	10	CL487523	CL487523 SAIL_454_
c1212	43.4	4.1	920	5	BQ683458	BQ683458 AGENCOURT
1213	43.4	4.1	920	10	CL471112	CL471112 SAIL_155b
1214	43.4	4.1	930	6	CA468280	CA468280 AGENCOURT
1215	43.4	4.1	938	10	CL477181	CL477181 SAIL_269_
c1216	43.4	4.1	942	5	BQ681469	BQ681469 AGENCOURT
1217	43.4	4.1	968	10	CL511872	CL511872 SAIL_854_
c1218	43.4	4.1	969	10	CL468996	CL468996 SAIL_1295
1219	43.4	4.1	978	10	CL465829	CL465829 SAIL_1246
c1220	43.4	4.1	986	8	DN563272	DN563272 92173388
c1221	43.4	4.1	1001	3	BM549244	BM549244 AGENCOURT
1222	43.4	4.1	1002	9	BZ051110	BZ051110 jnr62e08.
c1223	43.4	4.1	1006	10	CL468767	CL468767 SAIL_1290
1224	43.4	4.1	1008	5	BQ680767	BQ680767 AGENCOURT
1225	43.4	4.1	1010	10	CL462485	CL462485 SAIL_1166
c1226	43.4	4.1	1014	6	CB204069	CB204069 AGENCOURT
1227	43.4	4.1	1015	5	BQ712431	BQ712431 AGENCOURT
c1228	43.4	4.1	1023	10	CW951358	CW951358 TcB36.4_C
1229	43.4	4.1	1029	10	CL478689	CL478689 SAIL_294_
1230	43.4	4.1	1043	11	CNS03MBE	AL250547 Tetraodon
c1231	43.4	4.1	1056	10	AG367644	AG367644 Mus muscu
c1232	43.4	4.1	1061	2	BE455291	BE455291 HVSMEh009
1233	43.4	4.1	1069	5	BQ642259	BQ642259 AGENCOURT
1234	43.4	4.1	1083	6	CB206984	CB206984 AGENCOURT
1235	43.4	4.1	1086	9	CC225085	CC225085 CH261-154
c1236	43.4	4.1	1096	6	CA977794	CA977794 AGENCOURT
1237	43.4	4.1	1101	10	AG039543	AG039543 Pan trogl
1238	43.4	4.1	1103	5	BQ717559	BQ717559 AGENCOURT
c1239	43.4	4.1	1118	5	BU901630	BU901630 AGENCOURT
c1240	43.4	4.1	1127	10	AG062801	AG062801 Pan trogl
c1241	43.4	4.1	1132	5	BQ672163	BQ672163 AGENCOURT
1242	43.4	4.1	1136	5	BQ671004	BQ671004 AGENCOURT
c1243	43.4	4.1	1141	10	AG441809	AG441809 Mus muscu
c1244	43.4	4.1	1162	3	BQ051092	BQ051092 AGENCOURT
c1245	43.4	4.1	1190	8	DN724270	DN724270 CNB18-B12
1246	43.4	4.1	1193	9	CC300050	CC300050 CH261-107
c1247	43.4	4.1	1201	5	BX444152	BX444152 BX444152
1248	43.4	4.1	1285	10	CL081442	CL081442 CH216-161
1249	43.4	4.1	1326	9	BZ697030	BZ697030 SP__Ba009
1250	43.4	4.1	1332	8	DN726754	DN726754 CNB32-A08
c1251	43.4	4.1	1400	10	CW937358	CW937358 TcB16.2_D
1252	43.4	4.1	1417	10	CL469742	CL469742 SAIL_133_
c1253	43.4	4.1	1462	10	AG441877	AG441877 Mus muscu
1254	43.4	4.1	1471	3	BM911091	BM911091 AGENCOURT
c1255	43.4	4.1	1509	10	AG397016	AG397016 Mus muscu
c1256	43.4	4.1	1547	10	CG755163	CG755163 P050-4-D0
c1257	43.4	4.1	1601	10	CG752479	CG752479 P047-2-A0
c1258	43.4	4.1	1853	10	AG382854	AG382854 Mus muscu
1259	43.2	4.1	207	8	DN350414	DN350414 LIB3579-0
c1260	43.2	4.1	220	11	CR052560	CR052560 Forward s
c1261	43.2	4.1	323	10	CG898803	CG898803 pastbac08
c1262	43.2	4.1	336	10	BX958997	BX958997 Forward s
c1263	43.2	4.1	393	9	CC460061	CC460061 SALK_1386

c1264	43.2	4.1	424	11	CR143839	CR143839 Reverse s
c1265	43.2	4.1	433	9	BH753302	BH753302 SALK_0285
c1266	43.2	4.1	461	6	CA952784	CA952784 iq13h10.y
c1267	43.2	4.1	511	8	DN434640	DN434640 LIB4217-1
1268	43.2	4.1	517	11	TA21B11Q	AL453768 T. brucei
c1269	43.2	4.1	553	6	CF754076	CF754076 EST-77-2-
c1270	43.2	4.1	585	11	CR152671	CR152671 Forward s
c1271	43.2	4.1	587	10	CNS02LVU	AL203331 Tetraodon
c1272	43.2	4.1	661	9	BZ003288	BZ003288 oed91a02.
c1273	43.2	4.1	675	11	CR152762	CR152762 Reverse s
c1274	43.2	4.1	677	10	CG772236	CG772236 TcB49.4_A
c1275	43.2	4.1	694	10	CW949021	CW949021 TcB33.3_B
1276	43.2	4.1	700	9	BZ051765	BZ051765 jnr58f12.
c1277	43.2	4.1	707	9	AZ196487	AZ196487 SP_1032_A
c1278	43.2	4.1	708	9	AQ751096	AQ751096 HS_5576_B
1279	43.2	4.1	724	8	DN425696	DN425696 LIB4216-0
c1280	43.2	4.1	729	6	CD901383	CD901383 G356.103K
c1281	43.2	4.1	741	10	AG049269	AG049269 Pan trogl
c1282	43.2	4.1	747	9	AQ738642	AQ738642 HS_5381_B
1283	43.2	4.1	794	9	BZ050856	BZ050856 jnr64f12.
1284	43.2	4.1	805	10	AG280718	AG280718 Mus muscu
1285	43.2	4.1	813	9	BZ052047	BZ052047 jnr56e08.
c1286	43.2	4.1	833	3	BI953739	BI953739 HVSMEm001
c1287	43.2	4.1	839	10	CNS004NB	AL054280 Drosophil
c1288	43.2	4.1	848	10	AG127686	AG127686 Pan trogl
1289	43.2	4.1	849	10	AG491273	AG491273 Mus muscu
c1290	43.2	4.1	862	10	AG859462	AG859462 Oryza sat
1291	43.2	4.1	866	11	CNS046E1	AL276562 Tetraodon
1292	43.2	4.1	878	10	CL475527	CL475527 SAIL_23_H
c1293	43.2	4.1	880	7	CV667844	CV667844 LCPE04EX0
1294	43.2	4.1	881	10	AG082418	AG082418 Pan trogl
1295	43.2	4.1	883	10	AG901898	AG901898 Oryza sat
c1296	43.2	4.1	887	10	CNS02SC6	AL211695 Tetraodon
c1297	43.2	4.1	891	9	AZ184409	AZ184409 SP_1002_B
c1298	43.2	4.1	891	10	AG423947	AG423947 Mus muscu
c1299	43.2	4.1	892	11	CNS03FFK	AL241625 Tetraodon
c1300	43.2	4.1	893	5	BX355212	BX355212 BX355212
c1301	43.2	4.1	899	10	AG418751	AG418751 Mus muscu
c1302	43.2	4.1	908	8	CV767484	CV767484 FGAS06187
1303	43.2	4.1	909	10	CL478658	CL478658 SAIL_294_
1304	43.2	4.1	926	10	AG060188	AG060188 Pan trogl
1305	43.2	4.1	929	10	CZ520964	CZ520964 GMW2-50H1
1306	43.2	4.1	931	10	CW957058	CW957058 TcB52.1_A
c1307	43.2	4.1	933	10	CL460569	CL460569 SAIL_108_
1308	43.2	4.1	935	10	CL495255	CL495255 SAIL_607_
1309	43.2	4.1	938	10	CL466121	CL466121 SAIL_1252
c1310	43.2	4.1	938	10	CL515999	CL515999 SAIL_910_
1311	43.2	4.1	939	10	CL482413	CL482413 SAIL_360_
c1312	43.2	4.1	940	5	BQ411405	BQ411405 GA__Ed003_
1313	43.2	4.1	940	10	CL460263	CL460263 SAIL_102_
c1314	43.2	4.1	946	10	CW958932	CW958932 TcB54.4_G
1315	43.2	4.1	957	3	BM461728	BM461728 AGENCOURT
1316	43.2	4.1	957	10	CL464498	CL464498 SAIL_1221
1317	43.2	4.1	962	10	CNS00K3S	AL077188 Drosophil
1318	43.2	4.1	968	10	CL480772	CL480772 SAIL_32_D
1319	43.2	4.1	969	10	CL477043	CL477043 SAIL_267_
c1320	43.2	4.1	979	10	CL468750	CL468750 SAIL_1290
1321	43.2	4.1	983	7	CK422393	CK422393 AUF_IpSpn
1322	43.2	4.1	1000	10	CL506558	CL506558 SAIL_769_
1323	43.2	4.1	1015	10	CL500693	CL500693 SAIL_688_
1324	43.2	4.1	1016	6	CA479693	CA479693 AGENCOURT
c1325	43.2	4.1	1029	5	BU944088	BU944088 AGENCOURT
c1326	43.2	4.1	1030	10	CW951269	CW951269 TcB36.3_H
1327	43.2	4.1	1033	5	BQ674699	BQ674699 AGENCOURT
1328	43.2	4.1	1033	5	BQ897345	BQ897345 AGENCOURT
1329	43.2	4.1	1046	5	BQ643604	BQ643604 AGENCOURT
1330	43.2	4.1	1059	5	BU192105	BU192105 AGENCOURT
1331	43.2	4.1	1076	5	BQ710564	BQ710564 AGENCOURT
c1332	43.2	4.1	1080	9	AQ893056	AQ893056 HS_4832_A
c1333	43.2	4.1	1080	10	AG136651	AG136651 Pan trogl
1334	43.2	4.1	1094	10	AG099072	AG099072 Pan trogl
1335	43.2	4.1	1101	10	CNS000U8	AL051971 Drosophil
1336	43.2	4.1	1101	10	CNS00DZT	AL067605 Drosophil
1337	43.2	4.1	1101	10	CNS0171J	AL107473 Drosophil
c1338	43.2	4.1	1101	10	CNS0181P	AL108775 Drosophil
c1339	43.2	4.1	1104	5	BQ671688	BQ671688 AGENCOURT
c1340	43.2	4.1	1107	3	BI416477	BI416477 hasp001xa
1341	43.2	4.1	1107	7	CK162505	CK162505 FGAS01510
c1342	43.2	4.1	1119	10	AG414879	AG414879 Mus muscu
1343	43.2	4.1	1128	9	CC209255	CC209255 CH261-74F
c1344	43.2	4.1	1144	10	AG365359	AG365359 Mus muscu
c1345	43.2	4.1	1152	3	BM556517	BM556517 AGENCOURT
1346	43.2	4.1	1157	8	DN671180	DN671180 CFW61-C02
c1347	43.2	4.1	1192	6	CB905423	CB905423 tric074xf
c1348	43.2	4.1	1192	7	CF876942	CF876942 tric074xf
c1349	43.2	4.1	1193	10	CG752559	CG752559 P047-2-D0
c1350	43.2	4.1	1198	6	CD497643	CD497643 CDA29-A04
c1351	43.2	4.1	1212	8	DN695394	DN695394 CGX99-G10
c1352	43.2	4.1	1212	10	CL644385	CL644385 CH213-72B
1353	43.2	4.1	1222	9	CC189787	CC189787 CH261-161
1354	43.2	4.1	1224	3	BM560595	BM560595 AGENCOURT
c1355	43.2	4.1	1233	10	CL081644	CL081644 CH216-163
c1356	43.2	4.1	1241	8	DN689789	DN689789 CGX66-F11
c1357	43.2	4.1	1244	10	CL118045	CL118045 ISB1-69N2
c1358	43.2	4.1	1248	8	DN734853	DN734853 CNB78-A08
1359	43.2	4.1	1288	6	CA974086	CA974086 AGENCOURT
1360	43.2	4.1	1301	10	AG393296	AG393296 Mus muscu
1361	43.2	4.1	1310	3	BM809102	BM809102 AGENCOURT
1362	43.2	4.1	1313	10	CG747660	CG747660 P041-2-C0
1363	43.2	4.1	1324	10	AG382082	AG382082 Mus muscu
c1364	43.2	4.1	1432	9	CC250857	CC250857 CH261-166
1365	43.2	4.1	1459	5	BU316357	BU316357 603487214
1366	43.2	4.1	1565	10	AG340866	AG340866 Mus muscu
c1367	43.2	4.1	1624	10	AG397050	AG397050 Mus muscu
1368	43.2	4.1	1656	10	AG430456	AG430456 Mus muscu
c1369	43.2	4.1	1806	10	CL063000	CL063000 CH216-99D
c1370	43.2	4.1	2054	10	AG441640	AG441640 Mus muscu
1371	43	4.1	235	10	BX216281	BX216281 Danio rer
1372	43	4.1	270	10	CNS01INF	AL145964 Anopheles
c1373	43	4.1	331	11	CR045384	CR045384 Forward s
1374	43	4.1	369	7	CN144695	CN144695 WOUND1_23
c1375	43	4.1	403	8	DN415102	DN415102 LIB4215-0
c1376	43	4.1	408	2	BG551110	BG551110 sad33d01.
c1377	43	4.1	412	5	BU095515	BU095515 rf74h05.y
c1378	43	4.1	420	5	CA034112	CA034112 pw25c01.y
c1379	43	4.1	436	5	CA034056	CA034056 pw47e08.y
c1380	43	4.1	439	10	BX979804	BX979804 Forward s
1381	43	4.1	449	11	CNS0398S	AL233605 Tetraodon
1382	43	4.1	460	9	AQ868591	AQ868591 nbeb0028F
1383	43	4.1	463	8	CX621673	CX621673 GABR1_59_
1384	43	4.1	506	2	BF594884	BF594884 naa70h11.
1385	43	4.1	511	6	CD429169	CD429169 ETH1_2_B0
c1386	43	4.1	529	8	DN370168	DN370168 LIB3733-0
c1387	43	4.1	535	11	CR044505	CR044505 Forward s
1388	43	4.1	588	8	CX615932	CX615932 GABR1_24_
1389	43	4.1	592	8	DN413160	DN413160 LIB4215-0
1390	43	4.1	595	8	DN432871	DN432871 LIB4217-0
1391	43	4.1	600	6	CA526593	CA526593 8013-66 M
c1392	43	4.1	645	7	CV663743	CV663743 LCPE04EX0
1393	43	4.1	649	6	CD426715	CD426715 SA1_22_C1
c1394	43	4.1	662	8	DN400403	DN400403 LIB4004-0
c1395	43	4.1	664	11	CNS05CNF	AL331332 Tetraodon
c1396	43	4.1	666	2	BG786337	BG786337 SEAUMC006
c1397	43	4.1	670	3	BI956167	BI956167 HVSMEm002
1398	43	4.1	674	8	DN425716	DN425716 LIB4216-0
c1399	43	4.1	706	10	AG570588	AG570588 Mus muscu
1400	43	4.1	723	10	AG123920	AG123920 Pan trogl
c1401	43	4.1	734	8	DN440265	DN440265 LIB4393-0
1402	43	4.1	735	8	CX623077	CX623077 GABR1_67_
c1403	43	4.1	740	9	AZ195718	AZ195718 SP_1030_B
c1404	43	4.1	748	9	AZ187748	AZ187748 SP_1009_B
1405	43	4.1	751	9	AQ853906	AQ853906 nbxb0046C
c1406	43	4.1	760	9	AZ194761	AZ194761 SP_1028_B
1407	43	4.1	762	11	CNS04NET	AL298622 Tetraodon
1408	43	4.1	769	10	AG133155	AG133155 Pan trogl
1409	43	4.1	782	9	B21874	B21874 T3D16-Sp6 T

c1410	43	4.1	785	7	CV663571	CV663571 LCPE04EX0
1411	43	4.1	787	10	AG046077	AG046077 Pan trogl
c1412	43	4.1	794	9	AZ198517	AZ198517 SP_1037_B
c1413	43	4.1	796	11	CNS04BGN	AL283136 Tetraodon
c1414	43	4.1	798	9	AZ175429	AZ175429 SP_0132_A
c1415	43	4.1	799	10	AG049309	AG049309 Pan trogl
1416	43	4.1	800	8	CX607402	CX607402 ANR1_8_A0
c1417	43	4.1	812	10	CW948929	CW948929 TcB33.2_F
1418	43	4.1	815	10	AG860065	AG860065 Oryza sat
1419	43	4.1	824	9	BZ412991	BZ412991 99h2_ctg7
1420	43	4.1	825	9	AZ195521	AZ195521 SP_1030_A
1421	43	4.1	830	10	AG497612	AG497612 Mus muscu
1422	43	4.1	832	7	CN126874	CN126874 RHOH1_19_
1423	43	4.1	841	9	BZ051701	BZ051701 jnr58h06.
1424	43	4.1	847	10	AG876453	AG876453 Oryza sat
c1425	43	4.1	854	10	CL486928	CL486928 SAIL_443_
1426	43	4.1	856	10	AG468082	AG468082 Mus muscu
1427	43	4.1	863	9	BZ051672	BZ051672 jnr58d11.
1428	43	4.1	865	10	AG846397	AG846397 Oryza sat
c1429	43	4.1	867	10	AG405861	AG405861 Mus muscu
1430	43	4.1	869	10	AG529297	AG529297 Mus muscu
1431	43	4.1	873	10	CL498274	CL498274 SAIL_654_
1432	43	4.1	874	7	CK160001	CK160001 FGAS04153
1433	43	4.1	882	10	AG471724	AG471724 Mus muscu
1434	43	4.1	884	10	CNS018NP	AL109567 Drosophil
c1435	43	4.1	893	7	CV662857	CV662857 LCPE04EX0
1436	43	4.1	893	10	CL489836	CL489836 SAIL_52b_
1437	43	4.1	895	10	CL460465	CL460465 SAIL_106b
c1438	43	4.1	896	11	CR151764	CR151764 Reverse s
c1439	43	4.1	897	3	BI952044	BI952044 HVSMEm000
1440	43	4.1	898	10	AG081215	AG081215 Pan trogl
c1441	43	4.1	899	8	CV765400	CV765400 FGAS05978
c1442	43	4.1	904	5	BU962874	BU962874 AGENCOURT
1443	43	4.1	906	5	BQ945939	BQ945939 AGENCOURT
c1444	43	4.1	921	10	CL461881	CL461881 SAIL_1154
1445	43	4.1	928	10	CL491269	CL491269 SAIL_554_
c1446	43	4.1	934	5	BX357880	BX357880 BX357880
1447	43	4.1	934	10	CL465219	CL465219 SAIL_1236
1448	43	4.1	940	10	CL480244	CL480244 SAIL_320_
1449	43	4.1	950	10	CL468981	CL468981 SAIL_1295
1450	43	4.1	953	10	CL473805	CL473805 SAIL_207_
c1451	43	4.1	956	6	CB208876	CB208876 AGENCOURT
c1452	43	4.1	956	10	CW941038	CW941038 TcB22.1_E
c1453	43	4.1	957	10	CNS018F9	AL109263 Drosophil
1454	43	4.1	960	5	BQ429353	BQ429353 AGENCOURT
c1455	43	4.1	979	9	AQ891992	AQ891992 HS_4831_B
c1456	43	4.1	979	10	AG136805	AG136805 Pan trogl
1457	43	4.1	979	10	CL464708	CL464708 SAIL_1225
c1458	43	4.1	983	5	BU838409	BU838409 AGENCOURT
c1459	43	4.1	984	10	AG136861	AG136861 Pan trogl
c1460	43	4.1	988	5	BQ411526	BQ411526 GA__Ed004
c1461	43	4.1	991	8	DN808009	DN808009 74115230
1462	43	4.1	995	5	BQ674625	BQ674625 AGENCOURT
c1463	43	4.1	1001	6	CA453651	CA453651 AGENCOURT
1464	43	4.1	1007	10	CL464054	CL464054 SAIL_1212
1465	43	4.1	1034	6	CA983175	CA983175 AGENCOURT
1466	43	4.1	1042	5	BU507291	BU507291 AGENCOURT
1467	43	4.1	1046	5	BU956304	BU956304 AGENCOURT
1468	43	4.1	1054	10	CL462507	CL462507 SAIL_1166
c1469	43	4.1	1056	7	CV662673	CV662673 LCPE04EX0
1470	43	4.1	1056	9	BZ051752	BZ051752 jnr58e08.
c1471	43	4.1	1061	5	BU930925	BU930925 AGENCOURT
1472	43	4.1	1069	5	BX354603	BX354603 BX354603
c1473	43	4.1	1073	8	W13735	W13735 ma94a02.r1
1474	43	4.1	1078	6	CA460394	CA460394 AGENCOURT
c1475	43	4.1	1079	9	CC283488	CC283488 CH261-55F
c1476	43	4.1	1086	7	CV520645	CV520645 0089P0048
1477	43	4.1	1086	10	CL484608	CL484608 SAIL_39_G
c1478	43	4.1	1096	8	DN669503	DN669503 CFW50-H11
1479	43	4.1	1101	10	CNS012S8	AL101954 Drosophil
1480	43	4.1	1101	10	CNS016R4	AL107098 Drosophil
c1481	43	4.1	1106	6	CB905422	CB905422 tric074xf
c1482	43	4.1	1106	7	CF876941	CF876941 tric074xf
c1483	43	4.1	1112	10	AG381245	AG381245 Mus muscu
1484	43	4.1	1121	6	CA455759	CA455759 AGENCOURT
1485	43	4.1	1121	10	AG078685	AG078685 Pan trogl
c1486	43	4.1	1123	10	CL470578	CL470578 SAIL_144_
c1487	43	4.1	1124	9	CC185785	CC185785 CH261-61J
c1488	43	4.1	1128	8	DR733228	DR733228 FGAS07898
c1489	43	4.1	1131	5	BU957459	BU957459 AGENCOURT
1490	43	4.1	1139	3	BQ064751	BQ064751 AGENCOURT
1491	43	4.1	1142	10	CL501710	CL501710 SAIL_702_
c1492	43	4.1	1151	5	BQ951254	BQ951254 AGENCOURT
1493	43	4.1	1158	9	CC251504	CC251504 CH261-84H
1494	43	4.1	1160	5	BU537937	BU537937 AGENCOURT
1495	43	4.1	1167	10	CL469727	CL469727 SAIL_133_
c1496	43	4.1	1172	5	BU902250	BU902250 AGENCOURT
1497	43	4.1	1200	8	DN660111	DN660111 CEC44-H09
c1498	43	4.1	1201	10	CNS015Z3	AL106089 Drosophil
c1499	43	4.1	1206	8	DN672092	DN672092 CFW66-E05
c1500	43	4.1	1223	10	AG441637	AG441637 Mus muscu

ALIGNMENTS

RESULT 1
BC069410
LOCUS BC069410 1027 bp mRNA linear HTC 11-JUL-2005
DEFINITION Homo sapiens cDNA clone IMAGE:7262201, with apparent retained intron.
ACCESSION BC069410
VERSION BC069410.1 GI:46854343
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1027)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRTM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 1027)
AUTHORS .
CONSRTM NIH MGC Project
TITLE Direct Submission
JOURNAL Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome

```
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBR Plate: 2 Row: b Column: 3
            This clone has the following problem: retained intron.
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:7262201"
                      /tissue_type="PCR rescued clones"
                      /clone_lib="NIH_MGC_277"
                      /note="Vector: pPCR-Script Amp SK(+) with reversed insert"
ORIGIN

  Query Match             60.9%;  Score 637.4;  DB 4;  Length 1027;
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  Matches  638;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         55 GCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCC 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 GCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCC 448

Qy        115 CTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACT 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 CTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACT 508

Qy        175 GCCCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTT 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 GCCCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTT 568

Qy        235 GCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCC 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        569 GCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCC 628

Qy        295 CTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCA 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 CTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCA 688

Qy        355 CCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACA 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 CCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACA 748

Qy        415 GAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGA 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 GAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGA 808

Qy        475 GACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCC 534
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Db        809 GACAGCTGCGCTCAACTCCGTGCGGCTGTTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCC 868

Qy        535 CTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTT 594
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 CTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTT 928

Qy        595 CATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCC 654
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Db        929 CATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCC 988

Qy        655 GTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG 693
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Db        989 GTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG 1027


RESULT 2

DQ030711
LOCUS       DQ030711                588 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Homo sapiens HC464 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ030711
VERSION     DQ030711.1  GI:66881915
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 588)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES              Location/Qualifiers
     source           1. .588
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /chromosome="16"
     gene             <1. .>588
                      /locus_tag="HC464"
ORIGIN

  Query Match             56.2%;  Score 588;  DB 11;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-132;
  Matches  588;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 CTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCC 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCC 60

Qy        116 TCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTG 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTG 120

Qy        176 CCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTG 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTG 180

Qy        236 CCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCC 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCC 240

Qy        296 TCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCAC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCAC 300

Qy        356 CAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAG 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAG 360

Qy        416 AAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAG 475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAG 420

Qy        476 ACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCC 535
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Db         421 ACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCC 480

Qy         536 TGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTC 595
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Db         481 TGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTC 540

Qy         596 ATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGA 643
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Db         541 ATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGA 588


RESULT 3
DQ030712
LOCUS       DQ030712                586 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes HC464 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ030712
VERSION     DQ030712.1  GI:66881916
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 586)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 586)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .586
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
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     gene            <1. .>586
                     /locus_tag="HC464"
ORIGIN

  Query Match           49.8%;  Score 521;  DB 11;  Length 586;
  Best Local Similarity  89.4%;  Pred. No. 1.3e-115;
  Matches  524;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy          58 CCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTC 117
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Db           1 CCTCCCTGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTC 60

Qy         118 CCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCC 177
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Db          61 CCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCC 120

Qy         178 CCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCC 237
               |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CCTCGGCCACGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCC 180

Qy         238 TGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTC 297
               |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         181 TGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCATAGGGGGAGGCACGAGAGGCCCTC 240

Qy         298 AGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCA 357
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Db         241 AGCTACGACCCAGTGCCCGGTGCTGCGGCCAGAGGAGGTGTTGGAGGCAGACACCCACCA 300

Qy         358 GCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAA 417
               ||||||||||||||||||||||||||||
Db         301 GCGCTCCATCTCACCCTGGAGATACCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 360

Qy         418 GCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGAC 477
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Db         361 NNTGGCCTTNNNCGAGTGCCTGTNNNNNGGCTGTATNNNTGCGCGGACGGGCCGCGANNN 420

Qy         478 AGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTG 537
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Db         421 NNCTGCGCTCNNNTCCGTGCGGCTGCTCCNNNGCCTGCTGGTGCTGCGCCGCCGGCCCTG 480

Qy         538 CTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCAT 597
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Db         481 CTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCAT 540

Qy         598 CCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGA 643
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Db         541 CCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGA 586


RESULT 4
BX281422
LOCUS       BX281422                466 bp    mRNA    linear   EST 04-MAR-2003
DEFINITION  BX281422 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGp998H057906 ;
            IMAGE:3232180, mRNA sequence.
ACCESSION   BX281422
VERSION     BX281422.1  GI:28612698
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 466)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998H057906.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998H057906 ; IMAGE:3232180"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu24"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Plasmid DNA from the normalized
                     library NCI_CGAP_Lu5 was prepared, and ss circles were
                     made in vitro. Following HAP purification, this DNA was
                     used as tracer in a subtractive hybridization reaction.
                     The driver was PCR-amplified cDNAs from a pool of 5,000
```

clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 44.1%; Score 462; DB 5; Length 466;
Best Local Similarity 99.1%; Pred. No. 2.8e-101;
Matches 462; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy        338 TTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGAT 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGAT 60

Qy        398 GAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGAT 457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGAT 120

Qy        458 GCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTG 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTG 180

Qy        518 GTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTT 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTT 240

Qy        578 GCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCA 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCA 300

Qy        638 GTGTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACC 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACC 360

Qy        698 CCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCCAACACTACCCTTGGGGTCT 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCCAACACTACCCTTGGGGTCT 420

Qy        758 GGGCATTCCCCGTGTCTGGAGGACAGCCCCCCCACTGTTCTCCTCAT 803
              || |||||||||||||| | |||||||||||||||| |||||||
Db        421 GGNCATTCCCCGTGTCTGNANGACAGCCCCCCCACTGTTNTCCTCAT 466
```

RESULT 5
AG139411/c
LOCUS AG139411 669 bp DNA linear GSS 04-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-153O06.F, genomic survey sequence.
ACCESSION AG139411
VERSION AG139411.1 GI:16669089
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 669)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES Location/Qualifiers
source 1. .669
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-153O06.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

Query Match 36.0%; Score 377; DB 10; Length 669;
Best Local Similarity 90.6%; Pred. No. 1.3e-80;
Matches 423; Conservative 0; Mismatches 42; Indels 2; Gaps 2;

```
Qy        410 CCACAGAAGCTGGCCTTCGCCGAGTGCC-TGTGCAGAGGCTGTATCGATGCACGGACGGG 468
              |||||| | |||||  ||||||  |||| ||||||||||||||||||||| | ||||
Db        505 CCACAGGATCTGGCTGTCGCCGGATGCCTTGTGCAGAGGCTGTATCGATGCGCTGACGNT 446

Qy        469 CCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCG 528
              |||||||||| |||||||||||||||||||||||||||||||||  | || |||||
Db        445 CCGCGAGACAGGTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCT-ATACTACGCCG 387

Qy        529 CCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACAC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 CCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACAC 327

Qy        589 CGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCC 648
              |||||||||||||||||||||||    |||| ||| | ||||||||||||||||||||||||
Db        326 CGAGTTCATCCACGTCCCCGTCGAAAGCACATGCATACTGCCCCGTTCAGTGTGACCGCC 267

Qy        649 GAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATG 708
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 GAGNCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATG 207

Qy        709 TGTATTTATTGTTATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCC 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 TGTATTTATTGTTATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCC 147

Qy        769 GTGTCTGGAGGACAGCCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAG 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 GTGTCTGGAGGACAGCCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAG 87

Qy        829 AAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGT 875
              ||||||||| |||   |  |  |  |||||   |||   || |
Db         86 AAGGAGCTCCGCAGACGTCGTACGTCGCGAAGCTTTCGAACGCGTAT 40
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RESULT 6
BE551188/c
LOCUS BE551188 264 bp mRNA linear EST 10-AUG-2000
DEFINITION 7b55g03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3232180 3', mRNA sequence.
ACCESSION BE551188
VERSION BE551188.1 GI:9792880
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 264)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 259.

FEATURES Location/Qualifiers
source 1. .264
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3232180"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 23.4%; Score 244.8; DB 2; Length 264;
Best Local Similarity 98.8%; Pred. No. 1.6e-48;
Matches 257; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy        780 ACAGCCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAG 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 ACAGCCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAG 205

Qy        840 CACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCT 899
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        204 CACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGAACCTTGGCT 145

Qy        900 CCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGG-CCCCGCAGGCTGCC 958
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db        144 CCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCC 85

Qy        959 TCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTA 1018
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         84 TCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGAACGTGTA 25

Qy       1019 TTATTAAACTGATGAACACA 1038
              ||||||||||||||||||||
Db         24 TTATTAAACTGATGAACACA 5
```

RESULT 7
CNS015Y4/c
LOCUS CNS015Y4 1203 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL106054
VERSION AL106054.1 GI:5619805
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1203)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

FEATURES Location/Qualifiers
source 1. .1203
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15E10"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"

ORIGIN

Query Match 6.3%; Score 66; DB 10; Length 1203;
Best Local Similarity 36.2%; Pred. No. 5.7e-05;
Matches 125; Conservative 63; Mismatches 157; Indels 0; Gaps 0;

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Qy         29 GCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTG 88
              :|| :::::|  ||| || ||    | : :: ||::: || ||:  : ::  || : : |
Db       1070 SCCSSSSSSGGGGCCCCCCCCCCCCCSSSSCCCSSKCCCCCCKNSKCSKCCCCCSCSSG 1011

Qy         89 CACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACC 148
                | |   ||::  || ||    ::|| ||: :   :::: :::||   ::| | :  |
Db       1010 GGCCCCCCCCKBCGCCBCCCCCCSSCCCCCSCSSCCSBSSSSBBCCKGGSKCCCCCBTKC 951

Qy        149 CCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCT 208
              |: | |::|  :::  |::    | :: || |  |    |||||| | |:  | :::
Db        950 CBKCCCKSCCCBKBCCCBBBCCCSCCSBKCCCCCCCNCCCCCCCCCCCCCCSCCCCSSSG 891

Qy        209 CGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCA 268
              || :  ||  : ||:||    |    ||     :   || : || |        | :
Db        890 CGSSCCCCCCCSGGGSGGGNCCCCCCCCCCCGGCSGGGGGGSCCCSGGGCCCCCCCCSGS 831

Qy        269 AGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCG 328
              ||| :  ||| ||| || :  ||| : ||  :  |||    |:|:| |  | || |
Db        830 GGCCCSCCCGGGGGGCCCGCSCCCCCCCSGGCCCSCCCCCCCCSCCSCSGGGGGGGGGGGG 771

Qy        329 GAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCC 373
              | || || |  || || :| | :|  || :| | ||  | | |||
Db        770 GGGGGGGGGGGGGGGGRGCCGSCGGCCCSCCCCCCCCCSCCCCC 726
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RESULT 8
CL505520
LOCUS CL505520 2656 bp DNA linear GSS 01-APR-2004
DEFINITION SAIL_751_G07.v1 SAIL Collection Arabidopsis thaliana genomic clone SAIL_751_G07.v1, genomic survey sequence.
ACCESSION CL505520
VERSION CL505520.1 GI:46002840
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 2656)
AUTHORS Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D., Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D., Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B., Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
TITLE A high-throughput Arabidopsis reverse genetics system
JOURNAL Plant Cell 14 (12), 2985-2994 (2002)
PUBMED 12468722
COMMENT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.

```
            3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
            Email: allen.sessions@syngenta.com
            ABRC Stock Number CS833558; T-DNA left border flanking sequences of
            Syngenta Arabidopsis Insertion Library (SAIL) lines are available
            through the Arabidopsis Biological Resource Center (ABRC).
            Sequences represent a pool of amplified genomic regions and not
            single contiguous sequences.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .2656
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /clone="SAIL_751_G07.v1"
                     /clone_lib="SAIL Collection"
                     /note="T-DNA left border sequences were isolated using a
                     modified TAIL-PCR strategy"
ORIGIN

  Query Match             5.9%;  Score 61.4;  DB 10;  Length 2656;
  Best Local Similarity   35.7%;  Pred. No. 0.00083;
  Matches  218;  Conservative    0;  Mismatches  390;  Indels    2;  Gaps    1;

Qy         25 CCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGTTTCTGACCTG 84
Db        418 CNNTNNCNNNCGGCCNGGNNCNCCCCCCNNNNGCCCCCCCCCCCCCCCGGNNCNNCCCCN 477

Qy         85 GCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCACAGTCACGG 144
Db        478 CCNCNCCNCGNNNCCCCCNNNCCCCNCNCCCNNNCCCCGGNNNCACNCGCCNCGNCCCGG 537

Qy        145 TACCCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAGGCCCCCCCACACCTGCT 204
Db        538 GGGGNNCCCCCGCNGNGNGGCCCCCNNNNNGCNNGCCGGCCGCNNNCTCCCGGCGCGGGN 597

Qy        205 GGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGCCT--GGAG 262
Db        598 GNCGCANNGNNCCCCGNGCGCCGNCCCNNNCCCCNGNNNCCGNGNCGCCGCNCNGCGNNN 657

Qy        263 GCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTG 322
Db        658 NCCGCGCGCCCCCGCGCNCNGACGCGCACGGCNCGCCGCACGGCGGCGNNGGGCGNGCGN 717

Qy        323 CGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCTGGAGATAC 382
Db        718 CGGCCGGGCNCGCNGNGNCNGGCGNACGCACGGCCNCGCCCCGCCNCGCCACNCACGGNC 777

Qy        383 CGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGC 442
Db        778 CGCNCCAGACNGNACCGCGCGCCNNCNCCACCCCCNGGNCNCNCNNCGCCNCCNCNCC 837

Qy        443 AGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTG 502
Db        838 NGCCGCCCCNNGCCGCGGCCGCNGNCNNACGGGGNNNNNNCNCNNNACNNNNNNCGCCCG 897

Qy        503 CTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCC 562
Db        898 CGCCCGCCCCAGCCGCCNCCGCGCCCNNNCCNCCGGNNCCCCCANGCGCCNGCCCNAGCN 957

Qy        563 ACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGC 622
Db        958 GACCCCNCGACGACNCCTGCGGCGAGCGAAGCGCGGCGCCCCGCCCCCCCCCGCGGCNGC 1017

Qy        623 GTGCTGCCCC 632
Db       1018 GNCCCAGCCC 1027


RESULT 9
CE738486/c
LOCUS       CE738486                 535 bp    DNA     linear   GSS 30-SEP-2003
DEFINITION  tigr-gss-dog-17000330285612 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE738486
VERSION     CE738486.1  GI:37078739
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
  TITLE     The dog genome: survey sequencing and comparative analysis
  JOURNAL   Science 301 (5641), 1898-1903 (2003)
   PUBMED   14512627
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .535
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

  Query Match             5.8%;  Score 61.2;  DB 10;  Length 535;
  Best Local Similarity   76.5%;  Pred. No. 0.00075;
  Matches   75;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy         55 GCTCCTCCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCC 114
Db         99 GCTCCTCCCCCGCCTCTTGCTTCTGTTCTGGCTGCCCGCCAGCCTGGCCCGCCACGGCCC 40

Qy        115 CTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCAC 152
Db         39 CCAGCTCTGGAGGGGCCTCCACACCCACGGGACCCCAC 2


RESULT 10
AG290167
LOCUS       AG290167                 1454 bp    DNA     linear   GSS 18-DEC-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-064M18.T7, genomic survey
            sequence.
ACCESSION   AG290167
VERSION     AG290167.1  GI:47863044
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
            Shiroishi,T.
  TITLE     Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
  JOURNAL   Genome Res. 14 (12), 2439-2447 (2004)
   PUBMED   15574823
REFERENCE   2  (bases 1 to 1454)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
```

```
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .1454
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-064M18.T7"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             5.8%;  Score 60.8;  DB 10;  Length 1454;
  Best Local Similarity   42.4%;  Pred. No. 0.0011;
  Matches  278;  Conservative    0;  Mismatches  377;  Indels    0;  Gaps    0;

Qy          8 GTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGC 67
              | |  | |  | ||  | || |||   |||   || || |     ||| || |||| ||
Db        669 GCGGCGCCGCCCCCCCGGCCCGCCCCGCCCNGCCCCCCCCCCGCCCCCGCGCCCCCCCCGC 728

Qy         68 CTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGG 127
                |  |   | | ||    |     |   |||  ||   |        ||  || |   | |
Db        729 GGCGCGCCCCCGCCCCCCCCCGCCGGCGGCCCCGCGGCCGCCCGGGCCCGCCCCGCCGCG 788

Qy        128 CACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAG 187
              |  |||| |   | ||   || | | | ||  | | |     |  | ||||| || || |
Db        789 CCGCCCCCCCCGCGCGCCCCCGCGCCCCGCGCCCCCGGGCGCGCCCGGCCCCGCGCCCCG 848

Qy        188 GCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTG 247
              |||||||  | |  ||   | |  |  |||    | |    | |    ||     |||
Db        849 CCCCCCCCGCCCNGGCGCCCCCCCGCCGCCCGCGGCGCCGGGCCCCCCCCCGCCGCCCCCC 908

Qy        248 GTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACC 307
              | ||  || |   ||  |    |  |    |  ||     |||||  |  |   |    |
Db        909 CCGCCCGCCCCGCCCGCGGNNCCCGCCCCCCGCCCGCCGCCCCGGCCCGCCNCGCCCCGC 968

Qy        308 CAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATC 367
              |   |||| |  |  ||  ||   |    |  |   |  | ||  || || | ||  |
Db        969 CCCCGCCCCGCCCGCCGCGCGCGCGCCCCGCGCGCCCCCCCCCCCGCCCGGCCCCCCCGC 1028

Qy        368 TCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTC 427
                ||  |   |||     | ||   | |     | | |  || |   |  |
Db       1029 GGGGCCGNGCCCCGCCGCCCCCGCCCGCGCGGGCGGGCGCGCGCCCGGGCGCCGCGCCGC 1088

Qy        428 GCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTC 487
              |  |   |    |    ||    || || ||  |      ||    |  | | | |  | |
Db       1089 CGCCCGGCGCGCGNCCCGCGCCCGCCCGNGGCGCGCGCCCCGGCCGCCGCGCCNGCCCCC 1148

Qy        488 AACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGAC 547
                ||  || | || |  | ||    |  | || ||  |  |    |  |  | |||| |
Db       1149 CGNCGCGCCCGCCCGCGCGGGCGCGCCCGCGCGCCGCCGCCGCCCGGCCGGCCGCGCGCC 1208

Qy        548 GGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCC 607
              | | | | || |||| |         ||    |  | | ||      |  |  || || |
Db       1209 GCCCCCGNGCCCCCCCCCGGCCCCCCCGGCCCGGCCNGCCCCCGCGCCCGCGCCGCCCGC 1268

Qy        608 GTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGGCC 662
              | | || || |  ||| |  || |    | | | |  ||  | | |     ||||
Db       1269 GCCCGCCGCGCGCGCGCGNGGCGCGCGCCGGCGCGCGCGGNGNGCCGCGCCGGCC 1323


RESULT 11
AG441911/c
LOCUS       AG441911               1177 bp    DNA     linear   GSS 22-DEC-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-323I03.T7, genomic survey
            sequence.
ACCESSION   AG441911
VERSION     AG441911.1  GI:48084974
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
            Shiroishi,T.
  TITLE     Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
  JOURNAL   Genome Res. 14 (12), 2439-2447 (2004)
   PUBMED   15574823
REFERENCE   2  (bases 1 to 1177)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .1177
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-323I03.T7"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             5.7%;  Score 59.4;  DB 10;  Length 1177;
  Best Local Similarity   40.7%;  Pred. No. 0.0023;
  Matches  279;  Conservative    0;  Mismatches  397;  Indels   10;  Gaps    2;

Qy         15 CCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGT 74
              || | ||   |||  ||  |||| |  || || ||    | | || |||| ||| ||
Db        875 CCCCGCCCGCCCCCCCCCCCCCCCCCGCCCCCCCCCCCCCCCCCCCCCCCCCGCCCCCCC 816

Qy         75 TTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCC 134
                |   ||  ||  | | |  ||  ||| ||  | ||||  || | |   | |||||
Db        815 CCCCCCCCCCGCGCCGCCCGCCCCCCCCCCCCCNCGCCCCCCGCCGCCCGNCCCCCCCCC 756
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Qy        135 ACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAGGCCCCCC 194
Db        755 GNCGCGCCCCGCCCGCCGCGCCCNNCCCCCCGCGCCCCCCCCGCCCNCCCCNNGNCCCCCC 696

Qy        195 CACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCA 254
Db        695 CNCCCCCCCCCGCCCCCCGGNNGCGNNCNCCCCGCCCCCCCCCCNCCCCCCGGCGGCCNC 636

Qy        255 GCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCC 314
Db        635 CCCCCCGGCCCCCCGGCCCCCCGCCGCCCNCGGCCNCNCCCGCGCCCGGCCCCCCGGGGC 576

Qy        315 CGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCT 374
Db        575 CGGCCCCCCGCCCCGGGCCCCCCCCG--------CCCGCNCCCCCGCCGCGCGCCGCCCC 524

Qy        375 GGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT 434
Db        523 CGCGGGGCCCCCCGGCCCCGGGGGGNCNNCNCCCGGCNNNGCCGCGCCCCCCCGCCGCNN 464

Qy        435 GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCG 494
Db        463 CCCCCCGNCCCNNGCCCGCGGCCGNNCGNGCCGGCCGCCCCCGGCCCCCCGCCGGCGCCG 404

Qy        495 TGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGG 554
Db        403 GGCCNCCCGCCCCCCCCCGGGCGGGNCCCCCCGGCCCGCCGCGNCCCCGCCCCGCCCGGN 344

Qy        555 GGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCT 614
Db        343 GCCGCGCCCNNNNGNNNNNNCCNNGCCNCNCCNNC--CCCCCCCCCCCCCCGCNCCCNGN 286

Qy        615 GCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGAC 674
Db        285 GCCCNNNNNNCCNCCCGCCNNNNGCGNNNCNCCNGCCGCCCCGGCGCCCCNCGCCNNCCC 226

Qy        675 ACGTGTGCTCCCCAGAGGGCACCCCC 700
Db        225 CCGCCCCCCCCCCCNCCCCCCCNCNCC 200


RESULT 12
AG043471/c
LOCUS       AG043471                873 bp    DNA     linear   GSS 01-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-021M18.F, genomic survey sequence.
ACCESSION   AG043471
VERSION     AG043471.1  GI:16572196
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 873)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: -21M13
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .873
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-021M18.F"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

  Query Match             5.6%;  Score 58.6;  DB 10;  Length 873;
  Best Local Similarity   41.3%;  Pred. No. 0.0034;
  Matches  258;  Conservative    0;  Mismatches  365;  Indels    1;  Gaps    1;

Qy         15 CCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGT 74
Db        642 CCGCGCCCCGNCGCGCGGCCCGCCCCCCCCCCCCCCCNCCCCCCCCCCCCCCCCGCCCCCC 583

Qy         75 TTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCC 134
Db        582 CCCCCCCCNNNCCCCCCCCCCCCCCCCCCCGNCCCCNCCCCCCCCCCCCNCCCNNNNCCCC 523

Qy        135 ACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAGGCCCCCC 194
Db        522 CCCCCCGCCGCCCCGGCCCCCNCNCGCNCCCNCCCCCGCCCNCCCCCCCCCCGCGCCCGCC 463

Qy        195 CACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCA 254
Db        462 CCCGCCCGCCGCCGCGGCGCGCCGCGCCCGGGGCGCGCCGGGCGGCCGCCCGCGCCGCCG 403

Qy        255 GCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCC 314
Db        402 GGCCCCGCCCCCGCGCGCGCCCGCCGCGCGCCGGGGGCCCGGCGGCCGCGCCCGCGGGCC 343

Qy        315 CGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCT 374
Db        342 CCGCCCCGCCCCCGCCCCCGCCGCGGCCCGCCGCCGCGCGCGCGGCGCGCCCCCGCGC 283

Qy        375 GGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT 434
Db        282 GCGGCCGCGGCNCCGGCGGCGCGNAAAAAACCCAGCCAAA-AATCCTTNCTCTGGGGCGT 224

Qy        435 GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCG 494
Db        223 TCCCGCGCCCCGCGCCCGGGCCCGCCGCGNCNGCCCTTTTCACNNGCGCGNGGCNCCCGN 164

Qy        495 TGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGG 554
Db        163 CGCGCNGCCCGCCGCGCGCCCCCCGCCGCCCCGCGCNCCCCNNCCCCCCCCCCCCCCCGC 104

Qy        555 GGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCT 614
Db        103 GNCGCCCCCCCAAACCCCCCCCCCCCCCCCCCCCCNAACCCCCCCNCCNCCNNNCCNTTT 44

Qy        615 GCACCTGCGTGCTGCCCCGTTCAG 638
Db         43 NGCNCTNNNCNNNGNNNCAAGCNG 20


RESULT 13
AG032979
LOCUS       AG032979                1452 bp    DNA     linear   GSS 01-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-007O04.F, genomic survey sequence.
ACCESSION   AG032979
VERSION     AG032979.1  GI:16559852
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1452)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-007004.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

Query Match 5.5%; Score 58; DB 10; Length 1452;
Best Local Similarity 46.3%; Pred. No. 0.0051;
Matches 304; Conservative 0; Mismatches 339; Indels 14; Gaps 4;

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Qy          8 GTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGC 67
              | ||   |||| |     || ||| |||||||  || || ||    ||| || | || ||
Db        710 GCGCCCNCCGCGCGCCCGCCCGGCCCCGCCCCCCCCCCCCCGCCCGCCCCCCGCCCGC 769

Qy         68 CTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGG 127
              |  |   | | |  ||  | | |  || ||| | |     || | | | | | |
Db        770 GCCGCGCGGCCGCGCGCGC-CCNCGCGCGCGCGGCGCGCGCGCGCCGCGCGCGCCGCGCC 828

Qy        128 CACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCG---GC 184
              |||  | | | |||  |||| | |  |  | || | |  |  | || || ||   ||
Db        829 GCCCCGCCCCGCCGCGGCGCCCCGCGCGCCGCCGCGCCCGCCGGCCCGCGCCCCGCGCGC 888

Qy        185 CAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCC 244
              |||  ||  |   |  ||  || || || |||  |  | |  ||  |||    ||
Db        889 GCCGCCGCCGCCGGCGCGCGCGCGCGCGGCGCCGCGGCCGCGGCCGCCGCGCCGCGCG 948

Qy        245 CTGGTGTCCAGCCTGGAG----GCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300
              |  |  | ||| |  |    || ||  ||     | |  || || |  | | |
Db        949 CCGCGGCGCCGCCCGCGGCCGGGCCGCGCGCGCGCCGCGCGCGCGCGCGCCCCGCCCCNG 1008

Qy        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360
              ||  || | || ||  || |||     | |   | |   | |||       || |   ||
Db       1009 NGCGCGCCCGGGCGCGCCGCCGCGCGGCGCGCGCGCGCGCGCGGCCCCGCGCCCCGCCCG 1068

Qy        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
              | ||  |  | |  | |   |  |  | |||  | | |      |  | |  ||
Db       1069 CGCCCGCGGCCGCGCGCGNCGCGCCGCCCGCGCGGCCGCNGCCGCGCCGCGCCGGGGGCC 1128

Qy        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
              |  |||| |  || | | | |  |  || | ||| |  |||||| | | ||
Db       1129 GCGGGCCGCCGCGGNCCGGCGCCGCGCGCGCGGCGCGNCGCGGGCCCGCCGCGCGCCCGC 1188

Qy        481 T------GCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCC 534
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Db       1189 NCGCGCGCCGCGCNGCCCGGCGCNCGCGCGCCNCGCGCCGCGCGCCCGCGCGCGCCGGCN 1248

Qy        535 CTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTT 594
              |  | | ||||  || ||  || |||  | ||  || |     |  |  | |
Db       1249 CGCCGCGCGCGGGCGCGCGCCGCGCCCGGCGCCCCGGCCGCCGCGCCGCGNCGCGCNCCA 1308

Qy        595 CATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAG 651
                ||    | ||   || || |  ||     || |||    | | | | |||| |
Db       1309 TCNCCNGCGGCGCGCGCGCCGCGCGCGCCGCGCGCGCCGNCGCGCGCGCCNGCCGCG 1365
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RESULT 14
CK404476
LOCUS CK404476 1331 bp mRNA linear EST 05-JAN-2004
DEFINITION AUF_IfHdk_245_i05 Ictalurus furcatus head kidney cDNA library Ictalurus furcatus cDNA 5', mRNA sequence.
ACCESSION CK404476
VERSION CK404476.1 GI:40563736
KEYWORDS EST.
SOURCE Ictalurus furcatus
ORGANISM Ictalurus furcatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.
REFERENCE 1 (bases 1 to 1331)
AUTHORS Liu,Z., Li,P., Liu,L., He,C., Kucuktas,H., Feng,J., Chen,L., Peatman,E., Baoprasertkul,P., Simmons,M., Muir,W., Grizzle,J., Dunham,R. and Brady,Y.
TITLE 30,000 new catfish ESTs: new resources for functional analysis of genes involved in aquaculture performance traits
JOURNAL Unpublished (2004)
COMMENT Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory, Department of Fisheries and Allied Aquacultures and Program of Cell and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: T7.
FEATURES Location/Qualifiers
source 1. .1331
/organism="Ictalurus furcatus"
/mol_type="mRNA"
/db_xref="taxon:66913"
/clone_lib="Ictalurus furcatus head kidney cDNA library"
/note="Organ: Head kidney; Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN

Query Match 5.5%; Score 57.6; DB 7; Length 1331;
Best Local Similarity 40.3%; Pred. No. 0.0063;
Matches 249; Conservative 0; Mismatches 369; Indels 0; Gaps 0;

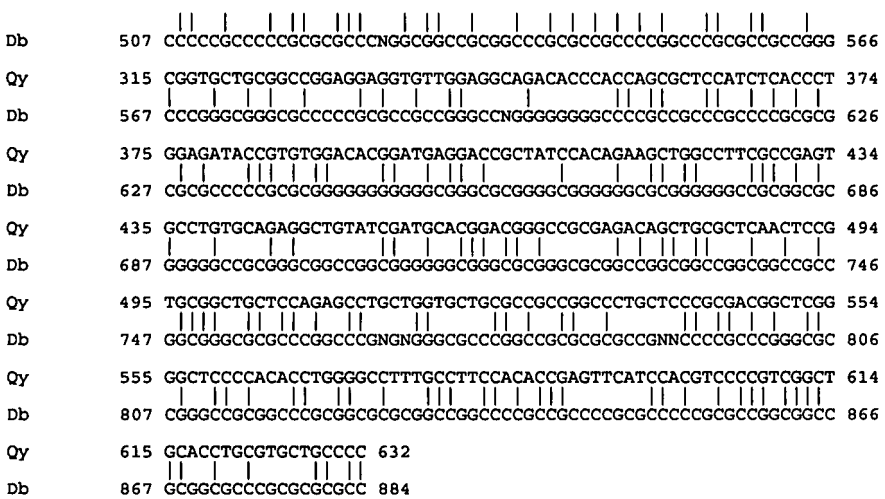
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Qy         15 CCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGT 74
              || | ||   |||  ||  |||| |   | || ||    | | ||  ||    | ||
Db        267 CCCCCCCCCCCCCCCCCCCCCCCCCCNNCNCCCCCCNCCCCCCCCCNCCNCCNCCCCCCC 326

Qy         75 TTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCC 134
                |  ||   | | | |   ||   ||| ||   || | | | |     | ||||||
Db        327 CCCNNCCCNNCCCCCCCCCCCCCCCCCCCCCNCCNNCNCCNCCCNCCCNCCCCCCCCCCC 386

Qy        135 ACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAGGCCCCCC 194
              |   | |      || | |  | |                  ||  |  ||  ||||||
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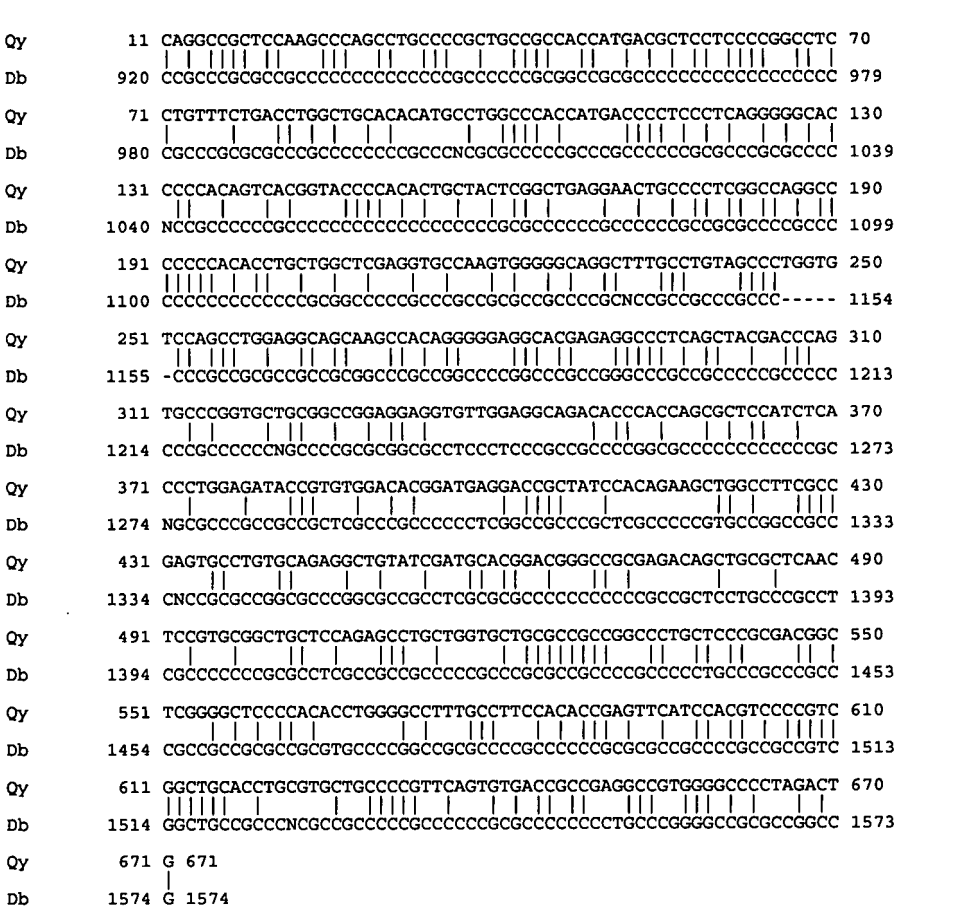
Qy        195 CACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCA 254
              |       |  | |       ||          |  |    ||     ||| |  | ||
Db        447 CNNNNNNCCCCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCGCCCCCCCCCCCCCCCGGCCCC 506

Qy        255 GCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCC 314
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RESULT 15
CC219595
LOCUS       CC219595               1785 bp    DNA     linear   GSS 12-MAY-2003
DEFINITION  CH261-62D17_RM1.2 CH261 Gallus gallus genomic clone CH261-62D17,
            genomic survey sequence.
ACCESSION   CC219595
VERSION     CC219595.1  GI:30541991
KEYWORDS    GSS.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1785)
  AUTHORS   Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
            Warren,W., Graves,T., Mardis,E. and Wilson,R.
  TITLE     Gallus gallus BAC End Reads
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 182000   Std Error: 0.00
            Seq primer: RM1 TACGACTCACTATAGGGAGA
            Class: BAC ends
            High quality sequence start: 521
            High quality sequence stop: 576.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="Red Jungle Fowl"
                     /db_xref="taxon:9031"
                     /clone="CH261-62D17"
                     /sex="female"
                     /cell_line="UCD001, inbred 256"
                     /clone_lib="CH261"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     CH261 Female Chicken library - for library and clone
                     ordering information: http://www.chori.org/bacpac"
ORIGIN

  Query Match             5.5%;  Score 57.6;  DB 9;  Length 1785;
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  Matches  289;  Conservative    0;  Mismatches  366;  Indels    6;  Gaps    1;
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Job time : 5058 secs
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Run on: April 30, 2006, 21:09:36 ; Search time 665 Seconds
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Perfect score: 1047
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description

RESULT 1
ID AAZ29728 standard; cDNA; 1047 BP.
DE Human Interleukin 17C, PRO1122 cDNA.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 3; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 2
ID AAA96338 standard; cDNA; 1047 BP.
DE cDNA encoding a novel polypeptide designated PRO1122.
PN WO200056889-A2.
PD 28-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 3; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 3
ID AAS46148 standard; cDNA; 1047 BP.
DE Human DNA encoding PRO polypeptide sequence #224.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 4; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 4
ID AAS09510 standard; cDNA; 1047 BP.
DE Human cDNA encoding Interleukin 17C ligand, IL-17C.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 4; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 5
ID ACA89598 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 6
ID ACA73608 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 7
ID ACA05923 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 8
ID ACA66757 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO protein #224.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 9
ID ACF20332 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 10
ID ACF19718 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 11
ID ACD22006 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 12
ID ACF13171 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 13
ID ACD28801 standard; cDNA; 1047 BP.
DE Human secreted / transmembrane polypeptide PRO1122 cDNA.
PN US2003027249-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 14
ID ACD25274 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 15
ID ACF00323 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054474-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 16
ID ACA72380 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 17
ID ACD04904 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 18
ID ACD18365 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 19
ID ACD08372 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 20
ID ACA88806 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 21
ID ACA70248 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 22
ID ACD12470 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 23
ID ACC74385 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 24
ID ACD16013 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 25
ID ACD25581 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 26
ID ACD18058 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 27
ID ACC88345 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 28
ID ACD21699 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 29
ID ACD18766 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 30
ID ABX98376 standard; cDNA; 1047 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 447.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 31
ID ACD14127 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 32
ID ACD09907 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 33
ID ACC88652 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 34
ID ACD21392 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 35
ID ABX75764 standard; cDNA; 1047 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1122.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 36

ID ABX97967 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 37
ID ACA97443 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 38
ID ACA57906 standard; cDNA; 1047 BP.
DE Human PRO1122 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 39
ID ACD14434 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 40
ID ACC91217 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 41
ID ACC88959 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 42
ID ACA06075 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003008348-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 43
ID ACD07156 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 44
ID ACA67607 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 45
ID ACC81662 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 46
ID ACC89266 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 47
ID ACC86622 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 48
ID ACC89880 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 49
ID ACC93059 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 50
ID ACA72687 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 51
ID ACA89205 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 52
ID ACA69941 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 53
ID ACA97084 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 54
ID ACA91080 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 55
ID ACA70862 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 56
ID ACA95372 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.

PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 57
ID ACC86315 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 58
ID ACC90187 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 59
ID ACD12795 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 60
ID ACF20025 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 61
ID ABX76969 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 62
ID ACA73301 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 63
ID ACA68844 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 64
ID ACA74688 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 65
ID ACA70555 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 66
ID ACD14741 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 67
ID ACA89851 standard; cDNA; 1047 BP.
DE Human cDNA (PRO1122) encoding h-IL17C.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 68
ID ACA68413 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 69
ID ABX98878 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 70
ID ACC81355 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 71
ID ACA95679 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 72
ID ACD04597 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 73
ID ACC88038 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 74
ID ACF12700 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 75
ID ACA96415 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 76
ID ACA65189 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;

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  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 77
ID   ACA73915 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003032129-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 78
ID   ACA74327 standard; cDNA; 1047 BP.
DE   Novel human secreted and transmembrane protein PRO1122 cDNA.
PN   US2003032131-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 79
ID   ACA96722 standard; cDNA; 1047 BP.
DE   Human PRO polynucleotide #224.
PN   US2003032103-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 80
ID   ACD10828 standard; cDNA; 1047 BP.
DE   cDNA encoding human PRO polypeptide #224.
PN   US2003032107-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 81
ID   ACC91524 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003032139-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 82
ID   ACD02859 standard; cDNA; 1047 BP.
DE   cDNA encoding human PRO polypeptide #224.
PN   US2003022301-A1.
PD   30-JAN-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 83
ID   ACC87424 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003036165-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 84
ID   ACC86008 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003027262-A1.
PD   06-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 85
ID   ACA65496 standard; cDNA; 1047 BP.
DE   Human PRO polynucleotide #224.
PN   US2003032110-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 86
ID   ACA94313 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003036142-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 87
ID   ACA98057 standard; cDNA; 1047 BP.
DE   Human PRO polynucleotide #224.
PN   US2003036145-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 88
ID   ACA91559 standard; cDNA; 1047 BP.
DE   Novel human secreted and transmembrane protein PRO1122 cDNA.
PN   US2003036154-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 89
ID   ACA90773 standard; cDNA; 1047 BP.
DE   Novel human secreted and transmembrane protein PRO1122 cDNA.
PN   US2003036153-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 90
ID   ACD16320 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003044931-A1.
PD   06-MAR-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 91
ID   ACD17481 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003036150-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 92
ID   ACC92138 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003040069-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 93
ID   ACA74995 standard; cDNA; 1047 BP.
DE   cDNA encoding human PRO polypeptide #224.
PN   US2003022293-A1.
PD   30-JAN-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 94
ID   ACA91866 standard; cDNA; 1047 BP.
DE   Human PRO polynucleotide #224.
PN   US2003032128-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 95
ID   ACA71510 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003032116-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 96
ID   ACC90910 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003032122-A1.
PD   13-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 97
ID   ACA65920 standard; cDNA; 1047 BP.
DE   cDNA encoding human PRO protein #224.
PN   US2003036139-A1.
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PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 98
ID ACA64635 standard; cDNA; 1047 BP.
DE Human cDNA encoding IL-17 family member, PRO1122.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 99
ID ACA95065 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 100
ID ACD16627 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 101
ID ACD15706 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 102
ID ABX16809 standard; cDNA; 1047 BP.
DE Human cDNA encoding secreted/transmembrane protein #224.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 8; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 103
ID ACA97750 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 104
ID ACA99199 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 105
ID ACC91831 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 106
ID ACA67698 standard; cDNA; 1047 BP.
DE cDNA encoding human secreted polypeptide PRO122.
PN US2002192751-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 107
ID ACD11242 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 108
ID ACD15092 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 109
ID ACD11856 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 110
ID ACC95985 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 111
ID ACF16548 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 112
ID ACF02666 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 113
ID ACF02973 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 114
ID ACF21560 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 115
ID ACF10244 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 116
ID ACF78137 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;

Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 117
ID ACD46842 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 118
ID ACD49605 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 119
ID ADA76535 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036114-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 120
ID ACF28372 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 121
ID ACD89062 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 122
ID ACD84457 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 123
ID ACD99231 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 124
ID ADA78199 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 125
ID ACF48973 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 126
ID ACD09293 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 127
ID ACF12086 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 128
ID ACF41320 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 129
ID ACF15934 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 130
ID ACF16241 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 131
ID ACD32068 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 132
ID ACF18876 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 133
ID ACF09323 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 134
ID ACF78444 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 135
ID ACF52043 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064440-A1.
PD 03-APR-2003.

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  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 136
ID   ADA43226 standard; cDNA; 1047 BP.
DE   Human interleukin 17 related mammalian cytokine polypeptide cDNA #2.
PN   US6579520-B2.
PD   17-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 137
ID   ACF26530 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003068704-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 138
ID   ACF24323 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 139
ID   ACF63634 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 140
ID   ACF50508 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 141
ID   ACH07979 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003049749-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 142
ID   ACF13785 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 143
ID   ACD41711 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 144
ID   ACF32124 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 145
ID   ACF23402 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 146
ID   ACF40092 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 147
ID   ACD45614 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003064451-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 148
ID   ACF53271 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003068721-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 149
ID   ACF27451 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003068699-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 150
ID   ACF45289 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003068707-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 151
ID   ACF29907 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003073175-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 152
ID   ACD89983 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003068695-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 153
ID   ACD84764 standard; cDNA; 1047 BP.
DE   Human PRO polynucleotide #224.
PN   US2003068703-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match            100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
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RESULT 154
ID ACD98924 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 155
ID ACF77216 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 156
ID ACF76909 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 157
ID ACF49894 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 158
ID ACF50201 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 159
ID ACD09600 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 160
ID ACD08679 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 161
ID ACF12393 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 162
ID ACC94901 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 163
ID ACD22620 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 164
ID ACF15320 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 165
ID ACC97415 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 166
ID ACC92445 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 167
ID ACF14092 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 168
ID ACF14399 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 169
ID ACF09630 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 170
ID ACD45921 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 171
ID ACD48070 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 172
ID ACD67801 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 173
ID ACF25609 standard; cDNA; 1047 BP.

DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 174
ID ACF29293 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 175
ID ACD85071 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 176
ID ACD84150 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 177
ID ACD88141 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 178
ID ACF30828 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 179
ID ACF32431 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 180
ID ACH12091 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 181
ID ACH12398 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 182
ID ACD40790 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 183
ID ACF18262 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 184
ID ACF08709 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 185
ID ACF31510 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 186
ID ACF52350 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 187
ID ACD50219 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 188
ID ACF38922 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 189
ID ACF26837 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 190
ID ACF24937 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 191
ID ACF46517 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068740-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 192
ID ACF28065 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 193
ID ACD89369 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 194
ID ACF63941 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 195
ID ACF60581 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 196
ID ACH12705 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 197
ID ACH10128 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 198
ID ACD03983 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 199
ID ACD10521 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 200
ID ACD12163 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 201
ID ACF42548 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 202
ID ACF18569 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 203
ID ACF02359 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 204
ID ACF21867 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 205
ID ACF10551 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 206
ID ACF34003 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 207
ID ACF44965 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 208
ID ACD90597 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 209
ID ACD91210 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 210
ID ACF30521 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003067478-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 211
ID ACD87220 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 212
ID ACF60274 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 213
ID ACF46824 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 214
ID ACF75681 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 215
ID ADA79991 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 216
ID ACF17341 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 217
ID ACF23095 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 218
ID ACF08095 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 219
ID ACF08402 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 220
ID ACF40706 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 221
ID ACF53885 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 222
ID ACD47149 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 223
ID ACF48052 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 224
ID ACF47438 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 225
ID ACF46210 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 226
ID ACD86299 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 227
ID ACF52657 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 228
ID ACF52964 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 229
ID ACF64957 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068737-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 230
ID ACF76602 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 231
ID ACF61502 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 232
ID ACF61809 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 233
ID ACD30840 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 234
ID ACD31761 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 235
ID ACD32682 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 236
ID ACF17648 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 237
ID ACF07481 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 238
ID ACF20639 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 239
ID ACF20946 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 240
ID ACF21253 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 241
ID ACD47763 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 242
ID ACF47745 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 243
ID ACF53578 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 244
ID ACD86913 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 245
ID ACH05161 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 246
ID ACF44658 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 247
ID ADA81718 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 248
ID ACD22313 standard; cDNA; 1047 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 249
ID ACD24660 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 250
ID ACD39863 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 251
ID ACD40170 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 252
ID ACF13478 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 253
ID ACF03280 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 254
ID ACF78751 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 255
ID ACF11472 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 256
ID ACF50815 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 257
ID ACF34310 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 258
ID ACD46535 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 259
ID ACD48377 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 260
ID ACF27758 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 261
ID ACF24630 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 262
ID ACD85685 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 263
ID ACD90290 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 264
ID ACD83843 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 265
ID ACF49280 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 266
ID ACH07365 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 267
ID ACH07672 standard; cDNA; 1047 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 268
ID ACH08286 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 269
ID ACH11477 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 270
ID ACH11784 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 271
ID ACH10435 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 272
ID ACF01438 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 273
ID ACF41013 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 274
ID ACD24353 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 275
ID ACD31454 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 276
ID ACF17955 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 277
ID ACF32738 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 278
ID ACF40399 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 279
ID ACF48359 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 280
ID ACF38308 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 281
ID ACF25244 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 282
ID ACF27144 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 283
ID ACF29600 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 284
ID ACD87834 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 285
ID ACF76295 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 286

ID ACF49587 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 287
ID ACF44044 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 288
ID ACH06389 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 289
ID ACH06696 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 290
ID ADA83516 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 291
ID ACC92752 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 292
ID ACC93366 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 293
ID ACF19411 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 294
ID ACD13102 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 295
ID ACF06560 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 296
ID ACC94594 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 297
ID ACC98022 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 298
ID ACC94287 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 299
ID ACF42241 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 300
ID ACD31147 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 301
ID ACD43176 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 302
ID ACD43483 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 303
ID ACF15013 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 304
ID ACF01745 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 305
ID ACF31817 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064469-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 306
ID ACD67494 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 307
ID ACD48684 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 308
ID ACD48991 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 309
ID ACF51429 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 310
ID ACF54192 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 311
ID ACF25916 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 312
ID ACF39229 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 313
ID ACF28986 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 314
ID ACD90903 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 315
ID ACD86606 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 316
ID ACH05468 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 317
ID ACF65264 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 318
ID ADB20559 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 319
ID ACF43737 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 320
ID ACH09207 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 321
ID ACH09514 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 322
ID ADA78811 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 323
ID ACF09937 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;

RESULT 324
ID ACF51122 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 325
ID ACF24016 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 326
ID ACD88448 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 327
ID ACH09821 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 328
ID ACH10742 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 329
ID ACD11549 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 330
ID ACC96599 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 331
ID ACD42260 standard; cDNA; 1047 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1122.
PN US2003044842-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 332
ID ACC98629 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 333
ID ACF41934 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 334
ID ACF16855 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 335
ID ACD32375 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 336
ID ACD30533 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 337
ID ACD41404 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 338
ID ACF07788 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 339
ID ACF31203 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 340
ID ACF77523 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 341
ID ACF11165 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 342
ID ACF33045 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 343

ID ACF26223 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 344
ID ACD83536 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 345
ID ACF23709 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 346
ID ACF43123 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 347
ID ACF43430 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 348
ID ACH06082 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 349
ID ACH08900 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 350
ID ACC90494 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 351
ID ACF10858 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 352
ID ACC93673 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 353
ID ACC96292 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 354
ID ACD24967 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 355
ID ACF02052 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 356
ID ACF22174 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 357
ID ACF22788 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 358
ID ACF09016 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 359
ID ACF33352 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 360
ID ACF54806 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 361
ID ADA49767 standard; cDNA; 1047 BP.
DE Human interleukin-17/interleukin-17 receptor related PRO1122 cDNA.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;

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  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 362
ID   ACF48666 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 363
ID   ACD47456 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003068697-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 364
ID   ACD49298 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003068710-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 365
ID   ACF38001 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003068686-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 366
ID   ACF30214 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003073178-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 367
ID   ACD87527 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003068774-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 368
ID   ACF62116 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003104538-A1.
PD   05-JUN-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 369
ID   ACH11049 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003049781-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 370
ID   ACD10214 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003036158-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 371
ID   ACD16939 standard; cDNA; 1047 BP.
DE   cDNA encoding human PRO polypeptide #224.
PN   US2003036151-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 372
ID   ACC99236 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003040067-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 373
ID   ACF00630 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003054456-A1.
PD   20-MAR-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 374
ID   ACD41097 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003054482-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 375
ID   ACF14706 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003054457-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 376
ID   ACF22481 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003059883-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 377
ID   ACF79058 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003049764-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 378
ID   ACF11779 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003073177-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 379
ID   ACF51736 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003064442-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 380
ID   ACF33659 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003064450-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
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  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 381
ID   ADA26960 standard; cDNA; 1047 BP.
DE   cDNA encoding human PRO polypeptide #2.
PN   US2002182673-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 382
ID   ACD49912 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003068731-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 383
ID   ACF37694 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003068683-A1.
PD   10-APR-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 384
ID   ACF28679 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003068754-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 385
ID   ACD88755 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003068681-A1.
PD   10-APR-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 386
ID   ACF75374 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003096351-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 387
ID   ACF61195 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003096358-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 388
ID   ACF44351 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003104556-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 389
ID   ACH08593 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003049756-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 390
ID   ACC93980 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003036122-A1.
PD   20-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 391
ID   ACD21085 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003036121-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 392
ID   ACF06867 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003040065-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 393
ID   ACD20778 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003044919-A1.
PD   06-MAR-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 394
ID   ACD22927 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003040077-A1.
PD   27-FEB-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 395
ID   ACF41627 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003044928-A1.
PD   06-MAR-2003.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 396
ID   ACF07174 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003049746-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 397
ID   ACF77830 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003054464-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 398
ID   ACD46228 standard; cDNA; 1047 BP.
DE   Human secreted/transmembrane protein (PRO) cDNA #224.
PN   US2003064459-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-239;
RESULT 399
ID   ACF47131 standard; cDNA; 1047 BP.
DE   Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN   US2003068757-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1047;  DB 9;  Length 1047;
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Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 400
ID ACF54499 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 401
ID ACF45903 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 402
ID ACF45596 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 403
ID ACF38615 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 404
ID ACD89676 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 405
ID ACD85378 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 406
ID ACD85992 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 407
ID ACF75988 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 408
ID ACF60888 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 409
ID ACH05775 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 410
ID ADA82882 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 411
ID ACF56034 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1047; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 412
ID ACF55420 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 413
ID ADB86190 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 414
ID ACF56341 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 415
ID ACF56648 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 416
ID ACF55727 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 417
ID ACF55113 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 418
ID ADB66894 standard; cDNA; 1047 BP.

DE cDNA encoding human PRO polypeptide #2.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 419
ID AAD59326 standard; cDNA; 1047 BP.
DE Human PRO1122 cDNA.
PN US2003049733-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 420
ID AAD59202 standard; cDNA; 1047 BP.
DE Human PRO1122 cDNA.
PN US2003049734-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 421
ID ADC29766 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003092063-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 422
ID ADD05920 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 423
ID ADC78792 standard; DNA; 1047 BP.
DE Human PRO protein coding sequence #11.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 424
ID AAD63608 standard; cDNA; 1047 BP.
DE Human IL-17C ligand (PRO1122) cDNA.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 425
ID ADG02915 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 426
ID ADG01622 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 427
ID ADF95797 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 428
ID ADG12612 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 429
ID ADG87378 standard; cDNA; 1047 BP.
DE Human PRO1122 cDNA from clone DNA62377-1381-1.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 430
ID ADH09272 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 431
ID ABX78751 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 432
ID ACA75723 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 433
ID ACA71203 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 434
ID ACC87731 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 435
ID ACC87117 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 436
ID ACD04290 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 437
ID ACA69621 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #224.

PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 438
ID ACA90466 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 439
ID ACC89573 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 440
ID ACA98364 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 441
ID ACA94006 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 442
ID ACA06132 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003032061-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 443
ID ACD15399 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 444
ID ACD08986 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 445
ID ACC96906 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 446
ID ACF15627 standard; cDNA; 1047 BP.
DE Human secreted polypeptide PRO1122-encoding cDNA, SEQ ID NO:447.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 447
ID ACA72994 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 448
ID ACD03166 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 449
ID ACD01981 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 450
ID ACA92173 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 451
ID ADL16674 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO1122 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 10; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 452
ID ADM30587 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 11; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 453
ID ADE74584 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 454
ID ADE75196 standard; cDNA; 1047 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #224.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 455
ID ADF09209 standard; cDNA; 1047 BP.
DE Human secreted and transmembrane protein PRO1122 cDNA.
PN US2003134327-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 456
ID ADF96409 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 457
ID ADG04680 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003215912-A1.

PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 458
ID ADG00840 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 459
ID ADG83096 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 460
ID ADH26377 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 461
ID ADH33346 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 462
ID ADJ55085 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 463
ID ADL16635 standard; cDNA; 1047 BP.
DE cDNA encoding human PRO1122 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 464
ID ADL71295 standard; cDNA; 1047 BP.
DE Human IL-17C (PRO1122) encoding cDNA, DNA62377-1381-1.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 465
ID ADJ64856 standard; cDNA; 1047 BP.
DE Human PRO polynucleotide #224.
PN US2004038337-A1.
26-FEB-2004.
(GETH) GENENTECH INC.
Match 100.0%; Score 1047; DB 12; Length 1047;
al Similarity 100.0%; Pred. No. 1.1e-239;
standard; cDNA; 1047 BP.
secreted and transmembrane protein PRO1122 cDNA.
1.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 467
ID ADM36799 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 468
ID ADM40604 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 469
ID ADN38212 standard; cDNA; 1047 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1047; DB 12; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 470
ID ADW12441 standard; cDNA; 1047 BP.
DE Human PRO1122 cDNA.
PN US2004265966-A1.
PD 30-DEC-2004.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (PANJ/) PAN J.
PA (STEW/) STEWART T A.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 100.0%; Score 1047; DB 14; Length 1047;
Best Local Similarity 100.0%; Pred. No. 1.1e-239;
RESULT 471
ID ADL33051 standard; cDNA; 1048 BP.
DE Novel human secreted and transmembrane protein PRO1122 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 98.9%; Score 1036; DB 11; Length 1048;
Best Local Similarity 99.9%; Pred. No. 4.5e-237;
RESULT 472
ID ADP10630 standard; DNA; 1048 BP.
DE Reference mRNA sequences for marker probe #307.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 98.9%; Score 1036; DB 12; Length 1048;
Best Local Similarity 99.9%; Pred. No. 4.5e-237;
RESULT 473
ID AAA59149 standard; cDNA; 1107 BP.
DE cDNA encoding a human interleukin-171 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 98.2%; Score 1028.4; DB 3; Length 1107;
Best Local Similarity 99.8%; Pred. No. 3e-235;
RESULT 474
ID AAA58991 standard; cDNA; 1107 BP.
DE cDNA encoding a human interleukin (IL) 171 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.

Query Match 2%; Score 1028.4; DB 3; Length 1107;
Best Local Similarity .8%; Pred. No. 3e-235;
RESULT 475
ID ADM31752 standard; cDNA; 1107 BP.
DE Novel human interleukin 171, IL-171.
PN US2004048334-A1.
PD 11-MAR-2004.
Query Match 98.2%; Score 1028.4; DB 10; Length 1107;
Best Local Similarity 99.8%; Pred. No. 3e-235;
RESULT 476
ID ADR13812 standard; cDNA; 1107 BP.
DE Human interleukin-171 (IL-171) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 98.2%; Score 1028.4; DB 12; Length 1107;
Best Local Similarity 99.8%; Pred. No. 3e-235;
RESULT 477
ID AEB55667 standard; cDNA; 1107 BP.
DE Human IL-17C cytokine receptor polypeptide encoding cDNA.
PN WO2005065711-A2.
PD 21-JUL-2005.
PA (SCHE) SCHERING CORP.
Query Match 98.2%; Score 1028.4; DB 14; Length 1107;
Best Local Similarity 99.8%; Pred. No. 3e-235;
RESULT 478
ID AAZ36836 standard; cDNA; 1067 BP.
DE Nucleotide sequence of human interleukin-21.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.1%; Score 1006.4; DB 3; Length 1067;
Best Local Similarity 98.9%; Pred. No. 5.2e-230;
RESULT 479
ID AAI67878 standard; DNA; 1067 BP.
DE Human interleukin (IL)-21 nucleotide sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Query Match 96.1%; Score 1006.4; DB 4; Length 1067;
Best Local Similarity 98.9%; Pred. No. 5.2e-230;
RESULT 480
ID ADJ61745 standard; cDNA; 1067 BP.
DE Human interleukin-21 (IL-21) cDNA #2.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.1%; Score 1006.4; DB 12; Length 1067;
Best Local Similarity 98.9%; Pred. No. 5.2e-230;
RESULT 481
ID AAD15291 standard; cDNA; 1177 BP.
DE Human interleukin (IL)-17 like cDNA.
PN WO200159120-A2.
PD 16-AUG-2001.
PA (AMGE-) AMGEN INC.
Query Match 88.2%; Score 923.4; DB 5; Length 1177;
Best Local Similarity 99.8%; Pred. No. 3.4e-210;
RESULT 482
ID AAZ36834 standard; cDNA; 705 BP.
DE Partial nucleotide sequence of human interleukin-21.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 640.4; DB 3; Length 705;
Best Local Similarity 98.3%; Pred. No. 9.5e-143;
RESULT 483
ID AAI67876 standard; DNA; 705 BP.
DE Human interleukin (IL)-21 partial nucleotide sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Query Match 61.2%; Score 640.4; DB 4; Length 705;
Best Local Similarity 98.3%; Pred. No. 9.5e-143;
RESULT 484
ID ADJ61718 standard; cDNA; 705 BP.
DE Human interleukin-21 (IL-21) cDNA #1.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 640.4; DB 12; Length 705;
Best Local Similarity 98.3%; Pred. No. 9.5e-143;
RESULT 485
ID ADV42797 standard; cDNA; 594 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 425.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 56.7%; Score 594; DB 14; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.1e-131;
RESULT 486
ID AAA09153 standard; DNA; 591 BP.
DE Human interleukin-17 (IL-17) homologue coding sequence.
PN WO200020593-A1.
PD 13-APR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 56.4%; Score 591; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 5.5e-131;
RESULT 487
ID AAD38083 standard; DNA; 591 BP.
DE Human LP-48 gene.
PN WO200233083-A2.
PD 25-APR-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 56.4%; Score 591; DB 6; Length 591;
Best Local Similarity 100.0%; Pred. No. 5.5e-131;
RESULT 488
ID AAA58990 standard; cDNA; 521 BP.
DE cDNA encoding a human interleukin (IL) 171 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 26.2%; Score 274.8; DB 3; Length 521;
Best Local Similarity 95.6%; Pred. No. 1.4e-55;
RESULT 489
ID AAA59148 standard; cDNA; 521 BP.
DE cDNA encoding a human interleukin-171 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 26.2%; Score 273.8; DB 3; Length 521;
Best Local Similarity 95.3%; Pred. No. 2.5e-55;
RESULT 490
ID AAA59147 standard; cDNA; 521 BP.
DE cDNA encoding a human interleukin-171 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 26.2%; Score 273.8; DB 3; Length 521;
Best Local Similarity 95.3%; Pred. No. 2.5e-55;
RESULT 491
ID AAA58989 standard; cDNA; 521 BP.
DE cDNA encoding a human interleukin (IL) 171 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 26.2%; Score 273.8; DB 3; Length 521;
Best Local Similarity 95.3%; Pred. No. 2.5e-55;
RESULT 492
ID ADB32007 standard; cDNA; 521 BP.
DE Human partial cDNA encoding interleukin 171, IL-171.
PN US6562578-B1.
PD 13-MAY-2003.

PA (SCHE) SCHERING CORP.
Query Match 26.2%; Score 273.8; DB 10; Length 521;
Best Local Similarity 95.3%; Pred. No. 2.5e-55;
RESULT 493
ID ADR13810 standard; cDNA; 521 BP.
DE Human interleukin-171 (IL-171) partial cDNA #2.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 26.2%; Score 273.8; DB 12; Length 521;
Best Local Similarity 95.3%; Pred. No. 2.5e-55;
RESULT 494
ID ADR13809 standard; cDNA; 521 BP.
DE Human interleukin-171 (IL-171) partial cDNA #1.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 26.2%; Score 273.8; DB 12; Length 521;
Best Local Similarity 95.3%; Pred. No. 2.5e-55;
RESULT 495
ID AAZ29731 standard; DNA; 230 BP.
DE Virtual DNA fragment DNA49665, for isolation of human PRO1122 cDNA.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Query Match 22.0%; Score 230; DB 3; Length 230;
Best Local Similarity 100.0%; Pred. No. 5.6e-45;
RESULT 496
ID AAZ36856 standard; DNA; 332 BP.
DE cDNA clone HTGED19RB related to human interleukin-22 CDNA sequence.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.7%; Score 143.8; DB 3; Length 332;
Best Local Similarity 72.4%; Pred. No. 2.2e-24;
RESULT 497
ID ADJ61747 standard; cDNA; 332 BP.
DE Interleukin-22 (IL-22) cDNA related human HTGED19RB cDNA.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.7%; Score 143.8; DB 12; Length 332;
Best Local Similarity 72.4%; Pred. No. 2.2e-24;
RESULT 498
ID ABN42315 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:15063.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 5.7%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00014;
RESULT 499
ID AAA59156 standard; cDNA; 454 BP.
DE cDNA encoding a rat interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 5.4%; Score 56.8; DB 3; Length 454;
Best Local Similarity 51.2%; Pred. No. 0.0014;
RESULT 500
ID AAA58982 standard; cDNA; 454 BP.
DE cDNA encoding a human interleukin (IL) 173 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 5.4%; Score 56.8; DB 3; Length 454;
Best Local Similarity 51.2%; Pred. No. 0.0014;
RESULT 501
ID ADB31993 standard; cDNA; 454 BP.
DE Human partial cDNA encoding interleukin 173, IL-173.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 5.4%; Score 56.8; DB 10; Length 454;
Best Local Similarity 51.2%; Pred. No. 0.0014;
RESULT 502
ID ADR13795 standard; cDNA; 454 BP.
DE Human interleukin-173 (IL-173) partial cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 5.4%; Score 56.8; DB 12; Length 454;
Best Local Similarity 51.2%; Pred. No. 0.0014;
RESULT 503
ID AAZ36837 standard; cDNA; 522 BP.
DE Partial nucleotide sequence of human interleukin-22.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 56.8; DB 3; Length 522;
Best Local Similarity 51.2%; Pred. No. 0.0014;
RESULT 504
ID AAI67888 standard; DNA; 522 BP.
DE Human interleukin (IL)-22 coding sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Query Match 5.4%; Score 56.8; DB 4; Length 522;
Best Local Similarity 51.2%; Pred. No. 0.0014;
RESULT 505
ID ADJ61748 standard; cDNA; 522 BP.
DE Human interleukin-22 (IL-22) cDNA #2.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 56.8; DB 12; Length 522;
Best Local Similarity 51.2%; Pred. No. 0.0014;
RESULT 506
ID ADF16328 standard; DNA; 609 BP.
DE Human albumin fusion protein-related DNA sequence SeqID1420.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Query Match 5.4%; Score 56.8; DB 10; Length 609;
Best Local Similarity 51.2%; Pred. No. 0.0015;
RESULT 507
ID ADF16330 standard; DNA; 609 BP.
DE Human albumin fusion protein-related DNA sequence SeqID1422.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Query Match 5.4%; Score 56.8; DB 10; Length 609;
Best Local Similarity 51.2%; Pred. No. 0.0015;
RESULT 508
ID ADH21717 standard; DNA; 609 BP.
DE Human interleukin-22 fragment-encoding DNA, SEQ ID NO:514.
PN WO2003059934-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 56.8; DB 10; Length 609;
Best Local Similarity 51.2%; Pred. No. 0.0015;
RESULT 509
ID ADH21715 standard; DNA; 609 BP.
DE Human interleukin-22 fragment-encoding DNA, SEQ ID NO:512.
PN WO2003059934-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 56.8; DB 10; Length 609;
Best Local Similarity 51.2%; Pred. No. 0.0015;
RESULT 510
ID ADV43377 standard; cDNA; 609 BP.

DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1005.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.4%; Score 56.8; DB 14; Length 609;
Best Local Similarity 51.2%; Pred. No. 0.0015;
RESULT 511
ID AAA59155 standard; cDNA; 1385 BP.
DE cDNA encoding a human interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 5.4%; Score 56.8; DB 3; Length 1385;
Best Local Similarity 51.2%; Pred. No. 0.0018;
RESULT 512
ID AAA58983 standard; cDNA; 1385 BP.
DE cDNA encoding a human interleukin (IL) 173 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 5.4%; Score 56.8; DB 3; Length 1385;
Best Local Similarity 51.2%; Pred. No. 0.0018;
RESULT 513
ID ADB31995 standard; cDNA; 1385 BP.
DE Human cDNA encoding interleukin 173, IL-173.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 5.4%; Score 56.8; DB 10; Length 1385;
Best Local Similarity 51.2%; Pred. No. 0.0018;
RESULT 514
ID ADR13797 standard; cDNA; 1385 BP.
DE Human interleukin-173 (IL-173) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 5.4%; Score 56.8; DB 12; Length 1385;
Best Local Similarity 51.2%; Pred. No. 0.0018;
RESULT 515
ID ADJ61720 standard; cDNA; 1641 BP.
DE Human interleukin-22 (IL-22) cDNA #1.
PN US2003186387-A1.
PD 02-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1641;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 516
ID AAZ36835 standard; cDNA; 1642 BP.
DE Partial nucleotide sequence of human interleukin-22.
PN WO9961617-A1.
PD 02-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 56.8; DB 3; Length 1642;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 517
ID AAI67877 standard; DNA; 1642 BP.
DE Human interleukin (IL)-22 nucleotide sequence.
PN US2001023070-A1.
PD 20-SEP-2001.
PA (EBNE/) EBNER R.
PA (RUBE/) RUBEN S M.
Query Match 5.4%; Score 56.8; DB 4; Length 1642;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 518
ID AAS09512 standard; cDNA; 1754 BP.
DE Human cDNA encoding Interleukin 17D ligand, IL-17D.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 4; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 519
ID ABK33579 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO protein, Seq ID No 87.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 6; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 520
ID ADY31827 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN WO200193983-A1.
PD 13-DEC-2001.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 7; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 521
ID ACA89853 standard; cDNA; 1754 BP.
DE Human cDNA (PRO21175) encoding h-IL17D.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 8; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 522
ID ACA68540 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 8; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 523
ID ACA64637 standard; cDNA; 1754 BP.
DE Human cDNA encoding IL-17 family member, PRO21175.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 8; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 524
ID ABT44269 standard; cDNA; 1754 BP.
DE Human PRO21175 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 525
ID ADA43230 standard; cDNA; 1754 BP.
DE Human interleukin 17 related mammalian cytokine polypeptide cDNA #4.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 526
ID ABT44552 standard; cDNA; 1754 BP.
DE Human PRO21175 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 527
ID ACD82219 standard; cDNA; 1754 BP.
DE Human secreted/transmembrane polypeptide PRO 21175 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 528
ID ADA49771 standard; cDNA; 1754 BP.
DE Human interleukin-17/interleukin-17 receptor related PRO21175 cDNA.

PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 529
ID ADA26964 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO polypeptide #4.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 530
ID ABT43925 standard; cDNA; 1754 BP.
DE Human membrane bound receptor/protein PRO21175 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 531
ID ADB83577 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 532
ID ADB80683 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 533
ID ADB73224 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 534
ID ADB78306 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 9; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 535
ID ADB84954 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 536
ID ADB78060 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 537
ID ADB87126 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 538
ID ADB84708 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 539
ID ADB83823 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 540
ID ADB72978 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 541
ID ADB66898 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO polypeptide #4.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 542
ID ADC36816 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 543
ID ADC21806 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 544
ID ADC49837 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 545
ID ADC49036 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 546
ID ADC49553 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 547
ID ADC47414 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 548
ID ADC47159 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 549
ID ADC78034 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 550
ID ADD06269 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 551
ID ADC77788 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 552
ID ADD50751 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 553
ID ADD50997 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 554
ID ADD50478 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 555
ID ADD50232 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 556
ID ADD51243 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 557
ID AAD63610 standard; cDNA; 1754 BP.
DE Human IL-17D ligand (PRO21175) cDNA.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 558
ID ADG87382 standard; cDNA; 1754 BP.
DE Human PRO21175 cDNA from clone DNA173894-2947.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 559
ID ACA66884 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO polypeptide #44.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 560
ID ACD68636 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 561
ID ADL16678 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO21175 polypeptide.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 562
ID ADC48790 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 563
ID ADE20961 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 564
ID ADE05805 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;

Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 565
ID ADD75034 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 566
ID ADD75780 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 567
ID ADD85012 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 568
ID ADD86838 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 569
ID ADE20715 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 570
ID ADE39012 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 571
ID ADE05559 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 572
ID ADD73544 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 573
ID ADD78384 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 574
ID ADE21207 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 575
ID ADD77322 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 576
ID ADE20469 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 577
ID ADD75534 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 578
ID ADD74050 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 579
ID ADD74296 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 580
ID ADD76026 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 581
ID ADD85518 standard; cDNA; 1754 BP..
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 582
ID ADE05067 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 583

ID ADD75280 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 584
ID ADD76824 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 585
ID ADD86592 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 586
ID ADD78060 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 587
ID ADD77568 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 588
ID ADD77814 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 589
ID ADD85272 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 590
ID ADD73804 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 591
ID ADD74542 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 592
ID ADD77070 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 593
ID ADD85764 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 594
ID ADE05313 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 595
ID ADD74788 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 596
ID ADG05600 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 597
ID ADG27154 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 598
ID ADG11217 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 599
ID ADG11996 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 600
ID ADF94553 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 601
ID ADG06649 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.

PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 602
ID ADH38993 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 603
ID ADG34083 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 604
ID ADI33553 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 605
ID ADH69647 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 606
ID ADI29808 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 607
ID ADL16639 standard; cDNA; 1754 BP.
DE cDNA encoding human PRO21175 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 608
ID ADL71299 standard; cDNA; 1754 BP.
DE Human IL-17D (PRO21175) encoding cDNA, DNA173894-2947.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 609
ID ADM27205 standard; cDNA; 1754 BP.
DE Novel human secreted and transmembrane protein PRO21175 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 610
ID ADK66563 standard; cDNA; 1754 BP.
DE Human PRO polynucleotide #44.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1754;
Best Local Similarity 51.2%; Pred. No. 0.0019;
RESULT 611
ID AAZ52195 standard; cDNA; 1819 BP.
DE Human transforming growth factor beta-9, Ztgfbeta-9 cDNA.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 5.4%; Score 56.8; DB 3; Length 1819;
Best Local Similarity 51.2%; Pred. No. 0.002;
RESULT 612
ID AAD54506 standard; DNA; 1819 BP.
DE Human interleukin-17D (IL-17D) DNA #1.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 5.4%; Score 56.8; DB 10; Length 1819;
Best Local Similarity 51.2%; Pred. No. 0.002;
RESULT 613
ID ADQ91998 standard; cDNA; 1819 BP.
DE Human transforming growth factor beta-9 (Ztgfbeta-9) cDNA.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 5.4%; Score 56.8; DB 12; Length 1819;
Best Local Similarity 51.2%; Pred. No. 0.002;
RESULT 614
ID AAZ52201 standard; cDNA; 2361 BP.
DE Human transforming growth factor beta-9, Ztgfbeta-9 variant cDNA.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 5.4%; Score 56.8; DB 3; Length 2361;
Best Local Similarity 51.2%; Pred. No. 0.0021;
RESULT 615
ID ADE34352 standard; DNA; 2361 BP.
DE Transforming growth factor beta-9 gene #SEQ ID 33.
PN WO2003048394-A1.
PD 12-JUN-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.4%; Score 56.8; DB 10; Length 2361;
Best Local Similarity 51.2%; Pred. No. 0.0021;
RESULT 616
ID AAD54507 standard; DNA; 2361 BP.
DE Human interleukin-17D (IL-17D) DNA #2.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 5.4%; Score 56.8; DB 10; Length 2361;
Best Local Similarity 51.2%; Pred. No. 0.0021;
RESULT 617
ID ADQ92013 standard; cDNA; 2361 BP.
DE Human transforming growth factor beta-9 (Ztgfbeta-9) variant cDNA.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 5.4%; Score 56.8; DB 12; Length 2361;
Best Local Similarity 51.2%; Pred. No. 0.0021;
RESULT 618
ID AAD28772 standard; cDNA; 1013 BP.
DE Mouse Interleukin-17 like (IL-17L) cDNA.
PN WO200208285-A2.
PD 31-JAN-2002.
PA (AMGE-) AMGEN INC.
Query Match 5.3%; Score 55.2; DB 6; Length 1013;
Best Local Similarity 57.1%; Pred. No. 0.0041;
RESULT 619
ID ADE83312 standard; cDNA; 1013 BP.
DE Mouse IL-17 like cDNA.
PN US2003124092-A1.
PD 03-JUL-2003.

PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 5.3%; Score 55.2; DB 12; Length 1013;
Best Local Similarity 57.1%; Pred. No. 0.0041;
RESULT 620
ID ADW64910 standard; cDNA; 1013 BP.
DE Mouse IL-17 like cDNA.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 5.3%; Score 55.2; DB 14; Length 1013;
Best Local Similarity 57.1%; Pred. No. 0.0041;
RESULT 621
ID ADZ14887 standard; cDNA; 1013 BP.
DE Mouse IL-17 like cDNA, SEQ ID NO: 3.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 5.3%; Score 55.2; DB 14; Length 1013;
Best Local Similarity 57.1%; Pred. No. 0.0041;
RESULT 622
ID AAD28773 standard; cDNA; 1496 BP.
DE Mouse non-secreted form of Interleukin-17 like (IL-17L) cDNA.
PN WO200208285-A2.
PD 31-JAN-2002.
PA (AMGE-) AMGEN INC.
Query Match 5.3%; Score 55.2; DB 6; Length 1496;
Best Local Similarity 57.1%; Pred. No. 0.0045;
RESULT 623
ID ADE83318 standard; cDNA; 1496 BP.
DE Non secreted mouse IL-17 like cDNA.
PN US2003124092-A1.
PD 03-JUL-2003.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 5.3%; Score 55.2; DB 12; Length 1496;
Best Local Similarity 57.1%; Pred. No. 0.0045;
RESULT 624
ID ADW64916 standard; cDNA; 1496 BP.
DE Non-secreted form of mouse IL-17 like cDNA.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 5.3%; Score 55.2; DB 14; Length 1496;
Best Local Similarity 57.1%; Pred. No. 0.0045;
RESULT 625
ID ADZ14893 standard; cDNA; 1496 BP.
DE Non-secreted form of mouse IL-17 like cDNA, SEQ ID NO: 9.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 5.3%; Score 55.2; DB 14; Length 1496;
Best Local Similarity 57.1%; Pred. No. 0.0045;
RESULT 626
ID ADX53251 standard; cDNA; 2055 BP.
DE Plant full length insert polynucleotide seqid 27991.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 5.2%; Score 54.6; DB 13; Length 2055;
Best Local Similarity 47.5%; Pred. No. 0.0068;
RESULT 627
ID AAA59158 standard; cDNA; 504 BP.
DE cDNA encoding a human interleukin-174 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 5.1%; Score 53.8; DB 3; Length 504;
Best Local Similarity 56.9%; Pred. No. 0.0073;
RESULT 628
ID AAA58986 standard; cDNA; 504 BP.
DE cDNA encoding a human interleukin (IL) 174 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 5.1%; Score 53.8; DB 3; Length 504;
Best Local Similarity 56.9%; Pred. No. 0.0073;
RESULT 629
ID ABA02393 standard; DNA; 504 BP.
DE Human interleukin 174 (IL-174)-encoding DNA.
PN WO200179288-A2.
PD 25-OCT-2001.
PA (SCHE) SCHERING CORP.
Query Match 5.1%; Score 53.8; DB 6; Length 504;
Best Local Similarity 56.9%; Pred. No. 0.0073;
RESULT 630
ID ADB32001 standard; cDNA; 504 BP.
DE Human cDNA encoding interleukin 174, IL-174.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 5.1%; Score 53.8; DB 10; Length 504;
Best Local Similarity 56.9%; Pred. No. 0.0073;
RESULT 631
ID ADR13803 standard; cDNA; 504 BP.
DE Human interleukin-174 (IL-174) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 5.1%; Score 53.8; DB 12; Length 504;
Best Local Similarity 56.9%; Pred. No. 0.0073;
RESULT 632
ID ADV42798 standard; cDNA; 534 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 426.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.1%; Score 53.8; DB 14; Length 534;
Best Local Similarity 56.9%; Pred. No. 0.0074;
RESULT 633
ID AAD28771 standard; cDNA; 644 BP.
DE Human Interleukin-17 like (IL-17L) cDNA.
PN WO200208285-A2.

PD 31-JAN-2002.
PA (AMGE-) AMGEN INC.
Query Match 5.1%; Score 53.8; DB 6; Length 644;
Best Local Similarity 56.9%; Pred. No. 0.0078;
RESULT 634
ID ABA03213 standard; cDNA; 644 BP.
DE Human IL-17 receptor like protein ligand, IL-17E, coding sequence.
PN WO200168705-A2.
PD 20-SEP-2001.
PA (AMGE-) AMGEN INC.
Query Match 5.1%; Score 53.8; DB 6; Length 644;
Best Local Similarity 56.9%; Pred. No. 0.0078;
RESULT 635
ID ADE83310 standard; cDNA; 644 BP.
DE Human IL-17 like cDNA.
PN US2003124092-A1.
PD 03-JUL-2003.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 5.1%; Score 53.8; DB 12; Length 644;
Best Local Similarity 56.9%; Pred. No. 0.0078;
RESULT 636
ID ADW64908 standard; cDNA; 644 BP.
DE Human IL-17 like cDNA.
PN US2005003451-A1.
PD 06-JAN-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 5.1%; Score 53.8; DB 14; Length 644;
Best Local Similarity 56.9%; Pred. No. 0.0078;
RESULT 637
ID ADZ14885 standard; cDNA; 644 BP.
DE Human IL-17 like cDNA, SEQ ID NO: 1.
PN US2005074427-A1.
PD 07-APR-2005.
PA (MEDL/) MEDLOCK E.
PA (YEHR/) YEH R.
PA (SILB/) SILBIGER S M.
PA (ELLI/) ELLIOTT G S.
PA (NGUY/) NGUYEN H Q.
PA (JING/) JING S.
Query Match 5.1%; Score 53.8; DB 14; Length 644;
Best Local Similarity 56.9%; Pred. No. 0.0078;
RESULT 638
ID AAA59160 standard; cDNA; 985 BP.
DE cDNA encoding a murine interleukin-174 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 5.1%; Score 53.6; DB 3; Length 985;
Best Local Similarity 56.6%; Pred. No. 0.0097;
RESULT 639
ID AAA58988 standard; cDNA; 985 BP.
DE cDNA encoding a murine interleukin (IL) 174 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 5.1%; Score 53.6; DB 3; Length 985;
Best Local Similarity 56.6%; Pred. No. 0.0097;
RESULT 640
ID ABA02394 standard; DNA; 985 BP.
DE Murine interleukin 174 (IL-174)-encoding DNA.
PN WO200179288-A2.
PD 25-OCT-2001.
PA (SCHE) SCHERING CORP.
Query Match 5.1%; Score 53.6; DB 6; Length 985;
Best Local Similarity 56.6%; Pred. No. 0.0097;
RESULT 641
ID ADB32005 standard; cDNA; 985 BP.
DE Mouse cDNA encoding interleukin 174, IL-174.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 5.1%; Score 53.6; DB 10; Length 985;
Best Local Similarity 56.6%; Pred. No. 0.0097;
RESULT 642
ID ADR13807 standard; cDNA; 985 BP.
DE Murine interleukin-174 (IL-174) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 5.1%; Score 53.6; DB 12; Length 985;
Best Local Similarity 56.6%; Pred. No. 0.0097;
RESULT 643
ID AAC85969 standard; cDNA; 1320 BP.
DE Native sequence of PRO10272 cDNA, clone DNA147531-2821.
PN WO200140465-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 4; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 644
ID AAF92135 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 4; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 645
ID AAS09511 standard; cDNA; 1320 BP.
DE Human cDNA encoding Interleukin 17E ligand, IL-17E.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 4; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 646
ID ABS74455 standard; cDNA; 1320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO10272.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 6; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 647
ID ACA91241 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 648
ID ACD81618 standard; cDNA; 1320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO10272.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 649
ID ACA60440 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;

Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 650
ID ACA58887 standard; cDNA; 1320 BP.
DE cDNA encoding human secreted polypeptide PRO10272.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 651
ID ACA64063 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #78.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 652
ID ACA91327 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #78.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 653
ID ACD45226 standard; cDNA; 1320 BP.
DE Human secreted/transmembrane polypeptide PRO10272 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 654
ID ACA93774 standard; cDNA; 1320 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO10272.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 655
ID ACA89852 standard; cDNA; 1320 BP.
DE Human cDNA (PRO102721) encoding h-IL17E.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 656
ID ACA67348 standard; cDNA; 1320 BP.
DE cDNA encoding human secreted polypeptide PRO10272.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 657
ID ACH66321 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 658
ID ACD02375 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 659
ID ACA89366 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 660
ID ACA69003 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 661
ID ACA64636 standard; cDNA; 1320 BP.
DE Human cDNA encoding IL-17 family member, PRO10272.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 662
ID ACA98525 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 8; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 663
ID ACA63450 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #78.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 664
ID ADA26943 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #9.
PN US2003087380-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 665
ID ADB17212 standard; cDNA; 1320 BP.
DE Human cDNA clone (SeqID 155) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 666
ID ADA43228 standard; cDNA; 1320 BP.
DE Human interleukin 17 related mammalian cytokine polypeptide cDNA #3.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 667
ID ACH03653 standard; cDNA; 1320 BP.
DE Human secreted/transmembrane polypeptide PRO 10272 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 668

ID ADA20017 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 669
ID ADB17400 standard; cDNA; 1320 BP.
DE Human cDNA clone (SeqID 155) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 670
ID ADA20189 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 671
ID ACD82167 standard; cDNA; 1320 BP.
DE Human secreted/transmembrane polypeptide PRO 10272 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 672
ID ADA00486 standard; cDNA; 1320 BP.
DE Human secreted/transmembrane polypeptide PRO 10272 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 673
ID ADA49769 standard; cDNA; 1320 BP.
DE Human interleukin-17/interleukin-17 receptor related PRO10272 cDNA.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 674
ID ACD27959 standard; cDNA; 1320 BP.
DE cDNA encoding novel human protein PRO10272.
PN US2003054484-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 675
ID ADA26962 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 676
ID ADB85728 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 9; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 677
ID ADB68407 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 678
ID ADB68214 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 679
ID ADB91031 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 680
ID ADB66896 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 681
ID ADC07111 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 682
ID ADC17290 standard; cDNA; 1320 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 155).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 683
ID ADC14988 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 684
ID ADC52483 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 685
ID ADD36159 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 686
ID ADE86210 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.

PN US2003153015-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 687
ID AAD63609 standard; cDNA; 1320 BP.
DE Human IL-17E ligand (PRO10272) cDNA.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 688
ID ADG01160 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 689
ID ADG08713 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 690
ID ADF95334 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 691
ID ADH24187 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 692
ID ADG87380 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA from clone DNA147531-2821.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 693
ID ADH34213 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 694
ID ADH30046 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 695
ID ADH24017 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 696
ID ADG85421 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 697
ID ADH24697 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 698
ID ADH37553 standard; cDNA; 1320 BP.
DE Human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 699
ID ADH02142 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 700
ID ADG87368 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA from clone DNA147531-2821.
PN US2003077738-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 701
ID ADH37723 standard; cDNA; 1320 BP.
DE Human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 702
ID ADG85761 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 703
ID ADH24357 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 704
ID ADH38651 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 705
ID ADG88790 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA.
PN US2003077737-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 706
ID ADG83772 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 707
ID ADH29580 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 708
ID ADH27696 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 709
ID ADH37893 standard; cDNA; 1320 BP.
DE Human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 710
ID ADH38070 standard; cDNA; 1320 BP.
DE Human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 711
ID ADH57490 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 712
ID ADH53632 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 713
ID ADH53802 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 714
ID ADH52138 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 715
ID ADH49993 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 716
ID ADI25503 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 717
ID ADH90296 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 718
ID ADI25673 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 719
ID ADH97847 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 720
ID ADI03695 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 721
ID ADI12052 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 722
ID ADH90126 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;

Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 723
ID ADH98527 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 724
ID ADI11202 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 725
ID ADI11712 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 726
ID ADH98357 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 727
ID ADH98697 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 728
ID ADH98187 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 729
ID ADI05175 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 730
ID ADI03525 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 731
ID ADI04920 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 732
ID ADH78374 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 733
ID ADI19718 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 734
ID ADH90466 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 735
ID ADI03185 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 736
ID ADH78034 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 737
ID ADH98017 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 738
ID ADI01402 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 739
ID ADI02097 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 740
ID ADI03355 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 741

ID ADI11542 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 742
ID ADI02444 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 743
ID ADI11882 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 744
ID ADI05519 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 745
ID ADH79591 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 746
ID ADI19548 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 747
ID ADI05349 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 748
ID ADH79761 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 749
ID ADI01587 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 750
ID ADI01757 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 751
ID ADI01927 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 752
ID ADH79931 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 753
ID ADI04749 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 754
ID ADI02885 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 755
ID ADH78204 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 756
ID ADI25843 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 757
ID ADI26013 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 758
ID ADK65525 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 759
ID ADL16676 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO10272 polypeptide.

PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 760
ID ADH98867 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 761
ID ADH80108 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 10; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 762
ID ADL93838 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 11; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 763
ID ADC52293 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 764
ID ADH06725 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 765
ID ADH06555 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 766
ID ADG68976 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 767
ID ADH27866 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 768
ID ADH25207 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 769
ID ADH33839 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 770
ID ADH02482 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 771
ID ADH08089 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 772
ID ADG69486 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 773
ID ADH39306 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 774
ID ADG84047 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 775
ID ADG47090 standard; cDNA; 1320 BP.
DE Human PRO10272 cDNA from clone DNA1475531-2821.
PN US2003100063-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 776
ID ADG85591 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 777
ID ADH06385 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 778
ID ADH30215 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 779
ID ADH24527 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 780
ID ADG69656 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 781
ID ADH07919 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 782
ID ADG85931 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 783
ID ADH39477 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 784
ID ADH33669 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 785
ID ADH34009 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 786
ID ADH01219 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 787
ID ADG69826 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 788
ID ADH02312 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 789
ID ADG69316 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 790
ID ADG86101 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 791
ID ADH25037 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 792
ID ADH39654 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 793
ID ADH02652 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 794
ID ADG69146 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 795
ID ADH07749 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;

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  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 796
ID   ADG86271 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003180863-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 797
ID   ADH24867 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003180908-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 798
ID   ADH25915 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003180911-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 799
ID   ADH38481 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003180922-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 800
ID   ADH57320 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003181642-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 801
ID   ADH52307 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003180921-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 802
ID   ADH49673 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003180857-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 803
ID   ADH90636 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003181700-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 804
ID   ADI11372 standard; cDNA; 1320 BP.
DE   Human PRO polynucleotide #78.
PN   US2003181683-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 805
ID   ADH99037 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003190698-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 806
ID   ADI02267 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003190699-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 807
ID   ADH90806 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003181701-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 808
ID   ADJ98681 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003187197-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 809
ID   ADJ98851 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003187228-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 810
ID   ADH79010 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003181703-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 811
ID   ADJ99244 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003186408-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 812
ID   ADJ99414 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003187196-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 813
ID   ADJ99032 standard; cDNA; 1320 BP.
DE   Novel human secreted and transmembrane protein PRO10272 cDNA.
PN   US2003187242-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             5.0%;  Score 52.2;  DB 12;  Length 1320;
  Best Local Similarity   56.5%;  Pred. No. 0.023;
RESULT 814
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ID ADH79179 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 815
ID ADK01040 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 816
ID ADL16637 standard; cDNA; 1320 BP.
DE cDNA encoding human PRO10272 polypeptide.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 817
ID ADK14561 standard; cDNA; 1320 BP.
DE Novel human secreted and transmembrane protein PRO10272 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 818
ID ADL71297 standard; cDNA; 1320 BP.
DE Human IL-17E (PRO10272) encoding cDNA, DNA147531-2821.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 819
ID ADM81010 standard; cDNA; 1320 BP.
DE Human PRO polynucleotide #78.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 52.2; DB 12; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 820
ID ADY77850 standard; cDNA; 1320 BP.
DE Neoplastic disease detection cDNA PRO10272.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 5.0%; Score 52.2; DB 14; Length 1320;
Best Local Similarity 56.5%; Pred. No. 0.023;
RESULT 821
ID ABZ04777 standard; DNA; 50 BP.
DE Human leukocyte gene expression profiling probe SEQ ID NO 4768.
PN WO200257414-A2.
PD 25-JUL-2002.
PA (BIOC-) BIOCARDIA INC.
Query Match 4.8%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.033;
RESULT 822
ID ADP10298 standard; DNA; 50 BP.
DE 50-mer oligonucleotide marker probe of the invention #307.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 4.8%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.033;
RESULT 823
ID AAA02477 standard; cDNA; 1127 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2468.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 49.8; DB 3; Length 1127;
Best Local Similarity 30.9%; Pred. No. 0.081;
RESULT 824
ID ADX62185 standard; cDNA; 2088 BP.
DE Plant full length insert polynucleotide seqid 33028.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 4.8%; Score 49.8; DB 13; Length 2088;
Best Local Similarity 46.6%; Pred. No. 0.095;
RESULT 825
ID AAA59159 standard; cDNA; 620 BP.
DE cDNA encoding a murine interleukin-174 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 4.7%; Score 49.4; DB 3; Length 620;
Best Local Similarity 58.7%; Pred. No. 0.087;
RESULT 826
ID AAA58987 standard; cDNA; 620 BP.
DE cDNA encoding a murine interleukin (IL) 174 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 4.7%; Score 49.4; DB 3; Length 620;
Best Local Similarity 58.7%; Pred. No. 0.087;
RESULT 827
ID ADB32003 standard; cDNA; 620 BP.
DE Mouse partial cDNA encoding interleukin 174, IL-174.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 4.7%; Score 49.4; DB 10; Length 620;
Best Local Similarity 58.7%; Pred. No. 0.087;
RESULT 828
ID ADR13805 standard; cDNA; 620 BP.
DE Murine interleukin-174 (IL-174) partial cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 4.7%; Score 49.4; DB 12; Length 620;
Best Local Similarity 58.7%; Pred. No. 0.087;
RESULT 829
ID ADS45919 standard; cDNA; 1839 BP.
DE Bacterial polynucleotide #662.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.6%; Score 48.4; DB 13; Length 1839;
Best Local Similarity 50.0%; Pred. No. 0.2;
RESULT 830

ID AAH26500 standard; cDNA; 2561 BP.
DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
PN WO200164874-A2.
PD 07-SEP-2001.
PA (BOST-) BOSTON HEART FOUND INC.
Query Match 4.5%; Score 47.4; DB 5; Length 2561;
Best Local Similarity 47.4%; Pred. No. 0.37;
RESULT 831
ID AAX53491 standard; DNA; 114955 BP.
DE Human adenosine A1 receptor antisense oligonucleotide fragment.
PN WO9913886-A1.
PD 25-MAR-1999.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 4.5%; Score 47.2; DB 2; Length 114955;
Best Local Similarity 29.3%; Pred. No. 1.1;
RESULT 832
ID ADJ44358 standard; cDNA; 669 BP.
DE Plant cDNA #5358.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 4.5%; Score 46.8; DB 12; Length 669;
Best Local Similarity 49.2%; Pred. No. 0.37;
RESULT 833
ID AAV50486 standard; DNA; 1032 BP.
DE Streptomyces clavuligerus DNA sequence of orfup1.
PN WO9833896-A2.
PD 06-AUG-1998.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYAL-) UNIV ALBERTA.
Query Match 4.5%; Score 46.8; DB 2; Length 1032;
Best Local Similarity 43.9%; Pred. No. 0.41;
RESULT 834
ID ADO15644 standard; DNA; 1032 BP.
DE Streptomyces clavuligerus orfup1.
PN US2004081960-A1.
PD 29-APR-2004.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYAL-) UNIV ALBERTA.
Query Match 4.5%; Score 46.8; DB 12; Length 1032;
Best Local Similarity 43.9%; Pred. No. 0.41;
RESULT 835
ID ADT75271 standard; DNA; 1035 BP.
DE Streptomyces clavuligerus cmv1 open reading frame.
PN WO2004092389-A2.
PD 28-OCT-2004.
PA (GLAX) GLAXO GROUP LTD.
PA (UYAL-) UNIV ALBERTA.
Query Match 4.5%; Score 46.8; DB 13; Length 1035;
Best Local Similarity 43.9%; Pred. No. 0.41;
RESULT 836
ID ADX50859 standard; cDNA; 1601 BP.
DE Plant full length insert polynucleotide seqid 25599.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 4.5%; Score 46.8; DB 13; Length 1601;
Best Local Similarity 49.2%; Pred. No. 0.46;

RESULT 837
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.5%; Score 46.8; DB 8; Length 2000;
Best Local Similarity 9.9%; Pred. No. 0.49;
RESULT 838
ID AAV50431 standard; DNA; 7193 BP.
DE Streptomyces clavuligerus DNA sequence of ORFs flanking cas1.
PN WO9833896-A2.
PD 06-AUG-1998.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYAL-) UNIV ALBERTA.
Query Match 4.5%; Score 46.8; DB 2; Length 7193;
Best Local Similarity 43.9%; Pred. No. 0.68;
RESULT 839
ID AAD61763 standard; DNA; 7193 BP.
DE Streptomyces clavuligerus chromosome including and flanking cas1 gene.
PN US2003109694-A1.
PD 12-JUN-2003.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 4.5%; Score 46.8; DB 10; Length 7193;
Best Local Similarity 43.9%; Pred. No. 0.68;
RESULT 840
ID ADO15641 standard; DNA; 7193 BP.
DE S. clavuligerus chromosome including and flanking the cas1 gene.
PN US2004081960-A1.
PD 29-APR-2004.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYAL-) UNIV ALBERTA.
Query Match 4.5%; Score 46.8; DB 12; Length 7193;
Best Local Similarity 43.9%; Pred. No. 0.68;
RESULT 841
ID ADT75281 standard; DNA; 18070 BP.
DE Streptomyces clavuligerus extended cmv cluster DNA.
PN WO2004092389-A2.
PD 28-OCT-2004.
PA (GLAX) GLAXO GROUP LTD.
PA (UYAL-) UNIV ALBERTA.
Query Match 4.5%; Score 46.8; DB 13; Length 18070;
Best Local Similarity 43.9%; Pred. No. 0.86;
RESULT 842
ID ADJ11749 standard; DNA; 1134 BP.
DE Rice cDNA modulated by post-transcriptional gene silencing SeqID 385.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 4.4%; Score 46.2; DB 11; Length 1134;
Best Local Similarity 44.1%; Pred. No. 0.59;
RESULT 843
ID ADJ11429 standard; DNA; 1137 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 65.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 4.4%; Score 46.2; DB 11; Length 1137;
Best Local Similarity 44.1%; Pred. No. 0.59;
RESULT 844
ID AAA10594 standard; DNA; 10732 BP.
DE Gene encoding a subunit of cellulose synthase.
PN JP2000060568-A.
PD 29-FEB-2000.
PA (MIZU/) MIZUNO K.
PA (OJIP) OJI PAPER CO.
Query Match 4.4%; Score 46.2; DB 3; Length 10732;
Best Local Similarity 14.4%; Pred. No. 1;
RESULT 845
ID ADJ11627 standard; DNA; 1161 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 263.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 4.4%; Score 45.8; DB 11; Length 1161;
Best Local Similarity 43.9%; Pred. No. 0.74;
RESULT 846
ID ADX49952 standard; cDNA; 1345 BP.
DE Plant full length insert polynucleotide seqid 24692.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 4.4%; Score 45.8; DB 13; Length 1345;
Best Local Similarity 44.9%; Pred. No. 0.76;
RESULT 847
ID ADX47228 standard; cDNA; 1420 BP.
DE Plant full length insert polynucleotide seqid 21968.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 4.4%; Score 45.8; DB 13; Length 1420;
Best Local Similarity 44.9%; Pred. No. 0.77;
RESULT 848
ID ADX53490 standard; cDNA; 1992 BP.
DE Plant full length insert polynucleotide seqid 28230.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 4.4%; Score 45.8; DB 13; Length 1992;
Best Local Similarity 44.9%; Pred. No. 0.85;
RESULT 849
ID ACA23975 standard; DNA; 615 BP.
DE Prokaryotic essential gene #5632.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 45.4; DB 8; Length 615;
Best Local Similarity 51.8%; Pred. No. 0.78;
RESULT 850
ID ACN54594 standard; cDNA; 629 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-K6-D2, SEQ:9375.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.3%; Score 45.2; DB 13; Length 629;
Best Local Similarity 52.7%; Pred. No. 0.87;
RESULT 851
ID ABS78661 standard; DNA; 5760 BP.
DE M. echinospora DNA encoding PKSE protein.
PN CA2387401-A1.
PD 04-SEP-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.3%; Score 45.2; DB 6; Length 5760;
Best Local Similarity 51.0%; Pred. No. 1.5;
RESULT 852
ID AEB12618 standard; DNA; 5760 BP.
DE Enediyne polyketide synthase, PKSE, coding sequence, SEQ ID 14.
PN US2005142601-A1.
PD 30-JUN-2005.
PA (FARN/) FARNET C M.
PA (STAF/) STAFFA A.
PA (ZAZO/) ZAZOPOULOS E.
Query Match 4.3%; Score 45.2; DB 14; Length 5760;
Best Local Similarity 51.0%; Pred. No. 1.5;
RESULT 853
ID AEC10211 standard; DNA; 5760 BP.
DE M. echinospora subsp. calichensis PKSE ORF, SEQ:14.
PN US2005170411-A1.
PD 04-AUG-2005.
PA (FARN/) FARNET C M.
PA (STAF/) STAFFA A.
PA (ZAZO/) ZAZOPOULOS E.
Query Match 4.3%; Score 45.2; DB 14; Length 5760;
Best Local Similarity 51.0%; Pred. No. 1.5;
RESULT 854
ID ABD09162 standard; DNA; 1074 BP.
DE Pseudomonas aeruginosa polynucleotide #7766.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 44.8; DB 11; Length 1074;
Best Local Similarity 43.8%; Pred. No. 1.2;
RESULT 855
ID ABD09309 standard; DNA; 1239 BP.
DE Pseudomonas aeruginosa polynucleotide #7913.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 44.8; DB 11; Length 1239;
Best Local Similarity 43.8%; Pred. No. 1.3;
RESULT 856
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.3%; Score 44.8; DB 8; Length 2000;
Best Local Similarity 9.1%; Pred. No. 1.5;

RESULT 857
ID AAQ61817 standard; DNA; 1578 BP.
DE Open reading frame of pseudorabies virus.
PN WO9408000-A1.
PD 14-APR-1994.
PA (ALKU) AKZO NV.
Query Match 4.3%; Score 44.6; DB 2; Length 1578;
Best Local Similarity 46.7%; Pred. No. 1.5;
RESULT 858
ID ADX46890 standard; cDNA; 1216 BP.
DE Plant full length insert polynucleotide seqid 21630.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 4.2%; Score 44.2; DB 13; Length 1216;
Best Local Similarity 44.7%; Pred. No. 1.8;
RESULT 859
ID ADX47236 standard; cDNA; 1239 BP.
DE Plant full length insert polynucleotide seqid 21976.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 4.2%; Score 44.2; DB 13; Length 1239;
Best Local Similarity 44.7%; Pred. No. 1.8;
RESULT 860
ID ADW87338 standard; DNA; 3008 BP.
DE Dog Lafora body disease associated protein EPM2B DNA.
PN WO2005012526-A1.
PD 10-FEB-2005.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
Query Match 4.2%; Score 44.2; DB 14; Length 3008;
Best Local Similarity 44.2%; Pred. No. 2.3;
RESULT 861
ID ACN44562 standard; DNA; 28544 BP.
DE Human genomic sequence hCG15331.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.2%; Score 44.2; DB 11; Length 28544;
Best Local Similarity 49.8%; Pred. No. 4;
RESULT 862
ID ADF83544 standard; cDNA; 2250 BP.
DE Human GRIM1 cDNA.
PN WO2003078463-A1.
PD 25-SEP-2003.
PA (UNIV-) UNIVERSITAETSKLINIKUM FREIBURG.
Query Match 4.2%; Score 44; DB 10; Length 2250;
Best Local Similarity 53.5%; Pred. No. 2.3;
RESULT 863
ID ACN37249 standard; cDNA; 2508 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA323721, SEQ ID NO:6.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.2%; Score 44; DB 13; Length 2508;
Best Local Similarity 53.5%; Pred. No. 2.4;
RESULT 864
ID AAH18559 standard; cDNA; 2753 BP.
DE Human cDNA sequence SEQ ID NO:18728.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.2%; Score 44; DB 4; Length 2753;
Best Local Similarity 53.5%; Pred. No. 2.5;
RESULT 865
ID ADX08083 standard; DNA; 2762 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 2648.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 4.2%; Score 44; DB 14; Length 2762;
Best Local Similarity 53.5%; Pred. No. 2.5;
RESULT 866
ID AAK52536 standard; cDNA; 3163 BP.
DE Human polynucleotide SEQ ID NO 2065.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.2%; Score 44; DB 4; Length 3163;
Best Local Similarity 53.5%; Pred. No. 2.6;
RESULT 867
ID AAK51552 standard; cDNA; 3236 BP.
DE Human polynucleotide SEQ ID NO 97.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.2%; Score 44; DB 4; Length 3236;
Best Local Similarity 53.5%; Pred. No. 2.6;
RESULT 868
ID ADQ23383 standard; DNA; 4560 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6203.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.2%; Score 44; DB 12; Length 4560;
Best Local Similarity 53.5%; Pred. No. 2.8;
RESULT 869
ID ABQ88187 standard; cDNA; 5504 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 94.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 4.2%; Score 44; DB 6; Length 5504;
Best Local Similarity 54.5%; Pred. No. 3;
RESULT 870
ID ABK84205 standard; cDNA; 5504 BP.
DE Human cDNA differentially expressed in granulocytic cells #776.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.2%; Score 44; DB 6; Length 5504;
Best Local Similarity 54.5%; Pred. No. 3;
RESULT 871
ID ADG32796 standard; DNA; 5504 BP.
DE Human DNA differentially expressed in patients with SLE SeqID120.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 4.2%; Score 44; DB 10; Length 5504;
Best Local Similarity 54.5%; Pred. No. 3;
RESULT 872
ID ADK61020 standard; DNA; 5504 BP.
DE Ovarian cancer-related DNA #175 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 4.2%; Score 44; DB 10; Length 5504;
Best Local Similarity 54.5%; Pred. No. 3;
RESULT 873
ID ADP13550 standard; DNA; 5504 BP.
DE Renal cell carcinoma differentially expressed gene #286.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.

PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Query Match 4.2%; Score 44; DB 12; Length 5504;
Best Local Similarity 54.5%; Pred. No. 3;
RESULT 874
ID AAZ17263 standard; cDNA; 1337 BP.
DE Human gene expression product cDNA sequence SEQ ID NO:4735.
PN WO9938972-A2.
PD 05-AUG-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.2%; Score 43.8; DB 2; Length 1337;
Best Local Similarity 22.7%; Pred. No. 2.3;
RESULT 875
ID ACN59490 standard; cDNA; 406 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-031-Q6-N6-H2, SEQ:14271.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.1%; Score 43.2; DB 13; Length 406;
Best Local Similarity 51.6%; Pred. No. 2.3;
RESULT 876
ID AAD36876 standard; DNA; 1017 BP.
DE S. clavuligerus clavulanic acid biosynthesis enzyme encoding DNA, ORF14.
PN WO2003040372-A2.
PD 15-MAY-2003.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYAL-) UNIV ALBERTA.
Query Match 4.1%; Score 43.2; DB 8; Length 1017;
Best Local Similarity 43.8%; Pred. No. 3;
RESULT 877
ID AAX02974 standard; DNA; 3198 BP.
DE Human IL-1ra BAC contiguous DNA sequence 19.
PN WO9906426-A1.
PD 11-FEB-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 4.1%; Score 43.2; DB 2; Length 3198;
Best Local Similarity 51.6%; Pred. No. 4;
RESULT 878
ID AAD36874 standard; DNA; 29870 BP.
DE Streptomyces clavuligerus clavulanic acid biosynthesis gene cluster.
PN WO2003040372-A2.
PD 15-MAY-2003.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYAL-) UNIV ALBERTA.
Query Match 4.1%; Score 43.2; DB 8; Length 29870;
Best Local Similarity 43.8%; Pred. No. 7.1;
RESULT 879
ID AAX53491 standard; DNA; 114955 BP.
DE Human adenosine A1 receptor antisense oligonucleotide fragment.
PN WO9913886-A1.
PD 25-MAR-1999.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 4.1%; Score 43.2; DB 2; Length 114955;
Best Local Similarity 31.9%; Pred. No. 10;
RESULT 880
ID AAA59157 standard; cDNA; 1143 BP.
DE cDNA encoding a murine interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 4.1%; Score 43; DB 3; Length 1143;
Best Local Similarity 52.5%; Pred. No. 3.4;
RESULT 881
ID AAA58985 standard; cDNA; 1143 BP.
DE cDNA encoding a murine interleukin (IL) 173 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 4.1%; Score 43; DB 3; Length 1143;
Best Local Similarity 52.5%; Pred. No. 3.4;
RESULT 882
ID ADB31999 standard; cDNA; 1143 BP.
DE Mouse cDNA encoding interleukin 173, IL-173.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 4.1%; Score 43; DB 10; Length 1143;
Best Local Similarity 52.5%; Pred. No. 3.4;
RESULT 883
ID ADR13801 standard; cDNA; 1143 BP.
DE Murine interleukin-173 (IL-173) cDNA.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 4.1%; Score 43; DB 12; Length 1143;
Best Local Similarity 52.5%; Pred. No. 3.4;
RESULT 884
ID AAZ52198 standard; cDNA; 1221 BP.
DE Murine transforming growth factor beta-9, Ztgfbeta-9 cDNA.
PN WO200015798-A2.
PD 23-MAR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.1%; Score 43; DB 3; Length 1221;
Best Local Similarity 52.5%; Pred. No. 3.5;
RESULT 885
ID AAD54508 standard; DNA; 1221 BP.
DE Mouse interleukin-17D (IL-17D) DNA.
PN WO2002102411-A2.
PD 27-DEC-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.1%; Score 43; DB 10; Length 1221;
Best Local Similarity 52.5%; Pred. No. 3.5;
RESULT 886
ID ADQ92005 standard; cDNA; 1221 BP.
DE Mouse transforming growth factor beta-9 (Ztgfbeta-9) cDNA.
PN US2004132136-A1.
PD 08-JUL-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.1%; Score 43; DB 12; Length 1221;
Best Local Similarity 52.5%; Pred. No. 3.5;
RESULT 887
ID AAD10108 standard; cDNA; 1258 BP.
DE Mouse ZCYTO7 cDNA.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 4.1%; Score 43; DB 4; Length 1258;
Best Local Similarity 52.5%; Pred. No. 3.5;
RESULT 888
ID ADS64152 standard; cDNA; 2919 BP.
DE Bacterial polynucleotide #16139.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.1%; Score 42.6; DB 13; Length 2919;
Best Local Similarity 50.2%; Pred. No. 5.4;
RESULT 889
ID ADS63401 standard; cDNA; 2919 BP.
DE Bacterial polynucleotide #15388.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.1%; Score 42.6; DB 13; Length 2919;
Best Local Similarity 50.2%; Pred. No. 5.4;
RESULT 890
ID ADS63769 standard; cDNA; 2919 BP.
DE Bacterial polynucleotide #15756.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.1%; Score 42.6; DB 13; Length 2919;
Best Local Similarity 50.2%; Pred. No. 5.4;
RESULT 891
ID AAX60505 standard; cDNA; 291 BP.
DE Human persephin protein encoding cDNA.
PN WO9914235-A1.
PD 25-MAR-1999.
PA (UNIW) UNIV WASHINGTON.
Query Match 4.0%; Score 42.4; DB 2; Length 291;
Best Local Similarity 55.4%; Pred. No. 3.3;
RESULT 892
ID ADW45164 standard; DNA; 405 BP.
DE Human albumin fusion-related persephin (PSPN;PSP) DNA - SEQ ID 168.
PN WO2005003296-A2.
PD 13-JAN-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 42.4; DB 14; Length 405;
Best Local Similarity 55.4%; Pred. No. 3.6;
RESULT 893
ID ADW45165 standard; DNA; 405 BP.
DE Human albumin fusion-related persephin (PSPN;PSP) DNA - SEQ ID 169.
PN WO2005003296-A2.
PD 13-JAN-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 42.4; DB 14; Length 405;
Best Local Similarity 55.4%; Pred. No. 3.6;
RESULT 894
ID AAX60509 standard; cDNA; 471 BP.
DE WO9914235 Seq ID No: 205.
PN WO9914235-A1.
PD 25-MAR-1999.
PA (UNIW) UNIV WASHINGTON.
Query Match 4.0%; Score 42.4; DB 2; Length 471;
Best Local Similarity 55.4%; Pred. No. 3.8;
RESULT 895
ID ADV42907 standard; cDNA; 471 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 535.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 4.0%; Score 42.4; DB 14; Length 471;
Best Local Similarity 55.4%; Pred. No. 3.8;
RESULT 896
ID ACL28360 standard; cDNA; 522 BP.
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:2316.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.0%; Score 42.4; DB 11; Length 522;
Best Local Similarity 46.3%; Pred. No. 3.9;
RESULT 897
ID AAK71511 standard; DNA; 951 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26323.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 42.4; DB 4; Length 951;
Best Local Similarity 51.6%; Pred. No. 4.5;
RESULT 898
ID ABL88016 standard; DNA; 1056 BP.
DE DNA polymerase III holoenzyme delta subunit related DNA SEQ ID NO:122.
PN WO200206532-A1.
PD 24-JAN-2002.
PA (REPL-) REPLIDYNE INC.
Query Match 4.0%; Score 42.4; DB 6; Length 1056;
Best Local Similarity 44.9%; Pred. No. 4.6;
RESULT 899
ID ABL88015 standard; DNA; 1056 BP.
DE DNA polymerase III holoenzyme delta subunit related DNA SEQ ID NO:121.
PN WO200206532-A1.
PD 24-JAN-2002.
PA (REPL-) REPLIDYNE INC.
Query Match 4.0%; Score 42.4; DB 6; Length 1056;
Best Local Similarity 44.9%; Pred. No. 4.6;
RESULT 900
ID ABK84674 standard; cDNA; 1629 BP.
DE Human cDNA differentially expressed in granulocytic cells #1245.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.0%; Score 42.4; DB 6; Length 1629;
Best Local Similarity 54.0%; Pred. No. 5.2;
RESULT 901
ID ABN97304 standard; DNA; 1629 BP.
DE Gene #3802 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.0%; Score 42.4; DB 6; Length 1629;
Best Local Similarity 54.0%; Pred. No. 5.2;
RESULT 902
ID ADC35128 standard; cDNA; 1629 BP.
DE Human breast cancer antigen polynucleotide seq id 12.
PN US2003108888-A1.
PD 12-JUN-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 4.0%; Score 42.4; DB 10; Length 1629;
Best Local Similarity 54.0%; Pred. No. 5.2;
RESULT 903
ID ADD14773 standard; cDNA; 1629 BP.
DE Human src biomarker polynucleotide SEQ ID NO:167.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 4.0%; Score 42.4; DB 10; Length 1629;
Best Local Similarity 54.0%; Pred. No. 5.2;
RESULT 904
ID ADA52854 standard; cDNA; 2180 BP.
DE Human coding sequence, SEQ ID 422.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.0%; Score 42.4; DB 10; Length 2180;
Best Local Similarity 55.4%; Pred. No. 5.6;
RESULT 905
ID ADC86738 standard; DNA; 3133 BP.
DE Human GPCR gene SEQ ID NO:1191.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 4.0%; Score 42.4; DB 10; Length 3133;
Best Local Similarity 30.8%; Pred. No. 6.1;
RESULT 906
ID ADG42706 standard; cDNA; 3492 BP.
DE Human cDNA encoding NOV7 #3.
PN US2003202971-A1.
PD 30-OCT-2003.
PA (MAJU/) MAJUMDER K.
Query Match 4.0%; Score 42.2; DB 10; Length 3492;
Best Local Similarity 53.3%; Pred. No. 7.1;

RESULT 907
ID ADG42707 standard; DNA; 3493 BP.
DE Human chromosome 22 DNA #2.
PN US2003202971-A1.
PD 30-OCT-2003.
PA (MAJU/) MAJUMDER K.
Query Match 4.0%; Score 42.2; DB 10; Length 3493;
Best Local Similarity 53.3%; Pred. No. 7.1;
RESULT 908
ID ADJ55775 standard; DNA; 3552 BP.
DE Fragment of human NOV7 DNA SeqID 67.
PN US2003199465-A1.
PD 23-OCT-2003.
PA (MALY/) MALYANKAR U M.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (SPYT/) SPYTEK K A.
PA (GUOX/) GUO X.
PA (SPAD/) SPADERNA S K.
PA (BOLD/) BOLDOG F L.
PA (GERL/) GERLACH V.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 4.0%; Score 42.2; DB 10; Length 3552;
Best Local Similarity 53.3%; Pred. No. 7.1;
RESULT 909
ID ADM76613 standard; DNA; 3552 BP.
DE Human NOV7 gene DNA fragment SeqID67.
PN WO2004009634-A2.
PD 29-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 42.2; DB 12; Length 3552;
Best Local Similarity 53.3%; Pred. No. 7.1;
RESULT 910
ID ADJ55776 standard; DNA; 3553 BP.
DE DNA sequence homologous to a fragment of human NOV7 DNA SeqID 68.
PN US2003199465-A1.
PD 23-OCT-2003.
PA (MALY/) MALYANKAR U M.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (SPYT/) SPYTEK K A.
PA (GUOX/) GUO X.
PA (SPAD/) SPADERNA S K.
PA (BOLD/) BOLDOG F L.
PA (GERL/) GERLACH V.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 4.0%; Score 42.2; DB 10; Length 3553;
Best Local Similarity 53.3%; Pred. No. 7.1;
RESULT 911
ID ADM76614 standard; DNA; 3553 BP.
DE Human NOV7 gene-related DNA fragment SeqID68.
PN WO2004009634-A2.
PD 29-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 42.2; DB 12; Length 3553;
Best Local Similarity 53.3%; Pred. No. 7.1;
RESULT 912
ID ADY85604 standard; DNA; 7406 BP.
DE DNA encoding human protocadherin flamingo 2 N-terminal protein Seq 5.
PN EP1517146-A2.
PD 23-MAR-2005.
PA (HINZ/) HINZMANN B.
PA (ROSE/) ROSENTHAL A.
PA (HEID/) HEIDEN E.
PA (LICH/) LICHTNER R.
Query Match 4.0%; Score 42.2; DB 14; Length 7406;
Best Local Similarity 53.3%; Pred. No. 8.6;

RESULT 913
ID AAS06332 standard; cDNA; 9045 BP.
DE DNA encoding seven-pass transmembrane receptor-like protein, MEM1.
PN WO200144473-A2.
PD 21-JUN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 42.2; DB 4; Length 9045;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 914
ID ADN49405 standard; DNA; 9045 BP.
DE Human seven-pass transmembrane receptor (MEM1) DNA.
PN US2004086931-A1.
PD 06-MAY-2004.
PA (SPAD/) SPADERNA S K.
PA (QUIN/) QUINN K E.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
Query Match 4.0%; Score 42.2; DB 12; Length 9045;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 915
ID ADO29840 standard; cDNA; 9045 BP.
DE Human GPCR CELSR1 polynucleotide, SEQ ID NO:942.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 4.0%; Score 42.2; DB 12; Length 9045;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 916
ID ADY85602 standard; DNA; 9057 BP.
DE Human protocadherin flamingo 2 DNA splice variant Seq 3.
PN EP1517146-A2.
PD 23-MAR-2005.
PA (HINZ/) HINZMANN B.
PA (ROSE/) ROSENTHAL A.
PA (HEID/) HEIDEN E.
PA (LICH/) LICHTNER R.
Query Match 4.0%; Score 42.2; DB 14; Length 9057;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 917
ID AAD14986 standard; DNA; 9087 BP.
DE Human NOV7 DNA.
PN WO200161009-A2.
PD 23-AUG-2001.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 42.2; DB 4; Length 9087;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 918
ID ADG42652 standard; cDNA; 9087 BP.
DE Human cDNA encoding NOV7.
PN US2003202971-A1.
PD 30-OCT-2003.
PA (MAJU/) MAJUMDER K.
Query Match 4.0%; Score 42.2; DB 10; Length 9087;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 919
ID ADJ55723 standard; cDNA; 9087 BP.
DE Human NOV6 cDNA SeqID 13.
PN US2003199465-A1.
PD 23-OCT-2003.
PA (MALY/) MALYANKAR U M.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (SPYT/) SPYTEK K A.
PA (GUOX/) GUO X.
PA (SPAD/) SPADERNA S K.
PA (BOLD/) BOLDOG F L.
PA (GERL/) GERLACH V.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 4.0%; Score 42.2; DB 10; Length 9087;

Best Local Similarity 53.3%; Pred. No. 9;
RESULT 920
ID ADH41732 standard; DNA; 9087 BP.
DE Novel human nucleic acid NOV21f.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 42.2; DB 12; Length 9087;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 921
ID ADH41722 standard; DNA; 9087 BP.
DE Novel human nucleic acid NOV21a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 42.2; DB 12; Length 9087;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 922
ID ADH41734 standard; DNA; 9087 BP.
DE Novel human nucleic acid NOV21g.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 42.2; DB 12; Length 9087;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 923
ID ADH41730 standard; DNA; 9087 BP.
DE Novel human nucleic acid NOV21e.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 42.2; DB 12; Length 9087;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 924
ID ADM78804 standard; DNA; 9087 BP.
DE DNA encoding human NOV7.
PN US2003224367-A1.
PD 04-DEC-2003.
PA (MAJU/) MAJUMDER K.
Query Match 4.0%; Score 42.2; DB 12; Length 9087;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 925
ID ADM76559 standard; DNA; 9087 BP.
DE Human NOV7 protein gene sequence SeqID13.
PN WO2004009634-A2.
PD 29-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 42.2; DB 12; Length 9087;
Best Local Similarity 53.3%; Pred. No. 9;
RESULT 926
ID AAS59825 standard; cDNA; 11389 BP.
DE Human novel cytokine encoding cDNA 790CIP2C_4 #1.
PN WO200175093-A1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 42.2; DB 4; Length 11389;
Best Local Similarity 53.3%; Pred. No. 9.6;
RESULT 927
ID ACC49543 standard; cDNA; 11389 BP.
DE Tumour-associated antigenic target protein TAT217 cDNA SEQ ID NO:51.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 42.2; DB 8; Length 11389;
Best Local Similarity 53.3%; Pred. No. 9.6;
RESULT 928
ID ABZ42827 standard; DNA; 11389 BP.
DE Human GPCR CELSR1/Flamingo nucleotide SEQ ID NO:443.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 4.0%; Score 42.2; DB 8; Length 11389;
Best Local Similarity 53.3%; Pred. No. 9.6;
RESULT 929
ID ADN39431 standard; cDNA; 11389 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:A31.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.0%; Score 42.2; DB 11; Length 11389;
Best Local Similarity 53.3%; Pred. No. 9.6;
RESULT 930
ID ADR25604 standard; DNA; 11389 BP.
DE Breast cancer prognosis marker #1465.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 4.0%; Score 42.2; DB 13; Length 11389;
Best Local Similarity 53.3%; Pred. No. 9.6;
RESULT 931
ID ADR43997 standard; DNA; 11389 BP.
DE Human breast tumour associated gene clone-08 SEQ ID NO:7.
PN WO2004074506-A2.
PD 02-SEP-2004.
PA (MERG-) MERGEN LTD.
Query Match 4.0%; Score 42.2; DB 13; Length 11389;
Best Local Similarity 53.3%; Pred. No. 9.6;
RESULT 932
ID ADP22959 standard; cDNA; 11389 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:53.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.0%; Score 42.2; DB 13; Length 11389;
Best Local Similarity 53.3%; Pred. No. 9.6;
RESULT 933
ID ADY85600 standard; DNA; 11389 BP.
DE Human protocadherin flamingo 2 DNA Seq 1.
PN EP1517146-A2.
PD 23-MAR-2005.
PA (HINZ/) HINZMANN B.
PA (ROSE/) ROSENTHAL A.
PA (HEID/) HEIDEN E.
PA (LICH/) LICHTNER R.
Query Match 4.0%; Score 42.2; DB 14; Length 11389;
Best Local Similarity 53.3%; Pred. No. 9.6;
RESULT 934
ID ADJ53165 standard; DNA; 25681 BP.
DE Saccharothrix aerocolonigenes rebeccamycin biosynthetic gene cluster.
PN WO2003033706-A1.
PD 24-APR-2003.
PA (UYOV-) UNIV OVIEDO.
Query Match 4.0%; Score 42.2; DB 10; Length 25681;
Best Local Similarity 44.2%; Pred. No. 12;
RESULT 935
ID AAA02484 standard; cDNA; 1000 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 42; DB 3; Length 1000;
Best Local Similarity 43.3%; Pred. No. 5.7;
RESULT 936
ID ADQ23807 standard; DNA; 1131 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6627.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.0%; Score 42; DB 12; Length 1131;
Best Local Similarity 42.6%; Pred. No. 5.9;
RESULT 937
ID AAI84343 standard; cDNA; 434 BP.
DE Human polynucleotide SEQ ID NO 4403.
PN WO200164835-A2.

PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 41.8; DB 4; Length 434;
Best Local Similarity 38.3%; Pred. No. 5.1;
RESULT 938
ID ACF06113 standard; DNA; 1173 BP.
DE Bacterial P450 enzyme encoding DNA SEQ ID NO:9.
PN WO2003052050-A2.
PD 26-JUN-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 4.0%; Score 41.8; DB 9; Length 1173;
Best Local Similarity 48.9%; Pred. No. 6.6;
RESULT 939
ID ACL68491 standard; DNA; 1194 BP.
DE M. xanthus gene sequence, seq id 4954.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 4.0%; Score 41.8; DB 14; Length 1194;
Best Local Similarity 47.3%; Pred. No. 6.7;
RESULT 940
ID ADU07907 standard; DNA; 1668 BP.
DE DNA sequence #285 encoding amylase.
PN WO2004091544-A2.
PD 28-OCT-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 4.0%; Score 41.8; DB 13; Length 1668;
Best Local Similarity 48.2%; Pred. No. 7.3;
RESULT 941
ID ACL64781 standard; DNA; 27219 BP.
DE M. xanthus DNA fragment, seq id 1244.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 4.0%; Score 41.8; DB 14; Length 27219;
Best Local Similarity 47.3%; Pred. No. 15;
RESULT 942
ID ADQ97180 standard; DNA; 118063 BP.
DE Mouse cancer associated sequence MD08-011, SEQ ID 156.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.0%; Score 41.8; DB 12; Length 118063;
Best Local Similarity 48.2%; Pred. No. 22;
RESULT 943
ID ABQ39038 standard; DNA; 653 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 25629.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 41.6; DB 6; Length 653;
Best Local Similarity 53.0%; Pred. No. 6.4;
RESULT 944
ID ABQ39039 standard; DNA; 653 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 25630.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 41.6; DB 6; Length 653;
Best Local Similarity 53.0%; Pred. No. 6.4;
RESULT 945
ID ACA25714 standard; DNA; 678 BP.
DE Prokaryotic essential gene #7371.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.0%; Score 41.6; DB 8; Length 678;
Best Local Similarity 48.0%; Pred. No. 6.4;
RESULT 946
ID ADC87060 standard; DNA; 3163 BP.
DE Human GPCR gene SEQ ID NO:1513.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 4.0%; Score 41.6; DB 10; Length 3163;
Best Local Similarity 47.2%; Pred. No. 9.6;
RESULT 947
ID ABQ52497 standard; DNA; 600 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 39088.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 41.4; DB 6; Length 600;
Best Local Similarity 50.8%; Pred. No. 6.9;
RESULT 948
ID ABQ52496 standard; DNA; 600 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 39087.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 41.4; DB 6; Length 600;
Best Local Similarity 50.8%; Pred. No. 6.9;
RESULT 949
ID AAH26495 standard; DNA; 12425 BP.
DE Human low density lipoprotein binding protein 2 (LBP-2) gene.
PN WO200164874-A2.
PD 07-SEP-2001.
PA (BOST-) BOSTON HEART FOUND INC.
Query Match 4.0%; Score 41.4; DB 5; Length 12425;
Best Local Similarity 45.1%; Pred. No. 15;
RESULT 950
ID AAS89507 standard; cDNA; 1196 BP.
DE DNA encoding novel human diagnostic protein #25311.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 41.2; DB 5; Length 1196;
Best Local Similarity 49.5%; Pred. No. 9.3;
RESULT 951
ID ADQ86205 standard; cDNA; 2531 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3077.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.9%; Score 41.2; DB 12; Length 2531;
Best Local Similarity 46.8%; Pred. No. 11;
RESULT 952
ID ADQ85045 standard; cDNA; 2531 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1859.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.9%; Score 41.2; DB 13; Length 2531;
Best Local Similarity 46.8%; Pred. No. 11;
RESULT 953
ID AAX21398 standard; DNA; 2538 BP.
DE Central fragment of AbsA operon from S.coelicolor.
PN US5876987-A.
PD 02-MAR-1999.
PA (UNMS) UNIV MICHIGAN STATE.
Query Match 3.9%; Score 41.2; DB 2; Length 2538;
Best Local Similarity 56.7%; Pred. No. 11;
RESULT 954
ID ADO25291 standard; cDNA; 191010 BP.
DE Human protein kinase C zeta I/zeta Ii genomic sequence.
PN WO2004041212-A2.
PD 21-MAY-2004.
PA (SACK/) SACKTOR T C.
PA (CRAR/) CRARY J F.
PA (HERN/) HERNANDEZ A I.
PA (MIRR/) MIRRA S.

PA (SHAO/) SHAO C.
Query Match 3.9%; Score 41.2; DB 12; Length 191010;
Best Local Similarity 53.8%; Pred. No. 34;
RESULT 955
ID ACC79037 standard; cDNA; 1780 BP.
DE Human secreted protein SECP-12 encoding cDNA SEQ ID NO:92.
PN WO2003016506-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.9%; Score 41; DB 10; Length 1780;
Best Local Similarity 56.2%; Pred. No. 11;
RESULT 956
ID ACA27006 standard; DNA; 3040 BP.
DE Prokaryotic essential gene #8663.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.9%; Score 41; DB 8; Length 3040;
Best Local Similarity 44.0%; Pred. No. 13;
RESULT 957
ID ACN44634 standard; DNA; 24525 BP.
DE Human genomic sequence hCG21734.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 41; DB 11; Length 24525;
Best Local Similarity 50.8%; Pred. No. 23;
RESULT 958
ID AAX60503 standard; cDNA; 291 BP.
DE Human persephin protein encoding cDNA.
PN WO9914235-A1.
PD 25-MAR-1999.
PA (UNIW) UNIV WASHINGTON.
Query Match 3.9%; Score 40.8; DB 2; Length 291;
Best Local Similarity 54.7%; Pred. No. 8;
RESULT 959
ID AAX60507 standard; cDNA; 471 BP.
DE Human pre-pro persephin cDNA sequence.
PN WO9914235-A1.
PD 25-MAR-1999.
PA (UNIW) UNIV WASHINGTON.
Query Match 3.9%; Score 40.8; DB 2; Length 471;
Best Local Similarity 54.7%; Pred. No. 9.1;
RESULT 960
ID ADC78862 standard; DNA; 471 BP.
DE Human PRO protein coding sequence #46.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 10; Length 471;
Best Local Similarity 54.7%; Pred. No. 9.1;
RESULT 961
ID AAZ50337 standard; DNA; 556 BP.
DE Human Persephin-ARF complementary DNA.
PN WO200006731-A2.
PD 10-FEB-2000.
PA (UNIW) UNIV WASHINGTON.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 3; Length 556;
Best Local Similarity 54.7%; Pred. No. 9.5;
RESULT 962
ID AAZ50334 standard; DNA; 556 BP.
DE Human Persephin-ARF encoding gene.
PN WO200006731-A2.
PD 10-FEB-2000.
PA (UNIW) UNIV WASHINGTON.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 3; Length 556;
Best Local Similarity 54.7%; Pred. No. 9.5;
RESULT 963
ID ADC76153 standard; DNA; 607 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1422.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.9%; Score 40.8; DB 10; Length 607;
Best Local Similarity 46.5%; Pred. No. 9.7;
RESULT 964
ID ADD17151 standard; DNA; 607 BP.
DE DNA (SeqID 1219) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.9%; Score 40.8; DB 10; Length 607;
Best Local Similarity 46.5%; Pred. No. 9.7;
RESULT 965
ID ADD17811 standard; DNA; 607 BP.
DE DNA (SeqID 1879) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.9%; Score 40.8; DB 10; Length 607;
Best Local Similarity 46.5%; Pred. No. 9.7;
RESULT 966
ID ADK58311 standard; DNA; 607 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #5694.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.9%; Score 40.8; DB 10; Length 607;
Best Local Similarity 46.5%; Pred. No. 9.7;
RESULT 967
ID ADD17814 standard; DNA; 872 BP.
DE DNA (SeqID 1882) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.9%; Score 40.8; DB 10; Length 872;
Best Local Similarity 46.5%; Pred. No. 11;
RESULT 968
ID ADC76149 standard; DNA; 873 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1418.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.9%; Score 40.8; DB 10; Length 873;
Best Local Similarity 46.5%; Pred. No. 11;
RESULT 969
ID ADD17156 standard; DNA; 873 BP.
DE DNA (SeqID 1224) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.9%; Score 40.8; DB 10; Length 873;
Best Local Similarity 46.5%; Pred. No. 11;
RESULT 970
ID ADK58312 standard; DNA; 873 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #5695.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.9%; Score 40.8; DB 10; Length 873;
Best Local Similarity 46.5%; Pred. No. 11;
RESULT 971
ID AAH03553 standard; cDNA; 890 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:388.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.9%; Score 40.8; DB 4; Length 890;

Best Local Similarity 56.8%; Pred. No. 11;
RESULT 972
ID ACL66375 standard; DNA; 1281 BP.
DE M. xanthus gene sequence, seq id 2838.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.9%; Score 40.8; DB 14; Length 1281;
Best Local Similarity 45.6%; Pred. No. 12;
RESULT 973
ID ACN44187 standard; cDNA; 1635 BP.
DE Human mRNA sequence hCT6815.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 40.8; DB 11; Length 1635;
Best Local Similarity 53.4%; Pred. No. 13;
RESULT 974
ID AAH13763 standard; cDNA; 1946 BP.
DE Human cDNA sequence SEQ ID NO:10678.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.9%; Score 40.8; DB 4; Length 1946;
Best Local Similarity 56.8%; Pred. No. 13;
RESULT 975
ID ADA19197 standard; cDNA; 1946 BP.
DE Human insulin resistance marker IRM12 (FLJ10110) cDNA.
PN WO200298355-A2.
PD 12-DEC-2002.
PA (CLIN-) CLINGENIX INC.
Query Match 3.9%; Score 40.8; DB 10; Length 1946;
Best Local Similarity 56.8%; Pred. No. 13;
RESULT 976
ID ACF34490 standard; DNA; 2528 BP.
DE Gene encoding angiogenesis protein BNO111.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match 3.9%; Score 40.8; DB 8; Length 2528;
Best Local Similarity 53.4%; Pred. No. 14;
RESULT 977
ID ADO19177 standard; cDNA; 2528 BP.
DE Human PRO polynucleotide #56.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 12; Length 2528;
Best Local Similarity 53.4%; Pred. No. 14;
RESULT 978
ID ADO19173 standard; cDNA; 2528 BP.
DE Human PRO polynucleotide #54.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 12; Length 2528;
Best Local Similarity 53.4%; Pred. No. 14;
RESULT 979
ID ADP54220 standard; cDNA; 2528 BP.
DE Human PRO cDNA sequence SEQ ID NO:196.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 13; Length 2528;
Best Local Similarity 53.4%; Pred. No. 14;
RESULT 980
ID ADX05927 standard; DNA; 2528 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 492.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 3.9%; Score 40.8; DB 14; Length 2528;
Best Local Similarity 53.4%; Pred. No. 14;
RESULT 981
ID ADY14501 standard; DNA; 2528 BP.
DE DNA encoding a PRO polypeptide, SEQ ID NO 307.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 14; Length 2528;
Best Local Similarity 53.4%; Pred. No. 14;
RESULT 982
ID ADY14497 standard; DNA; 2528 BP.
DE DNA encoding a PRO polypeptide, SEQ ID NO 303.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 14; Length 2528;
Best Local Similarity 53.4%; Pred. No. 14;
RESULT 983
ID AAL62474 standard; DNA; 2943 BP.
DE Human glutamate receptor subunit DNA.
PN WO2003051180-A2.
PD 26-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.9%; Score 40.8; DB 9; Length 2943;
Best Local Similarity 51.7%; Pred. No. 15;
RESULT 984
ID ACC72655 standard; cDNA; 2943 BP.
DE Human glutamate receptor subunit encoding cDNA.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 3.9%; Score 40.8; DB 10; Length 2943;
Best Local Similarity 51.7%; Pred. No. 15;
RESULT 985
ID AAQ36930 standard; DNA; 3694 BP.
DE Human KA-2 receptor gene.
PN EP529995-A1.
PD 03-MAR-1993.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 3.9%; Score 40.8; DB 2; Length 3694;
Best Local Similarity 51.7%; Pred. No. 15;
RESULT 986
ID ADF14506 standard; DNA; 4707 BP.
DE Human endometrial-specific DNA - SEQ ID 471.
PN WO2003059927-A1.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 3.9%; Score 40.8; DB 10; Length 4707;
Best Local Similarity 53.4%; Pred. No. 16;
RESULT 987
ID ADP54222 standard; cDNA; 5458 BP.
DE Human PRO cDNA sequence SEQ ID NO:198.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 13; Length 5458;
Best Local Similarity 53.4%; Pred. No. 17;
RESULT 988
ID ADO19175 standard; cDNA; 5533 BP.
DE Human PRO polynucleotide #55.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 12; Length 5533;
Best Local Similarity 53.4%; Pred. No. 17;
RESULT 989
ID ADY14499 standard; DNA; 5533 BP.
DE DNA encoding a PRO polypeptide, SEQ ID NO 305.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.8; DB 14; Length 5533;
Best Local Similarity 53.4%; Pred. No. 17;
RESULT 990

ID ACL64673 standard; DNA; 16047 BP.
DE M. xanthus DNA fragment, seq id 1136.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.9%; Score 40.8; DB 14; Length 16047;
Best Local Similarity 45.6%; Pred. No. 23;
RESULT 991
ID ACN44186 standard; DNA; 22147 BP.
DE Human genomic sequence hCG15786.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 40.8; DB 11; Length 22147;
Best Local Similarity 53.4%; Pred. No. 25;
RESULT 992
ID ADW38519 standard; cDNA; 37476 BP.
DE Immunomodulatory gene CAB56184 cDNA.
PN WO2005000099-A2.
PD 06-JAN-2005.
PA (GENZ) GENZYME CORP.
Query Match 3.9%; Score 40.8; DB 14; Length 37476;
Best Local Similarity 54.7%; Pred. No. 28;
RESULT 993
Query Match 3.9%; Score 40.8; DB 12; Length 55211;
Best Local Similarity 53.4%; Pred. No. 31;
RESULT 994
ID ACH91936 standard; DNA; 1015 BP.
DE Human genome derived single exon probe #25131.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 3.9%; Score 40.6; DB 12; Length 1015;
Best Local Similarity 53.5%; Pred. No. 12;
RESULT 995
ID ABX70475 standard; DNA; 1026 BP.
DE DNA encoding human GPCR related protein NOV34a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 3.9%; Score 40.6; DB 8; Length 1026;
Best Local Similarity 53.5%; Pred. No. 12;
RESULT 996
ID ABX70476 standard; DNA; 1026 BP.
DE DNA encoding human GPCR related protein NOV34b.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 3.9%; Score 40.6; DB 8; Length 1026;
Best Local Similarity 53.5%; Pred. No. 12;
RESULT 997
ID ADL24102 standard; cDNA; 1026 BP.
DE Human NOVX cDNA #74.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 3.9%; Score 40.6; DB 12; Length 1026;
Best Local Similarity 53.5%; Pred. No. 12;
RESULT 998
ID ADL24104 standard; cDNA; 1026 BP.
DE Human NOVX cDNA #75.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 3.9%; Score 40.6; DB 12; Length 1026;
Best Local Similarity 53.5%; Pred. No. 12;
RESULT 999
ID ACH87203 standard; DNA; 1026 BP.
DE Human genome derived single exon probe #20398.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 3.9%; Score 40.6; DB 12; Length 1026;
Best Local Similarity 53.5%; Pred. No. 12;
RESULT 1000
ID ADC30226 standard; cDNA; 1083 BP.
DE Human novel cDNA sequence, SEQ ID NO:308.
PN WO2003029271-A2.

PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 40.6; DB 10; Length 1083;
Best Local Similarity 53.5%; Pred. No. 13;
RESULT 1001
ID AAS78194 standard; cDNA; 1117 BP.
DE DNA encoding novel human diagnostic protein #13998.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 40.6; DB 5; Length 1117;
Best Local Similarity 53.5%; Pred. No. 13;
RESULT 1002
ID ADC32130 standard; cDNA; 1117 BP.
DE Human novel cDNA contig sequence, SEQ ID NO:2212.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 40.6; DB 10; Length 1117;
Best Local Similarity 53.5%; Pred. No. 13;
RESULT 1003
ID ADJ40432 standard; cDNA; 1215 BP.
DE Plant cDNA #1432.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 3.9%; Score 40.6; DB 12; Length 1215;
Best Local Similarity 49.0%; Pred. No. 13;
RESULT 1004
ID ADT19216 standard; cDNA; 1786 BP.
DE Plant cDNA, Seq ID 4542.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 3.9%; Score 40.6; DB 13; Length 1786;
Best Local Similarity 44.0%; Pred. No. 14;
RESULT 1005
ID ADI31739 standard; cDNA; 2941 BP.
DE Human cDNA #1065.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.9%; Score 40.6; DB 11; Length 2941;
Best Local Similarity 44.6%; Pred. No. 16;
RESULT 1006
ID ADS83806 standard; cDNA; 2941 BP.
DE Human lymph node cDNA #1065.
PN US2004077003-A1.
PD 22-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.9%; Score 40.6; DB 13; Length 2941;
Best Local Similarity 44.6%; Pred. No. 16;
RESULT 1007
ID ADQ63624 standard; cDNA; 2954 BP.
DE Novel human cDNA sequence #785.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.9%; Score 40.6; DB 12; Length 2954;
Best Local Similarity 53.5%; Pred. No. 16;
RESULT 1008
ID ADP44618 standard; DNA; 4349 BP.
DE Human dentatorubral-pallidoluysian atrophy (DRPLA;atrophin-1) DNA.
PN WO2004047872-A2.
PD 10-JUN-2004.
PA (MEDT) MEDTRONIC INC.
Query Match 3.9%; Score 40.6; DB 12; Length 4349;
Best Local Similarity 50.3%; Pred. No. 18;
RESULT 1009
ID ADQ84487 standard; cDNA; 4349 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1301.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.9%; Score 40.6; DB 12; Length 4349;
Best Local Similarity 50.3%; Pred. No. 18;
RESULT 1010
ID ADQ85295 standard; cDNA; 4349 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2109.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.9%; Score 40.6; DB 12; Length 4349;
Best Local Similarity 50.3%; Pred. No. 18;
RESULT 1011
ID ACN39362 standard; cDNA; 4349 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325594, SEQ ID NO:3457.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.6; DB 13; Length 4349;
Best Local Similarity 50.3%; Pred. No. 18;
RESULT 1012
ID ADQ84687 standard; cDNA; 4408 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1501.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.9%; Score 40.6; DB 12; Length 4408;
Best Local Similarity 44.6%; Pred. No. 18;
RESULT 1013
ID ADQ85603 standard; cDNA; 4408 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2417.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.9%; Score 40.6; DB 12; Length 4408;
Best Local Similarity 44.6%; Pred. No. 18;
RESULT 1014
ID ADQ86704 standard; cDNA; 4408 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3579.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.9%; Score 40.6; DB 13; Length 4408;
Best Local Similarity 44.6%; Pred. No. 18;
RESULT 1015
ID ADQ83458 standard; cDNA; 4408 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #272.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.9%; Score 40.6; DB 13; Length 4408;
Best Local Similarity 44.6%; Pred. No. 18;

RESULT 1016
ID ACN40386 standard; cDNA; 4408 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326503, SEQ ID NO:5132.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 40.6; DB 13; Length 4408;
Best Local Similarity 44.6%; Pred. No. 18;
RESULT 1017
ID ADX98574 standard; DNA; 95050 BP.
DE Human LOC145197 genomic DNA.
Query Match 3.9%; Score 40.6; DB 14; Length 95050;
Best Local Similarity 48.9%; Pred. No. 40;
RESULT 1018
ID ABK84349 standard; cDNA; 222930 BP.
DE Human cDNA differentially expressed in granulocytic cells #920.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.9%; Score 40.6; DB 6; Length 222930;
Best Local Similarity 50.3%; Pred. No. 50;
RESULT 1019
ID ADP75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.9%; Score 40.6; DB 11; Length 304905;
Best Local Similarity 54.3%; Pred. No. 54;
RESULT 1020
ID AAA59151 standard; cDNA; 403 BP.
DE cDNA encoding a human interleukin-175 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 3.9%; Score 40.4; DB 3; Length 403;
Best Local Similarity 59.6%; Pred. No. 11;
RESULT 1021
ID AAA59150 standard; cDNA; 403 BP.
DE cDNA encoding a human interleukin-175 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 3.9%; Score 40.4; DB 3; Length 403;
Best Local Similarity 59.6%; Pred. No. 11;
RESULT 1022
ID AAA58992 standard; cDNA; 403 BP.
DE cDNA encoding a human interleukin (IL) 175 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 3.9%; Score 40.4; DB 3; Length 403;
Best Local Similarity 59.6%; Pred. No. 11;
RESULT 1023
ID AAA58993 standard; cDNA; 403 BP.
DE cDNA encoding a human interleukin (IL) 175 polypeptide.
PN WO200042188-A2.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 3.9%; Score 40.4; DB 3; Length 403;
Best Local Similarity 59.6%; Pred. No. 11;
RESULT 1024
ID ADB32011 standard; cDNA; 403 BP.
DE Human partial cDNA encoding interleukin 175, IL-175.
PN US6562578-B1.
PD 13-MAY-2003.
PA (SCHE) SCHERING CORP.
Query Match 3.9%; Score 40.4; DB 10; Length 403;
Best Local Similarity 59.6%; Pred. No. 11;
RESULT 1025
ID ADR13815 standard; cDNA; 403 BP.
DE Human interleukin-175 (IL-175) cDNA #2.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 3.9%; Score 40.4; DB 12; Length 403;
Best Local Similarity 59.6%; Pred. No. 11;
RESULT 1026
ID ADR13814 standard; cDNA; 403 BP.
DE Human interleukin-175 (IL-175) cDNA #1.
PN US2004122221-A1.
PD 24-JUN-2004.
PA (SCHE) SCHERING CORP.
Query Match 3.9%; Score 40.4; DB 12; Length 403;
Best Local Similarity 59.6%; Pred. No. 11;
RESULT 1027
ID AEA27152 standard; DNA; 888 BP.
DE Stress tolerant plant-related transcription factor gene SeqID993.
PN WO2005047516-A2.
PD 26-MAY-2005.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 3.9%; Score 40.4; DB 14; Length 888;
Best Local Similarity 49.1%; Pred. No. 13;
RESULT 1028
ID ACL67726 standard; DNA; 1083 BP.
DE M. xanthus gene sequence, seq id 4189.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.9%; Score 40.4; DB 14; Length 1083;
Best Local Similarity 42.6%; Pred. No. 14;
RESULT 1029
ID ABT08122 standard; DNA; 1168 BP.
DE Myb-related transcription factor DNA SEQ ID No 23.
PN US2002066120-A1.
PD 30-MAY-2002.
PA (CAHO/) CAHOON R E.
PA (LIUZ/) LIU Z.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (SHIJ/) SHI J.
PA (WENG/) WENG Z.
Query Match 3.9%; Score 40.4; DB 6; Length 1168;
Best Local Similarity 49.1%; Pred. No. 14;
RESULT 1030
ID ADH50119 standard; DNA; 1168 BP.
DE Rice Myb-related transcription factor coding sequence #2.
PN US2002187539-A1.
PD 12-DEC-2002.
PA (CAHO/) CAHOON R E.
PA (WENG/) WENG Z.
Query Match 3.9%; Score 40.4; DB 12; Length 1168;
Best Local Similarity 49.1%; Pred. No. 14;
RESULT 1031
ID ADI42591 standard; DNA; 1200 BP.
DE Plant transcription factor polynucleotide #680.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 3.9%; Score 40.4; DB 12; Length 1200;
Best Local Similarity 49.1%; Pred. No. 14;
RESULT 1032

ID ADO02892 standard; cDNA; 1200 BP.
DE Rice orthologue of Thalecress transcription factor, cDNA #47.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 3.9%; Score 40.4; DB 12; Length 1200;
Best Local Similarity 49.1%; Pred. No. 14;
RESULT 1033
ID ADG33863 standard; DNA; 1392 BP.
DE Actinomycetes dual condensation/epimerisation NRPS domain DNA ID 122.
PN WO2003089641-A2.
PD 30-OCT-2003.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 3.9%; Score 40.4; DB 10; Length 1392;
Best Local Similarity 45.5%; Pred. No. 15;
RESULT 1034
ID ADT16394 standard; cDNA; 1767 BP.
DE Plant cDNA, Seq ID 1720.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 3.9%; Score 40.4; DB 13; Length 1767;
Best Local Similarity 50.0%; Pred. No. 16;
RESULT 1035
ID ABI99476 standard; cDNA; 1907 BP.
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:433.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 3.9%; Score 40.4; DB 6; Length 1907;
Best Local Similarity 53.3%; Pred. No. 16;
RESULT 1036
ID AAL44297 standard; DNA; 8651 BP.
DE Agromyces mediolanus Y1 operon (C50 carotenoid producing operon).
PN WO200241833-A2.
PD 30-MAY-2002.
PA (CRGI) CARGILL INC.
Query Match 3.9%; Score 40.4; DB 6; Length 8651;
Best Local Similarity 47.8%; Pred. No. 24;
RESULT 1037
ID ACL64745 standard; DNA; 22301 BP.
DE M. xanthus DNA fragment, seq id 1208.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.9%; Score 40.4; DB 14; Length 22301;
Best Local Similarity 42.6%; Pred. No. 31;
RESULT 1038
ID ADS55949 standard; cDNA; 855 BP.
DE Bacterial polynucleotide #7936.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.8%; Score 40.2; DB 13; Length 855;
Best Local Similarity 44.6%; Pred. No. 15;
RESULT 1039
ID ADU01860 standard; cDNA; 876 BP.
DE Novel human polynucleotide seqid 327.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 3.8%; Score 40.2; DB 13; Length 876;
Best Local Similarity 53.5%; Pred. No. 15;
RESULT 1040
ID ACL34805 standard; cDNA; 1023 BP.
DE Rice abiotic stress response related polynucleotide SEQ ID NO:13368.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.8%; Score 40.2; DB 11; Length 1023;
Best Local Similarity 47.4%; Pred. No. 15;
RESULT 1041
ID ADC86688 standard; DNA; 1117 BP.
DE Human GPCR gene SEQ ID NO:1141.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.8%; Score 40.2; DB 10; Length 1117;
Best Local Similarity 42.2%; Pred. No. 16;
RESULT 1042
ID ABZ20967 standard; DNA; 1416 BP.
DE Animal test kit marker DNA 127-sp6.
PN DE20206477-U1.
PD 10-OCT-2002.
PA (GAGB-) GAG BIOSCIENCE GMBH.
Query Match 3.8%; Score 40.2; DB 8; Length 1416;
Best Local Similarity 50.8%; Pred. No. 17;
RESULT 1043
ID ABZ37535 standard; DNA; 1431 BP.
DE Streptomyces viridochromogenes AviJ encoding polynucleotide.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 3.8%; Score 40.2; DB 8; Length 1431;
Best Local Similarity 48.1%; Pred. No. 17;
RESULT 1044
ID AAZ77506 standard; cDNA; 2188 BP.
DE Human ovarian tumor cDNA library derived EST fragment 57.
PN DE19817557-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 3.8%; Score 40.2; DB 2; Length 2188;
Best Local Similarity 49.8%; Pred. No. 19;
RESULT 1045
ID ABK83742 standard; cDNA; 2685 BP.
DE Human cDNA differentially expressed in granulocytic cells #313.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.8%; Score 40.2; DB 6; Length 2685;
Best Local Similarity 48.1%; Pred. No. 20;
RESULT 1046
ID ABZ37516 standard; DNA; 59816 BP.
DE Streptomyces viridochromogenes Avi gene cluster sense strand.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 3.8%; Score 40.2; DB 8; Length 59816;
Best Local Similarity 48.1%; Pred. No. 44;
RESULT 1047
ID ABZ37515 standard; DNA; 59816 BP.
DE Streptomyces viridochromogenes Avi gene cluster sense strand.
PN WO200268436-A1.
PD 06-SEP-2002.

PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 3.8%; Score 40.2; DB 8; Length 59816;
Best Local Similarity 48.1%; Pred. No. 44;
RESULT 1048
ID AAZ29734 standard; DNA; 40 BP.
DE Hybridisation probe used for isolation of human PRO1122 cDNA.
PN WO9960127-A2.
PD 25-NOV-1999.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1049
ID AAA96309 standard; DNA; 40 BP.
DE Probe for cDNA encoding novel polypeptide PRO1122.
PN WO200056889-A2.
PD 28-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1050
ID AAS09520 standard; DNA; 40 BP.
DE Human IL-17C hybridisation probe.
PN WO200146420-A2.
PD 28-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1051
ID ACD28804 standard; DNA; 40 BP.
DE Human secreted / transmembrane polypeptide PRO1122 probe.
PN US2003027249-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1052
ID ACA06078 standard; DNA; 40 BP.
DE Hybridisation probe #2 for DNA encoding human PRO polypeptide.
PN US2003008348-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1053
ID ACA89861 standard; DNA; 40 BP.
DE Human interleukin 17 homologue h-IL17-B/PRO1031 probe.
PN US2003003546-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1054
ID ACA64645 standard; DNA; 40 BP.
DE Human IL-17 family member, PRO1122/h-IL17C, probe.
PN US2003008815-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1055
ID ACA67701 standard; DNA; 40 BP.
DE Human secreted polypeptide PRO1122 probe.
PN US2002192751-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1056
ID ADA76539 standard; DNA; 40 BP.
DE Secreted and transmembrane protein related probe #2.
PN US2003036114-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1057
ID ADA43244 standard; DNA; 40 BP.
DE Human interleukin 17 related mammalian cytokine probe #1.
PN US6579520-B2.
PD 17-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1058
ID ACD42263 standard; DNA; 40 BP.
DE Human secreted/transmembrane protein PRO1122 probe.
PN US2003044842-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1059
ID ADA49785 standard; DNA; 40 BP.
DE Human interleukin-17/interleukin-17 receptor homologue probe #1.
PN US2002177188-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1060
ID ADA26978 standard; DNA; 40 BP.
DE Human PRO polypeptide associated hybridisation probe #1.
PN US2002182673-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1061
ID ADB66912 standard; DNA; 40 BP.
DE Human PRO DNA probe #1.
PN US2003054442-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1062
ID AAD59329 standard; DNA; 40 BP.
DE Hybridisation probe to isolate human PRO1122 cDNA.
PN US2003049733-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1063
ID AAD59205 standard; DNA; 40 BP.
DE Hybridisation probe used to isolate human PRO1122 cDNA.
PN US2003049734-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1064
ID ADC29770 standard; DNA; 40 BP.
DE Human secreted and transmembrane protein related probe seq id 14.
PN US2003092063-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1065
ID AAD63618 standard; DNA; 40 BP.
DE Human IL-17C ligand (PRO1122) cDNA clone specific probe.
PN US2003199044-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 10; Length 40;

Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1066
ID ADG87396 standard; DNA; 40 BP.
DE Hybridisation probe used to isolate human PRO1122 cDNA clone.
PN US2003180255-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1067
ID ACA06135 standard; DNA; 40 BP.
DE Hybridisation probe #2 for DNA encoding human PRO polypeptide.
PN US2003032061-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1068
ID ADL16692 standard; DNA; 40 BP.
DE Hybridisation probe used to isolate human PRO1122 cDNA.
PN US2003186306-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1069
ID ADF09213 standard; DNA; 40 BP.
DE Secreted and transmembrane protein PRO1122 probe seqid 14.
PN US2003134327-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 12; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1070
ID ADL16653 standard; DNA; 40 BP.
DE Hybridisation probe used to isolate human PRO1122 cDNA.
PN US2003203451-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 12; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1071
ID ADL71313 standard; DNA; 40 BP.
DE Human IL-17C (PRO1122) cDNA amplifying PCR probe.
PN US2004043397-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 40; DB 12; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1072
ID ADW12445 standard; DNA; 40 BP.
DE Human PRO1122 cDNA isolating hybridization probe.
PN US2004265966-A1.
PD 30-DEC-2004.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (PANJ/) PAN J.
PA (STEW/) STEWART T A.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 3.8%; Score 40; DB 14; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 1073
ID ADG33843 standard; DNA; 1389 BP.
DE Actinomycetes dual condensation/epimerisation NRPS domain DNA ID 102.
PN WO2003089641-A2.
PD 30-OCT-2003.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 3.8%; Score 40; DB 10; Length 1389;
Best Local Similarity 43.7%; Pred. No. 19;
RESULT 1074
ID ADL61802 standard; DNA; 1888 BP.
DE Human ovarian cancer DNA marker #20014.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.8%; Score 40; DB 5; Length 1888;
Best Local Similarity 47.9%; Pred. No. 20;
RESULT 1075
ID AAN92408 standard; DNA; 2061 BP.
DE Sequence encoding pseudorabies virus (PRV) glycoprotein gH.
PN WO8910965-A.
PD 16-NOV-1989.
PA (UPJO) UPJOHN CO.
Query Match 3.8%; Score 40; DB 1; Length 2061;
Best Local Similarity 45.1%; Pred. No. 21;
RESULT 1076
ID ADL45203 standard; DNA; 2344 BP.
DE Human ovarian cancer DNA marker #19093.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.8%; Score 40; DB 5; Length 2344;
Best Local Similarity 47.2%; Pred. No. 21;
RESULT 1077
ID ADE52577 standard; DNA; 4545 BP.
DE Human SQV DNA sequence #3.
PN WO2003062448-A2.
PD 31-JUL-2003.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 3.8%; Score 40; DB 10; Length 4545;
Best Local Similarity 50.0%; Pred. No. 25;
RESULT 1078
ID ABD33445 standard; cDNA; 4545 BP.
DE Human cancer-associated (CA) cDNA HR07-084.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.8%; Score 40; DB 13; Length 4545;
Best Local Similarity 50.0%; Pred. No. 25;
RESULT 1079
ID ADC86736 standard; DNA; 5452 BP.
DE Human GPCR gene SEQ ID NO:1189.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.8%; Score 40; DB 10; Length 5452;
Best Local Similarity 28.7%; Pred. No. 26;
RESULT 1080
ID ADP64454 standard; DNA; 76994 BP.
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.
PN WO2004053065-A2.
PD 24-JUN-2004.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 3.8%; Score 40; DB 12; Length 76994;
Best Local Similarity 42.8%; Pred. No. 52;
RESULT 1081
ID AAA14651 standard; DNA; 77536 BP.
DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.
Query Match 3.8%; Score 40; DB 3; Length 77536;
Best Local Similarity 57.0%; Pred. No. 53;
RESULT 1082
ID ABD33444 standard; DNA; 95914 BP.
DE Human cancer-associated (CA) gene HD07-084.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.8%; Score 40; DB 13; Length 95914;
Best Local Similarity 50.0%; Pred. No. 56;
RESULT 1083
ID AAD54645 standard; DNA; 113193 BP.

DE Streptomyces nodosus amphotericin (amph) biosynthetic gene cluster.
PN WO200297082-A2.
PD 05-DEC-2002.
PA (UYDU-) UNIV COLLEGE DUBLIN.
Query Match 3.8%; Score 40; DB 8; Length 113193;
Best Local Similarity 44.6%; Pred. No. 58;
RESULT 1084
ID AAI82007 standard; cDNA; 344 BP.
DE Human polynucleotide SEQ ID NO 2067.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.8%; Score 39.8; DB 4; Length 344;
Best Local Similarity 46.6%; Pred. No. 14;
RESULT 1085
ID ACL67591 standard; DNA; 954 BP.
DE M. xanthus gene sequence, seq id 4054.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.8%; Score 39.8; DB 14; Length 954;
Best Local Similarity 49.3%; Pred. No. 19;
RESULT 1086
ID ACL69645 standard; DNA; 1515 BP.
DE M. xanthus gene sequence, seq id 6108.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.8%; Score 39.8; DB 14; Length 1515;
Best Local Similarity 45.0%; Pred. No. 21;
RESULT 1087
ID ACL63816 standard; DNA; 1519 BP.
DE M. xanthus DNA fragment, seq id 279.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.8%; Score 39.8; DB 14; Length 1519;
Best Local Similarity 45.0%; Pred. No. 21;
RESULT 1088
ID ACL72611 standard; DNA; 1640 BP.
DE M. xanthus gene sequence, seq id 9074.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.8%; Score 39.8; DB 14; Length 1640;
Best Local Similarity 47.4%; Pred. No. 22;
RESULT 1089
ID ADX53487 standard; cDNA; 1754 BP.
DE Plant full length insert polynucleotide seqid 28227.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.8%; Score 39.8; DB 13; Length 1754;
Best Local Similarity 49.8%; Pred. No. 22;
RESULT 1090
ID ACL64507 standard; DNA; 8180 BP.
DE M. xanthus DNA fragment, seq id 970.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.8%; Score 39.8; DB 14; Length 8180;
Best Local Similarity 47.4%; Pred. No. 33;
RESULT 1091
ID ACL64562 standard; DNA; 10871 BP.
DE M. xanthus DNA fragment, seq id 1025.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.8%; Score 39.8; DB 14; Length 10871;
Best Local Similarity 49.3%; Pred. No. 35;
RESULT 1092
ID AAA38186 standard; DNA; 320 BP.
DE Primer used in the analysis of a BVDV genome fragment.
PN WO200020628-A1.
PD 13-APR-2000.
PA (BIOI-) BIO-ID DIAGNOSTIC INC.
Query Match 3.8%; Score 39.6; DB 3; Length 320;
Best Local Similarity 50.0%; Pred. No. 16;
RESULT 1093
ID ACN39130 standard; cDNA; 2425 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325388, SEQ ID NO:3078.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 39.6; DB 13; Length 2425;
Best Local Similarity 61.8%; Pred. No. 27;
RESULT 1094
ID ADH61319 standard; DNA; 4284 BP.
DE INTSIG encoding DNA 3010745CB1, SEQ ID 36.
PN WO2004001005-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.8%; Score 39.6; DB 12; Length 4284;
Best Local Similarity 61.8%; Pred. No. 31;
RESULT 1095
ID ADL61887 standard; DNA; 5165 BP.
DE Human ovarian cancer DNA marker #20099.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.8%; Score 39.6; DB 5; Length 5165;
Best Local Similarity 56.0%; Pred. No. 33;
RESULT 1096
ID AAA92058 standard; DNA; 8867 BP.
DE Human Lhx3 genomic DNA SEQ ID NO:22.
PN WO200050868-A2.
PD 31-AUG-2000.
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
Query Match 3.8%; Score 39.6; DB 3; Length 8867;
Best Local Similarity 49.1%; Pred. No. 37;
RESULT 1097
ID AAA14651 standard; DNA; 77536 BP.
DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.
Query Match 3.8%; Score 39.6; DB 3; Length 77536;
Best Local Similarity 46.4%; Pred. No. 66;
RESULT 1098
ID ACN61884 standard; cDNA; 263 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-022-Q6-N6-C3, SEQ:16665.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.8%; Score 39.4; DB 13; Length 263;
Best Local Similarity 50.8%; Pred. No. 17;
RESULT 1099
ID AAS93559 standard; cDNA; 1355 BP.
DE DNA encoding novel human diagnostic protein #29363.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.8%; Score 39.4; DB 5; Length 1355;
Best Local Similarity 56.2%; Pred. No. 26;
RESULT 1100
ID ADU40516 standard; cDNA; 1355 BP.
DE Novel human polynucleotide seq id 301.
PN US2004219521-A1.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.

PA (WENG/) WENG G.
PA (BOYL/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Query Match 3.8%; Score 39.4; DB 14; Length 1355;
Best Local Similarity 56.2%; Pred. No. 26;
RESULT 1101
ID AAH26499 standard; DNA; 1614 BP.
DE Human low density lipoprotein binding protein 2 (LBP-2) DNA.
PN WO200164874-A2.
PD 07-SEP-2001.
PA (BOST-) BOSTON HEART FOUND INC.
Query Match 3.8%; Score 39.4; DB 5; Length 1614;
Best Local Similarity 45.6%; Pred. No. 27;
RESULT 1102
ID ADX61936 standard; cDNA; 1746 BP.
DE Plant full length insert polynucleotide seqid 32779.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.8%; Score 39.4; DB 13; Length 1746;
Best Local Similarity 42.5%; Pred. No. 27;
RESULT 1103
ID ABK28670 standard; cDNA; 2085 BP.
DE Human cDNA encoding secreted potein SECP37.
PN WO200198353-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.8%; Score 39.4; DB 6; Length 2085;
Best Local Similarity 49.8%; Pred. No. 29;
RESULT 1104
ID ADA53215 standard; cDNA; 2142 BP.
DE Human coding sequence, SEQ ID 783.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.8%; Score 39.4; DB 10; Length 2142;
Best Local Similarity 49.8%; Pred. No. 29;
RESULT 1105
ID ABN59916 standard; cDNA; 2258 BP.
DE Novel human coding sequence SEQ ID NO: 327.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 3.8%; Score 39.4; DB 6; Length 2258;
Best Local Similarity 49.8%; Pred. No. 29;
RESULT 1106
ID AEB11880 standard; cDNA; 3260 BP.
DE Testis specific-protein Y-like protein 457_458insG polynucleotide.
PN WO2005056838-A1.
PD 23-JUN-2005.
PA (CLIN-) CLINIC FOR SPECIAL CHILDREN.
Query Match 3.8%; Score 39.4; DB 14; Length 3260;
Best Local Similarity 52.1%; Pred. No. 32;
RESULT 1107
ID ADN05853 standard; cDNA; 5128 BP.
DE Antipsoriatic cDNA sequence #1158.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.8%; Score 39.4; DB 12; Length 5128;
Best Local Similarity 51.6%; Pred. No. 36;
RESULT 1108
ID ADR83539 standard; DNA; 5128 BP.
DE Human Yes-associated protien 1 DNA, target gene of miRNA.
PN WO2004076622-A2.
PD 10-SEP-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 3.8%; Score 39.4; DB 13; Length 5128;
Best Local Similarity 51.6%; Pred. No. 36;
RESULT 1109
ID AAT30347 standard; cDNA; 5153 BP.
DE Human YAP cDNA.
PN WO9617061-A1.
PD 06-JUN-1996.
PA (UYRQ) UNIV ROCKEFELLER.
PA (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.
Query Match 3.8%; Score 39.4; DB 2; Length 5153;
Best Local Similarity 51.6%; Pred. No. 36;
RESULT 1110
ID ADD14716 standard; cDNA; 5153 BP.
DE Human src biomarker polynucleotide SEQ ID NO:110.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 3.8%; Score 39.4; DB 10; Length 5153;
Best Local Similarity 51.6%; Pred. No. 36;
RESULT 1111
ID AAK66243 standard; DNA; 5541 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21055.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 39.4; DB 4; Length 5541;
Best Local Similarity 49.8%; Pred. No. 37;
RESULT 1112
ID ADZ13116 standard; DNA; 241748 BP.
DE Murine cancer-associated genomic DNA #54.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.8%; Score 39.4; DB 14; Length 241748;
Best Local Similarity 52.1%; Pred. No. 98;
RESULT 1113
ID ABT10409 standard; cDNA; 451 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 543.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.7%; Score 39.2; DB 6; Length 451;
Best Local Similarity 44.1%; Pred. No. 22;
RESULT 1114
ID ACN59482 standard; cDNA; 566 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-031-Q6-N6-F6, SEQ:14263.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.7%; Score 39.2; DB 13; Length 566;
Best Local Similarity 46.7%; Pred. No. 23;
RESULT 1115
ID AAD19588 standard; cDNA; 704 BP.
DE Human Lung cancer Specific Gene (LSG) cDNA #5.
PN WO200172775-A2.
PD 04-OCT-2001.
PA (DIAD-) DIADEXUS INC.
Query Match 3.7%; Score 39.2; DB 4; Length 704;
Best Local Similarity 51.1%; Pred. No. 24;
RESULT 1116
ID ACA37817 standard; DNA; 2145 BP.
DE Prokaryotic essential gene #19474.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.7%; Score 39.2; DB 8; Length 2145;
Best Local Similarity 49.5%; Pred. No. 32;
RESULT 1117
ID ADC03387 standard; DNA; 2238 BP.
DE Rice flowering time-related gene #14.

PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.7%; Score 39.2; DB 10; Length 2238;
Best Local Similarity 49.0%; Pred. No. 33;
RESULT 1118
ID ACL28646 standard; cDNA; 2238 BP.
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:2602.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.7%; Score 39.2; DB 11; Length 2238;
Best Local Similarity 49.0%; Pred. No. 33;
RESULT 1119
ID ABZ20368 standard; cDNA; 2365 BP.
DE Oncofoetal cDNA sequence overexpressed in tumour tissue SEQ ID NO:2795.
PN WO200278516-A2.
PD 10-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.7%; Score 39.2; DB 8; Length 2365;
Best Local Similarity 46.0%; Pred. No. 33;
RESULT 1120
ID AAS67720 standard; cDNA; 2701 BP.
DE DNA encoding novel human diagnostic protein #3524.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.7%; Score 39.2; DB 5; Length 2701;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 1121
ID AAA95944 standard; DNA; 11820 BP.
DE Human KLK-L5 gene.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 3.7%; Score 39.2; DB 3; Length 11820;
Best Local Similarity 45.1%; Pred. No. 50;
RESULT 1122
ID ADN10929 standard; DNA; 11820 BP.
DE Human kallikrein 12 gene, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 3.7%; Score 39.2; DB 12; Length 11820;
Best Local Similarity 45.1%; Pred. No. 50;
RESULT 1123
ID ACL29290 standard; cDNA; 360 BP.
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:3246.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.7%; Score 39; DB 11; Length 360;
Best Local Similarity 46.8%; Pred. No. 23;
RESULT 1124
ID ACF90965 standard; DNA; 418 BP.
DE Human SIRS/sepsis diagnostic marker DNA fragment 9825.
PN WO2004087949-A2.
PD 14-OCT-2004.
PA (SIRS-) SIRS LAB GMBH.
Query Match 3.7%; Score 39; DB 13; Length 418;
Best Local Similarity 48.4%; Pred. No. 24;
RESULT 1125
ID ABI99656 standard; cDNA; 1286 BP.
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:686.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 3.7%; Score 39; DB 6; Length 1286;
Best Local Similarity 48.4%; Pred. No. 32;
RESULT 1126
ID AAS59858 standard; cDNA; 1349 BP.
DE Human novel cytokine encoding cDNA 790CIP2A_12 #2.
PN WO200175093-A1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.7%; Score 39; DB 4; Length 1349;
Best Local Similarity 61.2%; Pred. No. 32;
RESULT 1127
ID AAQ13670 standard; cDNA; 1352 BP.
DE E12 cDNA of subclone pE12P.
PN WO9113172-A.
PD 05-SEP-1991.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 3.7%; Score 39; DB 2; Length 1352;
Best Local Similarity 44.3%; Pred. No. 32;
RESULT 1128
ID AAS59815 standard; cDNA; 1535 BP.
DE Human novel cytokine encoding cDNA 790CIP2A_12 #1.
PN WO200175093-A1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.7%; Score 39; DB 4; Length 1535;
Best Local Similarity 61.2%; Pred. No. 33;
RESULT 1129
ID AAQ13669 standard; DNA; 2954 BP.
DE E2A gene.
PN WO9113172-A.
PD 05-SEP-1991.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 3.7%; Score 39; DB 2; Length 2954;
Best Local Similarity 44.3%; Pred. No. 39;
RESULT 1130
ID AAQ13674 standard; DNA; 3518 BP.
DE E2A.E12 transcript.
PN WO9113172-A.
PD 05-SEP-1991.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 3.7%; Score 39; DB 2; Length 3518;
Best Local Similarity 44.3%; Pred. No. 41;
RESULT 1131
ID ABN95831 standard; DNA; 4396 BP.
DE Gene #2329 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.7%; Score 39; DB 6; Length 4396;
Best Local Similarity 44.3%; Pred. No. 43;
RESULT 1132
ID ADH28778 standard; DNA; 4396 BP.
DE Human chronic myclogenous leukaemia (CML) gene marker #46.
PN US2003104426-A1.
PD 05-JUN-2003.
PA (LINS/) LINSLEY P S.
PA (MAOM/) MAO M.
PA (DAIH/) DAI H.
PA (HEYY/) HE Y.
PA (RADI/) RADICH J P.
Query Match 3.7%; Score 39; DB 10; Length 4396;
Best Local Similarity 44.3%; Pred. No. 43;
RESULT 1133
ID ADS64458 standard; DNA; 4396 BP.
DE Human transcription factor E2-alpha (TCF-3) gene.
PN US2004185489-A1.
PD 23-SEP-2004.
PA (CERT/) CERTA U.
PA (FOSE/) FOSER S.
PA (WEYE/) WEYER K.
Query Match 3.7%; Score 39; DB 13; Length 4396;
Best Local Similarity 44.3%; Pred. No. 43;
RESULT 1134
ID ADX05495 standard; DNA; 4396 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 60.
PN WO2005012875-A2.

PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 3.7%; Score 39; DB 14; Length 4396;
Best Local Similarity 44.3%; Pred. No. 43;
RESULT 1135
ID ADG37080 standard; DNA; 28198 BP.
DE Mouse plakoglobin polynucleotide seq id 2.
PN JP2003189850-A.
PD 08-JUL-2003.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 3.7%; Score 39; DB 10; Length 28198;
Best Local Similarity 49.0%; Pred. No. 70;
RESULT 1136
ID ADX51347 standard; cDNA; 515 BP.
DE Plant full length insert polynucleotide seqid 26087.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.7%; Score 38.8; DB 13; Length 515;
Best Local Similarity 52.4%; Pred. No. 28;
RESULT 1137
ID ADX51265 standard; cDNA; 581 BP.
DE Plant full length insert polynucleotide seqid 26005.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.7%; Score 38.8; DB 13; Length 581;
Best Local Similarity 52.4%; Pred. No. 29;
RESULT 1138
ID ADA49118 standard; DNA; 756 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.7%; Score 38.8; DB 9; Length 756;
Best Local Similarity 53.2%; Pred. No. 31;
RESULT 1139
ID ABQ68452 standard; DNA; 1327 BP.
DE Listeria monocytogenes 4b contig DNA sequence #1218.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 3.7%; Score 38.8; DB 6; Length 1327;
Best Local Similarity 50.5%; Pred. No. 36;
RESULT 1140
ID ADA70610 standard; DNA; 1599 BP.
DE Rice gene, SEQ ID 3933.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.7%; Score 38.8; DB 8; Length 1599;
Best Local Similarity 45.0%; Pred. No. 37;
RESULT 1141
ID ACL72419 standard; DNA; 1697 BP.
DE M. xanthus gene sequence, seq id 8882.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.7%; Score 38.8; DB 14; Length 1697;
Best Local Similarity 52.5%; Pred. No. 38;
RESULT 1142
ID ADD01251 standard; cDNA; 1802 BP.
DE Human nucleic acid-associated protein NAAP-32 cDNA SEQ ID NO:89.
PN WO2003054219-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.7%; Score 38.8; DB 10; Length 1802;
Best Local Similarity 50.5%; Pred. No. 38;
RESULT 1143
ID ADQ67505 standard; cDNA; 2235 BP.
DE Novel human cDNA sequence #2478.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.7%; Score 38.8; DB 12; Length 2235;
Best Local Similarity 50.5%; Pred. No. 41;
RESULT 1144
ID ADC37599 standard; DNA; 2264 BP.
DE Human nucleic acid associated protein NAAP-6 coding sequence.
PN WO2003046151-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.7%; Score 38.8; DB 10; Length 2264;
Best Local Similarity 50.5%; Pred. No. 41;
RESULT 1145
ID AAH26500 standard; cDNA; 2561 BP.
DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
PN WO200164874-A2.
PD 07-SEP-2001.
PA (BOST-) BOSTON HEART FOUND INC.
Query Match 3.7%; Score 38.8; DB 5; Length 2561;
Best Local Similarity 50.4%; Pred. No. 42;
RESULT 1146
ID ACN39392 standard; cDNA; 4018 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325616, SEQ ID NO:3504.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 38.8; DB 13; Length 4018;
Best Local Similarity 50.5%; Pred. No. 47;
RESULT 1147
ID ADU66651 standard; DNA; 4380 BP.
DE Human kinase and phosphatase DNA, Incyte polynucleotide ID: 7526196CB1.
PN WO2004098539-A2.
PD 18-NOV-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.7%; Score 38.8; DB 13; Length 4380;
Best Local Similarity 49.0%; Pred. No. 48;
RESULT 1148
ID ADQ23117 standard; DNA; 4868 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5937.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.7%; Score 38.8; DB 12; Length 4868;
Best Local Similarity 46.1%; Pred. No. 50;
RESULT 1149
ID ACL64483 standard; DNA; 9937 BP.
DE M. xanthus DNA fragment, seq id 946.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.7%; Score 38.8; DB 14; Length 9937;
Best Local Similarity 52.5%; Pred. No. 60;
RESULT 1150
ID ADS36457 standard; DNA; 17809 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1671.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.7%; Score 38.8; DB 13; Length 17809;
Best Local Similarity 44.8%; Pred. No. 70;
RESULT 1151
ID AAT93095 standard; cDNA; 24379 BP.
DE Streptomyces frenolicin gene cluster.

PN EP806480-A2.
PD 12-NOV-1997.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 3.7%; Score 38.8; DB 2; Length 24379;
Best Local Similarity 47.2%; Pred. No. 75;
RESULT 1152
ID AAV25925 standard; cDNA; 24379 BP.
DE Streptomyces roseofulvus frenolicin gene cluster.
PN JP10094395-A.
PD 14-APR-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 3.7%; Score 38.8; DB 2; Length 24379;
Best Local Similarity 47.2%; Pred. No. 75;
RESULT 1153
ID ACN45166 standard; DNA; 87687 BP.
DE Human genomic sequence hCG37872.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.7%; Score 38.8; DB 11; Length 87687;
Best Local Similarity 47.5%; Pred. No. 1e+02;
RESULT 1154
ID ACN61773 standard; cDNA; 291 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-020-Q6-N6-H3, SEQ:16554.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.7%; Score 38.6; DB 13; Length 291;
Best Local Similarity 48.7%; Pred. No. 27;
RESULT 1155
ID ADB68842 standard; DNA; 536 BP.
DE Minority luxI consensus sequence DNA 14.
PN WO2003057902-A2.
PD 17-JUL-2003.
PA (FRAU) FRAUNHOFER USA INC.
Query Match 3.7%; Score 38.6; DB 10; Length 536;
Best Local Similarity 10.9%; Pred. No. 31;
RESULT 1156
ID ADA48609 standard; DNA; 1023 BP.
DE Rice gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.7%; Score 38.6; DB 9; Length 1023;
Best Local Similarity 44.1%; Pred. No. 37;
RESULT 1157
ID ACL27665 standard; cDNA; 1191 BP.
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:1621.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.7%; Score 38.6; DB 11; Length 1191;
Best Local Similarity 47.7%; Pred. No. 39;
RESULT 1158
ID ADX46251 standard; cDNA; 1302 BP.
DE Plant full length insert polynucleotide seqid 20991.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.7%; Score 38.6; DB 13; Length 1302;
Best Local Similarity 53.7%; Pred. No. 40;
RESULT 1159
ID ADA69408 standard; DNA; 2232 BP.
DE Rice gene, SEQ ID 2731.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.7%; Score 38.6; DB 8; Length 2232;
Best Local Similarity 51.4%; Pred. No. 45;
RESULT 1160
ID ABZ23911 standard; DNA; 3108 BP.
DE Human 3OST4 polypeptide encoding DNA.
PN WO200292849-A2.
PD 21-NOV-2002.
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
Query Match 3.7%; Score 38.6; DB 8; Length 3108;
Best Local Similarity 51.6%; Pred. No. 49;
RESULT 1161
ID AAX37250 standard; DNA; 3658 BP.
DE Human 3-OST-4 encoding DNA.
PN WO9922005-A2.
PD 06-MAY-1999.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 3.7%; Score 38.6; DB 2; Length 3658;
Best Local Similarity 51.6%; Pred. No. 52;
RESULT 1162
ID AAX37251 standard; DNA; 4045 BP.
DE Human 3-OST-4 5' promoter and exon sequence.
PN WO9922005-A2.
PD 06-MAY-1999.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 3.7%; Score 38.6; DB 2; Length 4045;
Best Local Similarity 51.6%; Pred. No. 53;
RESULT 1163
ID AAV62934 standard; cDNA to mRNA; 5822 BP.
DE Human mDia Rho targeting protein cDNA #2.
PN JP10262680-A.
PD 06-OCT-1998.
PA (KIRI) KIRIN BREWERY KK.
Query Match 3.7%; Score 38.6; DB 2; Length 5822;
Best Local Similarity 50.3%; Pred. No. 58;
RESULT 1164
ID AAV62933 standard; cDNA to mRNA; 5822 BP.
DE Human mDia Rho targeting protein cDNA.
PN JP10262680-A.
PD 06-OCT-1998.
PA (KIRI) KIRIN BREWERY KK.
Query Match 3.7%; Score 38.6; DB 2; Length 5822;
Best Local Similarity 50.3%; Pred. No. 58;
RESULT 1165
ID AAZ30163 standard; DNA; 34094 BP.
DE Complete nucleotide sequence of the PAV-3 genome.
PN WO9953047-A2.
PD 21-OCT-1999.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 3.7%; Score 38.6; DB 2; Length 34094;
Best Local Similarity 50.3%; Pred. No. 92;
RESULT 1166
ID ACC78130 standard; DNA; 34094 BP.
DE Nucleotide sequence of porcine adenovirus type 3 (PAV-3) genome.
PN WO2003040305-A2.
PD 15-MAY-2003.
PA (UYSA-) UNIV SASKATCHEWAN.
Query Match 3.7%; Score 38.6; DB 9; Length 34094;
Best Local Similarity 50.3%; Pred. No. 92;
RESULT 1167
ID AEB77455 standard; DNA; 48775 BP.
DE Human TGF beta receptor I antisense sequence SEQ ID NO 96.
PN WO2005074981-A2.
PD 18-AUG-2005.
PA (BOGD/) BOGDAHN U.
Query Match 3.7%; Score 38.6; DB 14; Length 48775;
Best Local Similarity 48.7%; Pred. No. 1e+02;
RESULT 1168
ID AAA29349 standard; DNA; 71989 BP.
DE Sorangium cellulosum epothilone polyketide synthase operon genomic DNA.
Query Match 3.7%; Score 38.6; DB 3; Length 71989;

Best Local Similarity 52.9%; Pred. No. 1.1e+02;
RESULT 1169
Query Match 3.7%; Score 38.6; DB 4; Length 110000;
Best Local Similarity 52.9%; Pred. No. 1.2e+02;
RESULT 1170
ID ADQ53553 standard; DNA; 567 BP.
DE Novel canine microarray-related DNA sequence SeqID4855.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
Query Match 3.7%; Score 38.4; DB 13; Length 567;
Best Local Similarity 50.5%; Pred. No. 36;
RESULT 1171
ID ACN87435 standard; DNA; 931 BP.
DE Breast cancer related marker, seq id 8585.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.7%; Score 38.4; DB 11; Length 931;
Best Local Similarity 43.5%; Pred. No. 40;
RESULT 1172
ID AAH21004 standard; DNA; 1008 BP.
DE Bovine-derived DNA fragment contig1 448_67_1218.
PN DE19959751-A1.
PD 13-JUN-2001.
PA (FRIE/) FRIES H R.
PA (DURS/) DURSTEWITZ G.
Query Match 3.7%; Score 38.4; DB 4; Length 1008;
Best Local Similarity 49.2%; Pred. No. 41;
RESULT 1173
ID ACL38874 standard; cDNA; 2000 BP.
DE Rice stress-regulated promoter SEQ ID NO:17437.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.7%; Score 38.4; DB 11; Length 2000;
Best Local Similarity 56.2%; Pred. No. 49;
RESULT 1174
ID AAV06594 standard; cDNA; 4580 BP.
DE Bovine N-proteinase cDNA.
PN WO9800555-A1.
PD 08-JAN-1998.
PA (PROC/) PROCKOP D J.
PA (COLI/) COLIGE A.
PA (LAPI/) LAPIERE C.
Query Match 3.7%; Score 38.4; DB 2; Length 4580;
Best Local Similarity 47.2%; Pred. No. 61;
RESULT 1175
ID ABS57456 standard; cDNA; 4580 BP.
DE Bovine N-proteinase cDNA.
PN US6428998-B1.
PD 06-AUG-2002.
PA (UYLI-) UNIV LIEGE.
Query Match 3.7%; Score 38.4; DB 10; Length 4580;
Best Local Similarity 47.2%; Pred. No. 61;
RESULT 1176
ID ADN95645 standard; DNA; 10905 BP.
DE Human BEC/LEC-related gene sequence SeqID568.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 3.7%; Score 38.4; DB 11; Length 10905;
Best Local Similarity 49.0%; Pred. No. 76;
RESULT 1177
ID AEB16864 standard; DNA; 10905 BP.
DE Human neuron-specific (gamma) enolase (NSE) 2 (ENO2) gene, SEQ ID NO: 2.
PN US2005142616-A1.
PD 30-JUN-2005.
PA (HANS/) HANSON V.
PA (SPIE/) SPIERA H.
Query Match 3.7%; Score 38.4; DB 14; Length 10905;
Best Local Similarity 49.0%; Pred. No. 76;
RESULT 1178
ID AAK82710 standard; DNA; 21313 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37522.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 38.4; DB 4; Length 21313;
Best Local Similarity 49.0%; Pred. No. 91;
RESULT 1179
ID ADF31997 standard; DNA; 39949 BP.
DE Full length cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 3.7%; Score 38.4; DB 12; Length 39949;
Best Local Similarity 45.6%; Pred. No. 1.1e+02;
RESULT 1180
ID ADW39403 standard; DNA; 40772 BP.
DE Herpes simplex virus type 1 cos6 DNA.
PN CN1461805-A.
PD 17-DEC-2003.
PA (BENY-) BENYUAN ZHENGYANG GENETIC TECHNOLOGY CO.
Query Match 3.7%; Score 38.4; DB 13; Length 40772;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
RESULT 1181
ID ADF31998 standard; DNA; 48200 BP.
DE Cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 3.7%; Score 38.4; DB 12; Length 48200;
Best Local Similarity 45.6%; Pred. No. 1.1e+02;
RESULT 1182
ID ACA44050 standard; DNA; 369 BP.
DE Prokaryotic essential gene #25707.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.6%; Score 38.2; DB 8; Length 369;
Best Local Similarity 51.5%; Pred. No. 36;
RESULT 1183
ID ACN51217 standard; cDNA; 420 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-H6, SEQ:5998.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.6%; Score 38.2; DB 13; Length 420;
Best Local Similarity 49.3%; Pred. No. 37;
RESULT 1184
ID ABD04273 standard; DNA; 639 BP.
DE Pseudomonas aeruginosa polynucleotide #2877.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 38.2; DB 11; Length 639;
Best Local Similarity 45.0%; Pred. No. 41;
RESULT 1185
ID ADA70465 standard; DNA; 930 BP.
DE Rice gene, SEQ ID 3788.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.6%; Score 38.2; DB 8; Length 930;
Best Local Similarity 47.7%; Pred. No. 45;
RESULT 1186
ID ACA38609 standard; DNA; 972 BP.
DE Prokaryotic essential gene #20266.
PN WO200277183-A2.
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.
Query Match 3.6%; Score 38.2; DB 8; Length 972;
Best Local Similarity 56.5%; Pred. No. 46;
RESULT 1187
ID ACA40342 standard; DNA; 975 BP.
DE Prokaryotic essential gene #21999.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.6%; Score 38.2; DB 8; Length 975;
Best Local Similarity 56.5%; Pred. No. 46;
RESULT 1188
ID ABD01834 standard; DNA; 1068 BP.
DE Pseudomonas aeruginosa polynucleotide #438.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 38.2; DB 11; Length 1068;
Best Local Similarity 46.4%; Pred. No. 47;
RESULT 1189
ID ADT18284 standard; cDNA; 1075 BP.
DE Plant cDNA, Seq ID 3610.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 3.6%; Score 38.2; DB 13; Length 1075;
Best Local Similarity 44.1%; Pred. No. 47;
RESULT 1190
ID ABD01759 standard; DNA; 1164 BP.
DE Pseudomonas aeruginosa polynucleotide #363.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 38.2; DB 11; Length 1164;
Best Local Similarity 46.4%; Pred. No. 48;
RESULT 1191
ID ACL29128 standard; cDNA; 1194 BP.
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:3084.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.6%; Score 38.2; DB 11; Length 1194;
Best Local Similarity 50.9%; Pred. No. 48;
RESULT 1192
ID ABA03009 standard; cDNA; 1356 BP.
DE Tomato phytase encoding cDNA.
PN CN1313392-A.
PD 19-SEP-2001.
PA (LIMM/) LI M.
Query Match 3.6%; Score 38.2; DB 6; Length 1356;
Best Local Similarity 47.7%; Pred. No. 50;
RESULT 1193
ID ADV43446 standard; cDNA; 1503 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1074.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 3.6%; Score 38.2; DB 14; Length 1503;
Best Local Similarity 50.3%; Pred. No. 51;
RESULT 1194
ID AAZ99989 standard; DNA; 1514 BP.
DE DNA encoding the chicken homeobox protein 9 (HB9).
PN WO200018884-A1.
PD 06-APR-2000.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 3.6%; Score 38.2; DB 3; Length 1514;
Best Local Similarity 52.1%; Pred. No. 51;
RESULT 1195
ID AAZ31672 standard; DNA; 1662 BP.
DE Human FKHL7 coding sequence open reading frame.
PN WO9952415-A2.
PD 21-OCT-1999.
PA (IOWA) UNIV IOWA RES FOUND.
Query Match 3.6%; Score 38.2; DB 2; Length 1662;
Best Local Similarity 42.1%; Pred. No. 52;
RESULT 1196
ID AAZ38080 standard; DNA; 1662 BP.
DE Human forkhead transcription factor gene, FKHL7 ORF sequence.
PN WO9953060-A2.
PD 21-OCT-1999.
PA (IOWA) UNIV IOWA RES FOUND.
Query Match 3.6%; Score 38.2; DB 2; Length 1662;
Best Local Similarity 42.1%; Pred. No. 52;
RESULT 1197
ID ADR24750 standard; DNA; 1662 BP.
DE Breast cancer prognosis marker #611.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 3.6%; Score 38.2; DB 13; Length 1662;
Best Local Similarity 42.1%; Pred. No. 52;
RESULT 1198
ID ABK84476 standard; cDNA; 2067 BP.
DE Human cDNA differentially expressed in granulocytic cells #1047.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 38.2; DB 6; Length 2067;
Best Local Similarity 50.3%; Pred. No. 55;
RESULT 1199
ID ADL82924 standard; cDNA; 2067 BP.
DE Human PRO12155 cDNA, SEQ ID 126.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.6%; Score 38.2; DB 12; Length 2067;
Best Local Similarity 50.3%; Pred. No. 55;
RESULT 1200
ID ADQ18543 standard; DNA; 2067 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1362.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.6%; Score 38.2; DB 12; Length 2067;
Best Local Similarity 50.3%; Pred. No. 55;
RESULT 1201
ID ADR25195 standard; DNA; 2067 BP.
DE Breast cancer prognosis marker #1056.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 3.6%; Score 38.2; DB 13; Length 2067;
Best Local Similarity 50.3%; Pred. No. 55;
RESULT 1202
ID ADY61135 standard; DNA; 2067 BP.
DE Breast cancer associated human polynucleotide sequence, SEQ ID No:19.
PN WO2005021788-A1.
PD 10-MAR-2005.
PA (IPSO-) IPSOGEN.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (PAOL-) INST PAOLI CALMETTES.
Query Match 3.6%; Score 38.2; DB 14; Length 2067;
Best Local Similarity 50.3%; Pred. No. 55;
RESULT 1203
ID ABQ54970 standard; cDNA; 2170 BP.
DE Human ovarian antigen HNOCH54 cDNA, SEQ ID NO:850.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 38.2; DB 6; Length 2170;
Best Local Similarity 49.7%; Pred. No. 56;
RESULT 1204
ID ADQ18001 standard; DNA; 2526 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 818.

PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.6%; Score 38.2; DB 12; Length 2526;
Best Local Similarity 52.1%; Pred. No. 58;
RESULT 1205
ID ADQ22602 standard; DNA; 2652 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5422.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.6%; Score 38.2; DB 12; Length 2652;
Best Local Similarity 52.1%; Pred. No. 59;
RESULT 1206
ID AAH99564 standard; cDNA; 2752 BP.
DE Human protein encoding cDNA sequence SEQ ID NO:399.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 38.2; DB 4; Length 2752;
Best Local Similarity 51.5%; Pred. No. 60;
RESULT 1207
ID AAZ31671 standard; DNA; 3946 BP.
DE Human FKHL7 coding sequence.
PN WO9952415-A2.
PD 21-OCT-1999.
PA (IOWA) UNIV IOWA RES FOUND.
Query Match 3.6%; Score 38.2; DB 2; Length 3946;
Best Local Similarity 42.1%; Pred. No. 66;
RESULT 1208
ID AAZ38079 standard; DNA; 3946 BP.
DE Human forkhead transcription factor gene, FKHL7 DNA sequence.
PN WO9953060-A2.
PD 21-OCT-1999.
PA (IOWA) UNIV IOWA RES FOUND.
Query Match 3.6%; Score 38.2; DB 2; Length 3946;
Best Local Similarity 42.1%; Pred. No. 66;
RESULT 1209
ID ADE60227 standard; DNA; 4523 BP.
DE Human gene M11167, SEQ ID NO 6133.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 38.2; DB 10; Length 4523;
Best Local Similarity 47.0%; Pred. No. 68;
RESULT 1210
ID ADE60229 standard; DNA; 4523 BP.
DE Human gene M11167, SEQ ID NO 6135.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 38.2; DB 10; Length 4523;
Best Local Similarity 47.0%; Pred. No. 68;
RESULT 1211
ID ADE60231 standard; DNA; 4523 BP.
DE Human gene M11167, SEQ ID NO 6137.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 38.2; DB 10; Length 4523;
Best Local Similarity 47.0%; Pred. No. 68;
RESULT 1212
ID ADE60233 standard; DNA; 4523 BP.
DE Human gene M11167, SEQ ID NO 6139.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 38.2; DB 10; Length 4523;
Best Local Similarity 47.0%; Pred. No. 68;
RESULT 1213
ID ADD45822 standard; DNA; 4523 BP.
DE Human gene M11167, SEQ ID NO 11491.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 38.2; DB 10; Length 4523;
Best Local Similarity 47.0%; Pred. No. 68;
RESULT 1214
ID ADR67197 standard; DNA; 5378 BP.
DE Human bladder cancer associated nucleotide sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 3.6%; Score 38.2; DB 13; Length 5378;
Best Local Similarity 49.7%; Pred. No. 71;
RESULT 1215
ID ADD14722 standard; cDNA; 5382 BP.
DE Human src biomarker polynucleotide SEQ ID NO:116.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 3.6%; Score 38.2; DB 10; Length 5382;
Best Local Similarity 49.7%; Pred. No. 71;
RESULT 1216
ID AAC85191 standard; DNA; 9994 BP.
DE S. avermitilis 10 kb genomic DNA.
PN WO200109155-A1.
PD 08-FEB-2001.
PA (MERI) MERCK & CO INC.
Query Match 3.6%; Score 38.2; DB 4; Length 9994;
Best Local Similarity 46.4%; Pred. No. 83;
RESULT 1217
ID AAS59545 standard; DNA; 61313 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #40.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.6%; Score 38.2; DB 4; Length 61313;
Best Local Similarity 47.3%; Pred. No. 1.3e+02;
RESULT 1218
ID ACF64474 standard; DNA; 61313 BP.
DE Propionibacterium acnes DNA contig sequence #40.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 3.6%; Score 38.2; DB 8; Length 61313;
Best Local Similarity 47.3%; Pred. No. 1.3e+02;
RESULT 1219
ID ADU47667 standard; DNA; 88400 BP.
DE S. cyaneogriseus LL-F28249 compound full-length biosynthetic gene.
PN EP1477563-A2.
PD 17-NOV-2004.
PA (AMHP) WYETH.
PA (FORT-) FORT DODGE ANIMAL HEALTH.
Query Match 3.6%; Score 38.2; DB 13; Length 88400;
Best Local Similarity 50.8%; Pred. No. 1.5e+02;
RESULT 1220
ID ADQ18615 standard; DNA; 104729 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1434.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.6%; Score 38.2; DB 12; Length 104729;
Best Local Similarity 42.1%; Pred. No. 1.5e+02;
RESULT 1221
Query Match 3.6%; Score 38.2; DB 4; Length 110000;

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  Best Local Similarity   56.5%;  Pred. No. 1.5e+02;
RESULT 1222
  Query Match             3.6%;  Score 38.2;  DB 4;  Length 110000;
  Best Local Similarity   56.5%;  Pred. No. 1.5e+02;
RESULT 1223
ID   ADK11756 standard; DNA; 519 BP.
DE   Breast cancer differentially expressed gene product #162.
PN   WO2003057926-A1.
PD   17-JUL-2003.
PA   (CHIR ) CHIRON CORP.
  Query Match             3.6%;  Score 38;  DB 10;  Length 519;
  Best Local Similarity   54.2%;  Pred. No. 43;
RESULT 1224
ID   ADP29185 standard; DNA; 555 BP.
DE   Human secreted protein encoding sequence SEQ ID #1183.
PN   WO2004035732-A2.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
  Query Match             3.6%;  Score 38;  DB 12;  Length 555;
  Best Local Similarity   52.5%;  Pred. No. 44;
RESULT 1225
ID   ADA70261 standard; DNA; 1023 BP.
DE   Rice gene, SEQ ID 3584.
PN   WO2003000898-A1.
PD   03-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match             3.6%;  Score 38;  DB 8;  Length 1023;
  Best Local Similarity   44.1%;  Pred. No. 52;
RESULT 1226
ID   ADA48209 standard; DNA; 1023 BP.
DE   Rice gene conferring disease resistance in plants.
PN   WO2003000906-A2.
PD   03-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match             3.6%;  Score 38;  DB 9;  Length 1023;
  Best Local Similarity   44.1%;  Pred. No. 52;
RESULT 1227
ID   ADJ11589 standard; DNA; 1023 BP.
DE   Rice DNA modulated by post-transcriptional gene silencing SeqID 225.
PN   US2003135888-A1.
PD   17-JUL-2003.
PA   (ZHUT/) ZHU T.
PA   (WANG/) WANG X.
PA   (CHAN/) CHANG H.
PA   (BRIG/) BRIGGS S P.
PA   (COOP/) COOPER B.
PA   (GLAZ/) GLAZEBROOK J.
PA   (GOFF/) GOFF S A.
PA   (KATA/) KATAGIRI F.
PA   (KREP/) KREPS J.
PA   (MOUG/) MOUGHAMER T.
PA   (PROV/) PROVART N.
PA   (RICK/) RICKE D.
  Query Match             3.6%;  Score 38;  DB 11;  Length 1023;
  Best Local Similarity   44.1%;  Pred. No. 52;
RESULT 1228
ID   ACL33952 standard; cDNA; 1053 BP.
DE   Rice abiotic stress response related polynucleotide SEQ ID NO:12515.
PN   WO2003008540-A2.
PD   30-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
  Query Match             3.6%;  Score 38;  DB 11;  Length 1053;
  Best Local Similarity   55.2%;  Pred. No. 52;
RESULT 1229
ID   AAX90747 standard; cDNA; 1271 BP.
DE   Maize pathogen resistance Hm2 polynucleotide.
PN   WO9936543-A1.
PD   22-JUL-1999.
PA   (PION-) PIONEER HI-BRED INT INC.
PA   (UMOR ) UNIV MISSOURI.
  Query Match             3.6%;  Score 38;  DB 2;  Length 1271;
  Best Local Similarity   55.2%;  Pred. No. 55;
RESULT 1230
ID   ADS14464 standard; DNA; 2040 BP.
DE   Pseudomonas aeruginosa quorum sensing controlled gene PA0176, SEQ ID 19.
PN   WO2004083385-A2.
PD   30-SEP-2004.
PA   (IOWA ) UNIV IOWA RES FOUND.
  Query Match             3.6%;  Score 38;  DB 13;  Length 2040;
  Best Local Similarity   51.8%;  Pred. No. 62;
RESULT 1231
ID   ABD13429 standard; DNA; 2055 BP.
DE   Pseudomonas aeruginosa polynucleotide #12033.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.6%;  Score 38;  DB 11;  Length 2055;
  Best Local Similarity   51.8%;  Pred. No. 62;
RESULT 1232
ID   ABD13401 standard; DNA; 2160 BP.
DE   Pseudomonas aeruginosa polynucleotide #12005.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.6%;  Score 38;  DB 11;  Length 2160;
  Best Local Similarity   51.8%;  Pred. No. 63;
RESULT 1233
ID   ADB62530 standard; cDNA; 2639 BP.
DE   Human cDNA encoding clone HHDPC20088160.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match             3.6%;  Score 38;  DB 10;  Length 2639;
  Best Local Similarity   60.8%;  Pred. No. 66;
RESULT 1234
ID   ABD13376 standard; DNA; 3366 BP.
DE   Pseudomonas aeruginosa polynucleotide #11980.
PN   US6551795-B1.
PD   22-APR-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
  Query Match             3.6%;  Score 38;  DB 11;  Length 3366;
  Best Local Similarity   51.8%;  Pred. No. 70;
RESULT 1235
ID   ABL67689 standard; DNA; 5432 BP.
DE   Oesophagus cancer related gene sequence SEQ ID NO:6026.
PN   WO200194629-A2.
PD   13-DEC-2001.
PA   (AVAL-) AVALON PHARM.
  Query Match             3.6%;  Score 38;  DB 6;  Length 5432;
  Best Local Similarity   53.3%;  Pred. No. 79;
RESULT 1236
ID   ABL64999 standard; DNA; 5432 BP.
DE   Lung cancer related gene sequence SEQ ID NO:3336.
PN   WO200194629-A2.
PD   13-DEC-2001.
PA   (AVAL-) AVALON PHARM.
  Query Match             3.6%;  Score 38;  DB 6;  Length 5432;
  Best Local Similarity   53.3%;  Pred. No. 79;
RESULT 1237
ID   ABK64387 standard; DNA; 5432 BP.
DE   Human benign prostatic hyperplasia gene #282.
PN   WO200212440-A2.
PD   14-FEB-2002.
PA   (GENE-) GENE LOGIC INC.
PA   (NISB ) JAPAN TOBACCO INC.
  Query Match             3.6%;  Score 38;  DB 6;  Length 5432;
  Best Local Similarity   53.3%;  Pred. No. 79;
RESULT 1238
ID   ADI61744 standard; cDNA; 5773 BP.
DE   Human cDNA upregulated in Alzheimer's disease, INCYTE 109082.18.
PN   US6682888-B1.
PD   27-JAN-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             3.6%;  Score 38;  DB 12;  Length 5773;
  Best Local Similarity   53.3%;  Pred. No. 81;
```

RESULT 1239
ID AEA43909 standard; cDNA; 5773 BP.
DE Human cDNA differentially expressed in brain tissue SEQ ID NO:112.
PN US2005130171-A1.
PD 16-JUN-2005.
PA (INCY-) INCYTE CORP.
Query Match 3.6%; Score 38; DB 14; Length 5773;
Best Local Similarity 53.3%; Pred. No. 81;
RESULT 1240
ID ADS10122 standard; DNA; 6277 BP.
DE Human therapeutic DNA - SEQ ID 359.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 3.6%; Score 38; DB 13; Length 6277;
Best Local Similarity 53.3%; Pred. No. 82;
RESULT 1241
ID AAK53013 standard; cDNA; 6282 BP.
DE Human polynucleotide SEQ ID NO 2542.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 38; DB 4; Length 6282;
Best Local Similarity 53.3%; Pred. No. 82;
RESULT 1242
ID AAK52029 standard; cDNA; 6286 BP.
DE Human polynucleotide SEQ ID NO 574.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 38; DB 4; Length 6286;
Best Local Similarity 53.3%; Pred. No. 82;
RESULT 1243
ID ADI23934 standard; DNA; 7185 BP.
DE Streptomyces refuineus 024A locus ORF7.
PN US2003198981-A1.
PD 23-OCT-2003.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 3.6%; Score 38; DB 10; Length 7185;
Best Local Similarity 48.9%; Pred. No. 85;
RESULT 1244
ID ADS36476 standard; DNA; 17804 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1690.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.6%; Score 38; DB 13; Length 17804;
Best Local Similarity 44.1%; Pred. No. 1.1e+02;
RESULT 1245
ID AAD54223 standard; DNA; 24081 BP.
DE Streptomyces platensis subspecies rosaceus dorrigocin ORF6 DNA.
PN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 3.6%; Score 38; DB 10; Length 24081;
Best Local Similarity 45.0%; Pred. No. 1.2e+02;
RESULT 1246
ID ACL68541 standard; DNA; 24459 BP.
DE M. xanthus gene sequence, seq id 5004.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.6%; Score 38; DB 14; Length 24459;
Best Local Similarity 49.5%; Pred. No. 1.2e+02;
RESULT 1247
ID ACL64784 standard; DNA; 32241 BP.
DE M. xanthus DNA fragment, seq id 1247.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.6%; Score 38; DB 14; Length 32241;
Best Local Similarity 49.5%; Pred. No. 1.3e+02;
RESULT 1248
ID ABL64982 standard; DNA; 43058 BP.
DE Lung cancer related gene sequence SEQ ID NO:3319.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.6%; Score 38; DB 6; Length 43058;
Best Local Similarity 53.7%; Pred. No. 1.4e+02;
RESULT 1249
ID ABL65219 standard; DNA; 43058 BP.
DE Lung cancer related gene sequence SEQ ID NO:3556.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.6%; Score 38; DB 6; Length 43058;
Best Local Similarity 53.7%; Pred. No. 1.4e+02;
RESULT 1250
ID ABN97455 standard; DNA; 43058 BP.
DE Gene #3953 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 38; DB 6; Length 43058;
Best Local Similarity 53.7%; Pred. No. 1.4e+02;
RESULT 1251
ID AAD54217 standard; DNA; 52101 BP.
DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.
PN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 3.6%; Score 38; DB 10; Length 52101;
Best Local Similarity 45.0%; Pred. No. 1.4e+02;
RESULT 1252
ID ADI23920 standard; DNA; 61944 BP.
DE Streptomyces refuineus 024A locus (NRRL 3143).
PN US2003198981-A1.
PD 23-OCT-2003.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 3.6%; Score 38; DB 10; Length 61944;
Best Local Similarity 48.9%; Pred. No. 1.5e+02;
RESULT 1253
ID AAA38184 standard; DNA; 318 BP.
DE Primer used in the analysis of a BVDV genome fragment.
PN WO200020628-A1.
PD 13-APR-2000.
PA (BIOI-) BIO-ID DIAGNOSTIC INC.
Query Match 3.6%; Score 37.8; DB 3; Length 318;
Best Local Similarity 50.3%; Pred. No. 43;
RESULT 1254
ID AAA38185 standard; DNA; 320 BP.
DE Primer used in the analysis of a BVDV genome fragment.
PN WO200020628-A1.
PD 13-APR-2000.
PA (BIOI-) BIO-ID DIAGNOSTIC INC.
Query Match 3.6%; Score 37.8; DB 3; Length 320;
Best Local Similarity 49.7%; Pred. No. 43;
RESULT 1255
ID ACN54596 standard; cDNA; 588 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-K6-D5, SEQ:9377.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.6%; Score 37.8; DB 13; Length 588;
Best Local Similarity 50.0%; Pred. No. 50;
RESULT 1256
ID AAA79300 standard; cDNA; 822 BP.
DE Eucalyptus grandis cell signalling involved polynucleotide SEQ ID NO:38.
PN WO200042171-A1.
PD 20-JUL-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 3.6%; Score 37.8; DB 3; Length 822;

Best Local Similarity 53.4%; Pred. No. 54;
RESULT 1257
ID ABD05041 standard; DNA; 939 BP.
DE Pseudomonas aeruginosa polynucleotide #3645.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 37.8; DB 11; Length 939;
Best Local Similarity 45.0%; Pred. No. 56;
RESULT 1258
ID ADJ39500 standard; cDNA; 1232 BP.
DE Plant cDNA #500.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 3.6%; Score 37.8; DB 12; Length 1232;
Best Local Similarity 48.6%; Pred. No. 60;
RESULT 1259
ID AAZ61590 standard; DNA; 1485 BP.
DE DNA encoding a human OC-3 protein.
PN WO200011159-A1.
PD 02-MAR-2000.
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
Query Match 3.6%; Score 37.8; DB 3; Length 1485;
Best Local Similarity 45.9%; Pred. No. 63;
RESULT 1260
ID AAZ61593 standard; DNA; 1485 BP.
DE DNA encoding a human OC-3 protein.
PN WO200011158-A1.
PD 02-MAR-2000.
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
Query Match 3.6%; Score 37.8; DB 3; Length 1485;
Best Local Similarity 45.9%; Pred. No. 63;
RESULT 1261
ID ACA37747 standard; DNA; 1716 BP.
DE Prokaryotic essential gene #19404.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.6%; Score 37.8; DB 8; Length 1716;
Best Local Similarity 44.0%; Pred. No. 66;
RESULT 1262
ID AAD34459 standard; cDNA; 1788 BP.
DE Human GPCR cDNA #2.
PN WO200224885-A2.
PD 28-MAR-2002.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 37.8; DB 6; Length 1788;
Best Local Similarity 50.3%; Pred. No. 67;
RESULT 1263
ID ABD05093 standard; DNA; 1881 BP.
DE Pseudomonas aeruginosa polynucleotide #3697.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 37.8; DB 11; Length 1881;
Best Local Similarity 45.0%; Pred. No. 67;
RESULT 1264
ID AAS84942 standard; cDNA; 1908 BP.
DE DNA encoding novel human diagnostic protein #20746.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 3.6%; Score 37.8; DB 5; Length 1908;
Best Local Similarity 50.8%; Pred. No. 68;
RESULT 1265
ID ABD05208 standard; DNA; 1998 BP.
DE Pseudomonas aeruginosa polynucleotide #3812.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 37.8; DB 11; Length 1998;
Best Local Similarity 45.0%; Pred. No. 68;
RESULT 1266
ID AAA79661 standard; cDNA; 2138 BP.
DE Eucalyptus grandis cell signalling involved polynucleotide SEQ ID NO:462.
PN WO200042171-A1.
PD 20-JUL-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 3.6%; Score 37.8; DB 3; Length 2138;
Best Local Similarity 53.4%; Pred. No. 70;
RESULT 1267
ID ADB87421 standard; DNA; 2500 BP.
DE Transgene expression regulatory element, STAR66F.
PN WO2003004704-A2.
PD 16-JAN-2003.
PA (CHRO-) CHROMAGENICS BV.
Query Match 3.6%; Score 37.8; DB 10; Length 2500;
Best Local Similarity 44.0%; Pred. No. 73;
RESULT 1268
ID ADJ35230 standard; DNA; 2500 BP.
DE Human stabilising anti-repression, STAR, element #66.
PN WO2003106674-A2.
PD 24-DEC-2003.
PA (CHRO-) CHROMAGENICS BV.
Query Match 3.6%; Score 37.8; DB 12; Length 2500;
Best Local Similarity 44.0%; Pred. No. 73;
RESULT 1269
ID ADL96848 standard; DNA; 2500 BP.
DE STablizing Anti-Repressor DNA sequence, T2F STAR 66F.
PN WO2003106684-A2.
PD 24-DEC-2003.
PA (CHRO-) CHROMAGENICS BV.
Query Match 3.6%; Score 37.8; DB 12; Length 2500;
Best Local Similarity 44.0%; Pred. No. 73;
RESULT 1270
ID ADT20151 standard; cDNA; 2973 BP.
DE Plant cDNA, Seq ID 5477.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 3.6%; Score 37.8; DB 13; Length 2973;
Best Local Similarity 50.3%; Pred. No. 76;
RESULT 1271
ID AAA09686 standard; DNA; 3957 BP.
DE HSV-2 immediate early protein ICP4 DNA sequence.
PN WO9516779-A1.
PD 22-JUN-1995.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 3.6%; Score 37.8; DB 5; Length 3957;
Best Local Similarity 51.6%; Pred. No. 82;
RESULT 1272
ID ADG75121 standard; DNA; 3957 BP.
DE Human herpesvirus 2 ICP4 ORF DNA - SEQ ID 193.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 3.6%; Score 37.8; DB 10; Length 3957;
Best Local Similarity 51.6%; Pred. No. 82;
RESULT 1273
ID AAD25519 standard; DNA; 154746 BP.
DE Human herpesvirus 2 complete DNA genome.
PN WO200176643-A1.
PD 18-OCT-2001.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 3.6%; Score 37.8; DB 6; Length 154746;

Best Local Similarity 51.6%; Pred. No. 2.1e+02;
RESULT 1274
ID AAD25519 standard; DNA; 154746 BP.
DE Human herpesvirus 2 complete DNA genome.
PN WO200176643-A1.
PD 18-OCT-2001.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 3.6%; Score 37.8; DB 6; Length 154746;
Best Local Similarity 51.6%; Pred. No. 2.1e+02;
RESULT 1275
ID ACL67554 standard; DNA; 780 BP.
DE M. xanthus gene sequence, seq id 4017.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.6%; Score 37.6; DB 14; Length 780;
Best Local Similarity 47.5%; Pred. No. 60;
RESULT 1276
ID ADX36380 standard; cDNA; 925 BP.
DE Plant full length insert polynucleotide seqid 19200.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.6%; Score 37.6; DB 13; Length 925;
Best Local Similarity 52.6%; Pred. No. 63;
RESULT 1277
ID AAA02488 standard; cDNA; 1218 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2479.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 37.6; DB 3; Length 1218;
Best Local Similarity 22.0%; Pred. No. 67;
RESULT 1278
ID ADI42681 standard; DNA; 1219 BP.
DE Plant transcription factor polynucleotide #735.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 3.6%; Score 37.6; DB 12; Length 1219;
Best Local Similarity 52.6%; Pred. No. 67;
RESULT 1279
ID ADO02930 standard; cDNA; 1219 BP.
DE Corn orthologue of Thalecress transcription factor, cDNA #98.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 3.6%; Score 37.6; DB 12; Length 1219;
Best Local Similarity 52.6%; Pred. No. 67;
RESULT 1280
ID ADT44580 standard; cDNA; 1251 BP.
DE Bacterial polynucleotide #19331.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.6%; Score 37.6; DB 13; Length 1251;
Best Local Similarity 55.3%; Pred. No. 68;
RESULT 1281
ID ACL73026 standard; DNA; 1308 BP.
DE M. xanthus gene sequence, seq id 9489.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.6%; Score 37.6; DB 14; Length 1308;
Best Local Similarity 55.3%; Pred. No. 69;
RESULT 1282
ID ACN40831 standard; cDNA; 1528 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326883, SEQ ID NO:5875.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.6%; Score 37.6; DB 13; Length 1528;
Best Local Similarity 53.4%; Pred. No. 71;
RESULT 1283
ID ADL12321 standard; cDNA; 1577 BP.
DE Human steroid-induced C3A liver cell cDNA #50.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.6%; Score 37.6; DB 12; Length 1577;
Best Local Similarity 53.4%; Pred. No. 72;
RESULT 1284
ID ABK84709 standard; cDNA; 1587 BP.
DE Human cDNA differentially expressed in granulocytic cells #1280.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 37.6; DB 6; Length 1587;
Best Local Similarity 53.4%; Pred. No. 72;
RESULT 1285
ID ADE85067 standard; DNA; 1587 BP.
DE Farnesyl transferase inhibitor modulated leukemia associated gene #286.
PN WO2003038129-A2.
PD 08-MAY-2003.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 3.6%; Score 37.6; DB 10; Length 1587;
Best Local Similarity 53.4%; Pred. No. 72;
RESULT 1286
ID ADI31552 standard; cDNA; 1587 BP.
DE Human cDNA #878.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.6%; Score 37.6; DB 11; Length 1587;
Best Local Similarity 53.4%; Pred. No. 72;

RESULT 1287
ID ADP21404 standard; DNA; 1587 BP.
DE Gene RGS19 for screening for cardiac therapeutic preparation.
PN WO2004050894-A2.
PD 17-JUN-2004.
PA (ARTE-) ARTESIAN THERAPEUTICS INC.
Query Match 3.6%; Score 37.6; DB 12; Length 1587;
Best Local Similarity 53.4%; Pred. No. 72;
RESULT 1288
ID ADR52680 standard; DNA; 1587 BP.
DE Drug therapy altered expressed gene #31.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 3.6%; Score 37.6; DB 13; Length 1587;
Best Local Similarity 53.4%; Pred. No. 72;
RESULT 1289
ID ADS83619 standard; cDNA; 1587 BP.
DE Human lymph node cDNA #878.
PN US2004077003-A1.
PD 22-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.6%; Score 37.6; DB 13; Length 1587;
Best Local Similarity 53.4%; Pred. No. 72;
RESULT 1290
ID ADX06227 standard; DNA; 1587 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 792.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 3.6%; Score 37.6; DB 14; Length 1587;
Best Local Similarity 53.4%; Pred. No. 72;
RESULT 1291
ID ADZ49392 standard; DNA; 1587 BP.
DE Insulin signaling pathway related gene, SEQ ID 721.
PN US2005085436-A1.
PD 21-APR-2005.
PA (LIHH/) LI H.
PA (MAJJ/) MA J.
Query Match 3.6%; Score 37.6; DB 14; Length 1587;
Best Local Similarity 53.4%; Pred. No. 72;
RESULT 1292
ID AAA02504 standard; cDNA; 1593 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2495.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.6%; Score 37.6; DB 3; Length 1593;
Best Local Similarity 33.2%; Pred. No. 72;
RESULT 1293
ID AEA19389 standard; cDNA; 1620 BP.
DE Novel human polynucleotide SEQ ID NO 83.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 3.6%; Score 37.6; DB 14; Length 1620;
Best Local Similarity 49.6%; Pred. No. 72;
RESULT 1294
ID AEA61238 standard; DNA; 1647 BP.
DE Human FLJ12768 gene genomic sequence SEQ ID NO:148.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 3.6%; Score 37.6; DB 14; Length 1647;
Best Local Similarity 46.8%; Pred. No. 73;
RESULT 1295
ID ADI61702 standard; cDNA; 1876 BP.
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 234151.1.
PN US6682888-B1.
PD 27-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 3.6%; Score 37.6; DB 12; Length 1876;
Best Local Similarity 49.6%; Pred. No. 75;
RESULT 1296
ID AEA43867 standard; cDNA; 1876 BP.
DE Human cDNA differentially expressed in brain tissue SEQ ID NO:70.
PN US2005130171-A1.
PD 16-JUN-2005.
PA (INCY-) INCYTE CORP.
Query Match 3.6%; Score 37.6; DB 14; Length 1876;
Best Local Similarity 49.6%; Pred. No. 75;
RESULT 1297
ID ADA70740 standard; DNA; 2310 BP.
DE Rice gene, SEQ ID 4063.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.6%; Score 37.6; DB 8; Length 2310;
Best Local Similarity 56.5%; Pred. No. 79;
RESULT 1298
ID ABD04394 standard; DNA; 2460 BP.
DE Pseudomonas aeruginosa polynucleotide #2998.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 37.6; DB 11; Length 2460;
Best Local Similarity 52.6%; Pred. No. 81;
RESULT 1299
ID ABD04265 standard; DNA; 2856 BP.
DE Pseudomonas aeruginosa polynucleotide #2869.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 37.6; DB 11; Length 2856;
Best Local Similarity 52.6%; Pred. No. 84;
RESULT 1300
ID AAD31053 standard; DNA; 3189 BP.
DE Human PAPAP gene.
PN WO200212279-A2.
PD 14-FEB-2002.
PA (GEST) GENSET.
Query Match 3.6%; Score 37.6; DB 6; Length 3189;
Best Local Similarity 49.6%; Pred. No. 86;
RESULT 1301
ID ABD04497 standard; DNA; 3387 BP.
DE Pseudomonas aeruginosa polynucleotide #3101.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 37.6; DB 11; Length 3387;
Best Local Similarity 52.6%; Pred. No. 88;
RESULT 1302
ID ADR07888 standard; cDNA; 3392 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1394.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 37.6; DB 13; Length 3392;
Best Local Similarity 51.2%; Pred. No. 88;
RESULT 1303
ID ABX71210 standard; cDNA; 5117 BP.
DE Novel human cDNA sequence #435.
PN WO200281731-A2.
PD 17-OCT-2002.
PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Query Match 3.6%; Score 37.6; DB 8; Length 5117;
Best Local Similarity 45.2%; Pred. No. 97;
RESULT 1304
ID AAA10594 standard; DNA; 10732 BP.
DE Gene encoding a subunit of cellulose synthase.

PN JP2000060568-A.
PD 29-FEB-2000.
PA (MIZU/) MIZUNO K.
PA (OJIP) OJI PAPER CO.
Query Match 3.6%; Score 37.6; DB 3; Length 10732;
Best Local Similarity 13.5%; Pred. No. 1.2e+02;
RESULT 1305
ID ACL64617 standard; DNA; 14101 BP.
DE M. xanthus DNA fragment, seq id 1080.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.6%; Score 37.6; DB 14; Length 14101;
Best Local Similarity 55.3%; Pred. No. 1.3e+02;
RESULT 1306
ID AEA61152 standard; DNA; 23490 BP.
DE Human FLJ12768 gene genomic sequence SEQ ID NO:62.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 3.6%; Score 37.6; DB 14; Length 23490;
Best Local Similarity 46.8%; Pred. No. 1.4e+02;
RESULT 1307
ID ACL64736 standard; DNA; 26533 BP.
DE M. xanthus DNA fragment, seq id 1199.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.6%; Score 37.6; DB 14; Length 26533;
Best Local Similarity 47.5%; Pred. No. 1.5e+02;
RESULT 1308
ID AAC87588 standard; DNA; 57728 BP.
DE Human 9p11 chromosomal region.
PN JP2000287684-A.
PD 17-OCT-2000.
PA (ASAK) ASAHI BREWERIES LTD.
Query Match 3.6%; Score 37.6; DB 4; Length 57728;
Best Local Similarity 50.6%; Pred. No. 1.8e+02;
RESULT 1309
ID ABD33428 standard; DNA; 68732 BP.
DE Human cancer-associated (CA) gene HD07-080.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.6%; Score 37.6; DB 13; Length 68732;
Best Local Similarity 55.3%; Pred. No. 1.9e+02;
RESULT 1310
Query Match 3.6%; Score 37.6; DB 4; Length 110000;
Best Local Similarity 47.8%; Pred. No. 2.2e+02;
RESULT 1311
Query Match 3.6%; Score 37.6; DB 4; Length 110000;
Best Local Similarity 47.8%; Pred. No. 2.2e+02;
RESULT 1312
ID AAA59154 standard; cDNA; 310 BP.
DE cDNA encoding a human interleukin-173 polypeptide.
PN WO200042187-A1.
PD 20-JUL-2000.
PA (SCHE) SCHERING CORP.
Query Match 3.6%; Score 37.4; DB 3; Length 310;
Best Local Similarity 55.9%; Pred. No. 53;
RESULT 1313
ID AAA38183 standard; DNA; 320 BP.
DE Primer used in the analysis of a BVDV genome fragment.
PN WO200020628-A1.
PD 13-APR-2000.
PA (BIOI-) BIO-ID DIAGNOSTIC INC.
Query Match 3.6%; Score 37.4; DB 3; Length 320;
Best Local Similarity 49.2%; Pred. No. 53;
RESULT 1314
ID AAX89576 standard; DNA; 405 BP.
DE Autonomously replicating sequence TEL135.
PN US5935789-A.
PD 10-AUG-1999.
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
Query Match 3.6%; Score 37.4; DB 2; Length 405;
Best Local Similarity 48.0%; Pred. No. 56;
RESULT 1315
ID AAL44929 standard; DNA; 405 BP.
DE Multiple tandem integration expression vector related DNA #3.
PN KR99033548-A.
PD 15-MAY-1999.
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
Query Match 3.6%; Score 37.4; DB 3; Length 405;
Best Local Similarity 48.0%; Pred. No. 56;
RESULT 1316
ID ACL14545 standard; DNA; 610 BP.
DE DNA clone originating in barley containing SNP encoding sequence #4536.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 3.6%; Score 37.4; DB 9; Length 610;
Best Local Similarity 50.2%; Pred. No. 63;
RESULT 1317
ID ABQ35494 standard; DNA; 840 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 22085.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 37.4; DB 6; Length 840;
Best Local Similarity 50.3%; Pred. No. 68;
RESULT 1318
ID ABQ35495 standard; DNA; 840 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 22086.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 37.4; DB 6; Length 840;
Best Local Similarity 50.3%; Pred. No. 68;
RESULT 1319
ID ADN98685 standard; cDNA; 882 BP.
DE Novel human cDNA sequence #285.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 3.6%; Score 37.4; DB 12; Length 882;
Best Local Similarity 47.3%; Pred. No. 69;
RESULT 1320
ID ADO00254 standard; cDNA; 882 BP.
DE Novel human cDNA sequence #1069.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 3.6%; Score 37.4; DB 12; Length 882;
Best Local Similarity 47.3%; Pred. No. 69;
RESULT 1321
ID AEB67185 standard; DNA; 947 BP.
DE Rice genome derived DNA sequence, SEQ ID 2330.
PN JP2005185101-A.
PD 14-JUL-2005.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
Query Match 3.6%; Score 37.4; DB 14; Length 947;
Best Local Similarity 47.3%; Pred. No. 70;
RESULT 1322
ID ADX48513 standard; cDNA; 1038 BP.
DE Plant full length insert polynucleotide seqid 23253.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.

Query Match 3.6%; Score 37.4; DB 13; Length 1038;
Best Local Similarity 48.8%; Pred. No. 72;
RESULT 1323
ID ADX59516 standard; cDNA; 1072 BP.
DE Plant full length insert polynucleotide seqid 30359.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.6%; Score 37.4; DB 13; Length 1072;
Best Local Similarity 48.8%; Pred. No. 73;
RESULT 1324
ID AAH45072 standard; cDNA; 1209 BP.
DE Human FM-3 coding sequence.
PN WO200140797-A1.
PD 07-JUN-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 3.6%; Score 37.4; DB 4; Length 1209;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1325
ID AAF76231 standard; cDNA; 1209 BP.
DE Human G-protein coupled receptor FM-3 cDNA.
PN WO200114883-A1.
PD 01-MAR-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 3.6%; Score 37.4; DB 5; Length 1209;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1326
ID AAZ49707 standard; DNA; 1212 BP.
DE Human growth hormone secretagogue related receptor DNA.
PN WO200002919-A1.
PD 20-JAN-2000.
PA (MERI) MERCK & CO INC.
Query Match 3.6%; Score 37.4; DB 3; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1327
ID AAA30739 standard; DNA; 1212 BP.
DE DNA encoding human mutant G protein-coupled receptor MIG (T273K).
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 3.6%; Score 37.4; DB 3; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1328
ID AAA30663 standard; cDNA; 1212 BP.
DE Human G protein-coupled receptor MIG cDNA.
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 3.6%; Score 37.4; DB 3; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1329
ID ABS73400 standard; DNA; 1212 BP.
DE DNA encoding human GPCR GPR66 mutant T273K.
PN WO200268600-A2.
PD 06-SEP-2002.
PA (AREN-) ARENA PHARM INC.
Query Match 3.6%; Score 37.4; DB 6; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1330
ID ABS73344 standard; cDNA; 1212 BP.
DE cDNA encoding human GPCR GPR66.
PN WO200268600-A2.
PD 06-SEP-2002.
PA (AREN-) ARENA PHARM INC.
Query Match 3.6%; Score 37.4; DB 6; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1331
ID ABZ42529 standard; DNA; 1212 BP.
DE Human G protein-coupled receptor GPR66 nucleotide SEQ ID NO:539.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 3.6%; Score 37.4; DB 8; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1332
ID ADA99009 standard; DNA; 1212 BP.
DE Human NMU1 receptor polynucleotide SEQ ID NO:1.
PN WO2003066077-A2.
PD 14-AUG-2003.
PA (FARB) BAYER AG.
Query Match 3.6%; Score 37.4; DB 9; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1333
ID ADC22742 standard; cDNA; 1212 BP.
DE Human G protein-coupled receptor cDNA #70.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 3.6%; Score 37.4; DB 10; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1334
ID ADC22632 standard; cDNA; 1212 BP.
DE Human G protein-coupled receptor cDNA #30.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 3.6%; Score 37.4; DB 10; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1335
ID ADE31652 standard; DNA; 1212 BP.
DE Human 14395 gene #SEQ ID 9.
PN WO2003065984-A2.
PD 14-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.6%; Score 37.4; DB 10; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1336
ID ADH14215 standard; cDNA; 1212 BP.
DE Mutated human MIG cDNA.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 3.6%; Score 37.4; DB 10; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1337
ID ADH14105 standard; cDNA; 1212 BP.
DE Human MIG cDNA.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 3.6%; Score 37.4; DB 10; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1338
ID ADO29933 standard; cDNA; 1212 BP.
DE Human GPCR GPR66 polynucleotide, SEQ ID NO:1035.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 3.6%; Score 37.4; DB 12; Length 1212;
Best Local Similarity 60.2%; Pred. No. 75;
RESULT 1339
ID ADR67059 standard; cDNA; 1281 BP.
DE Human cancer associated gene cDNA sequence SEQ ID NO:105.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.6%; Score 37.4; DB 13; Length 1281;

Best Local Similarity 60.2%; Pred. No. 76;
RESULT 1340
ID AAD08007 standard; cDNA; 1318 BP.
DE Human G-protein coupled receptor, SNORF62 cDNA.
PN WO200144297-A1.
PD 21-JUN-2001.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 3.6%; Score 37.4; DB 5; Length 1318;
Best Local Similarity 60.2%; Pred. No. 77;
RESULT 1341
ID ADX50173 standard; cDNA; 1341 BP.
DE Plant full length insert polynucleotide seqid 24913.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.6%; Score 37.4; DB 13; Length 1341;
Best Local Similarity 49.2%; Pred. No. 77;
RESULT 1342
ID ADT19387 standard; cDNA; 1533 BP.
DE Plant cDNA, Seq ID 4713.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 3.6%; Score 37.4; DB 13; Length 1533;
Best Local Similarity 47.1%; Pred. No. 80;
RESULT 1343
ID AAD24956 standard; cDNA; 2374 BP.
DE Human G-protein coupled receptor-1 (GCREC-1) cDNA.
PN WO200198351-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 37.4; DB 6; Length 2374;
Best Local Similarity 60.2%; Pred. No. 89;
RESULT 1344
ID ADA70747 standard; DNA; 2562 BP.
DE Rice gene, SEQ ID 4070.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.6%; Score 37.4; DB 8; Length 2562;
Best Local Similarity 52.2%; Pred. No. 91;
RESULT 1345
ID ADB62298 standard; cDNA; 2569 BP.
DE Human cDNA encoding clone FCBBF20038230.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 37.4; DB 10; Length 2569;
Best Local Similarity 49.2%; Pred. No. 91;
RESULT 1346
ID AAL61172 standard; DNA; 4770 BP.
DE Actinosynnema pretiosum polyketide synthase (PKS) gene #3.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 3.6%; Score 37.4; DB 8; Length 4770;
Best Local Similarity 41.7%; Pred. No. 1.1e+02;
RESULT 1347
ID ADR67058 standard; DNA; 23965 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:104.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.6%; Score 37.4; DB 13; Length 23965;
Best Local Similarity 60.2%; Pred. No. 1.6e+02;
RESULT 1348
ID ADA02594 standard; DNA; 24873 BP.
DE Human BMI1 carcinoma associated gene, SEQ ID NO:1112.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 37.4; DB 9; Length 24873;
Best Local Similarity 48.3%; Pred. No. 1.6e+02;
RESULT 1349
ID ADB72332 standard; DNA; 24873 BP.
DE Human BMI1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 37.4; DB 10; Length 24873;
Best Local Similarity 48.3%; Pred. No. 1.6e+02;
RESULT 1350
ID ADE95842 standard; DNA; 24873 BP.
DE Human BMI1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 37.4; DB 10; Length 24873;
Best Local Similarity 48.3%; Pred. No. 1.6e+02;
RESULT 1351
ID ACL64776 standard; DNA; 25048 BP.
DE M. xanthus DNA fragment, seq id 1239.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.6%; Score 37.4; DB 14; Length 25048;
Best Local Similarity 50.3%; Pred. No. 1.6e+02;
RESULT 1352
ID ABV75558 standard; DNA; 36538 BP.
DE Saccharopolyspora butenyl-spinosyn biosynthetic gene cluster 2.
PN WO200279477-A2.
PD 10-OCT-2002.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.6%; Score 37.4; DB 10; Length 36538;
Best Local Similarity 52.2%; Pred. No. 1.8e+02;
RESULT 1353
ID AAL61224 standard; DNA; 82746 BP.
DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 3.6%; Score 37.4; DB 8; Length 82746;
Best Local Similarity 41.7%; Pred. No. 2.2e+02;
RESULT 1354
ID ADC85301 standard; DNA; 96591 BP.
DE Mouse Sos1 coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 37.4; DB 10; Length 96591;
Best Local Similarity 47.3%; Pred. No. 2.3e+02;
RESULT 1355
ID ADA02822 standard; DNA; 96592 BP.
DE Human SOS1 carcinoma associated gene, SEQ ID NO:1340.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 37.4; DB 9; Length 96592;
Best Local Similarity 47.3%; Pred. No. 2.3e+02;
RESULT 1356
ID ADB72560 standard; DNA; 96592 BP.
DE Human SOS1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 37.4; DB 10; Length 96592;
Best Local Similarity 47.3%; Pred. No. 2.3e+02;
RESULT 1357
ID ADM74417 standard; DNA; 96592 BP.
DE Human carcinoma associated (CA) nucleic acid #43.

PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 3.6%; Score 37.4; DB 12; Length 96592;
Best Local Similarity 47.3%; Pred. No. 2.3e+02;
RESULT 1358
ID ABD04997 standard; DNA; 519 BP.
DE Pseudomonas aeruginosa polynucleotide #3601.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.6%; Score 37.2; DB 11; Length 519;
Best Local Similarity 46.0%; Pred. No. 67;
RESULT 1359
ID ABX73107 standard; cDNA; 727 BP.
DE Monkey variant of human GPCR #4, Incyte clone 703021534H1.
PN US2002106655-A1.
PD 08-AUG-2002.
PA (BAND/) BANDMAN O.
PA (LALP/) LAL P G.
PA (TANG/) TANG Y T.
PA (BAUG/) BAUGHN M R.
Query Match 3.6%; Score 37.2; DB 6; Length 727;
Best Local Similarity 48.6%; Pred. No. 73;
RESULT 1360
ID ABT09678 standard; DNA; 1064 BP.
DE Human PAL-18 polynucleotide SEQ ID NO: 29.
PN US2002106765-A1.
PD 08-AUG-2002.
PA (KIND/) KINDERS R J.
PA (CORE/) COREY M J.
Query Match 3.6%; Score 37.2; DB 6; Length 1064;
Best Local Similarity 46.0%; Pred. No. 81;
RESULT 1361
ID ADW50867 standard; DNA; 1155 BP.
DE Nocardiopsis sp. DSM 16424 DNA encoding a protease L2a Seq 9.
PN WO2004111220-A1.
PD 23-DEC-2004.
PA (NOVO) NOVOZYMES AS.
Query Match 3.6%; Score 37.2; DB 14; Length 1155;
Best Local Similarity 46.0%; Pred. No. 83;
RESULT 1362
ID ADT17394 standard; cDNA; 1608 BP.
DE Plant cDNA, Seq ID 2720.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 3.6%; Score 37.2; DB 13; Length 1608;
Best Local Similarity 53.4%; Pred. No. 90;
RESULT 1363
ID ACL27608 standard; cDNA; 1719 BP.
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:1564.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.6%; Score 37.2; DB 11; Length 1719;
Best Local Similarity 55.4%; Pred. No. 92;
RESULT 1364
ID ADX62612 standard; cDNA; 1815 BP.
DE Plant full length insert polynucleotide seqid 33455.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.6%; Score 37.2; DB 13; Length 1815;
Best Local Similarity 46.8%; Pred. No. 93;
RESULT 1365
ID ACA41017 standard; DNA; 2556 BP.
DE Prokaryotic essential gene #22674.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.6%; Score 37.2; DB 8; Length 2556;
Best Local Similarity 59.4%; Pred. No. 1e+02;
RESULT 1366
ID ABZ40207 standard; DNA; 2556 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 5003.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 3.6%; Score 37.2; DB 10; Length 2556;
Best Local Similarity 59.4%; Pred. No. 1e+02;
RESULT 1367
ID ADR07928 standard; cDNA; 2890 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1434.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 37.2; DB 13; Length 2890;
Best Local Similarity 45.0%; Pred. No. 1e+02;
RESULT 1368
ID AAC77294 standard; cDNA; 3362 BP.
DE Human ORFX ORF2849 polynucleotide sequence SEQ ID NO:5697.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 3.6%; Score 37.2; DB 3; Length 3362;
Best Local Similarity 48.6%; Pred. No. 1.1e+02;
RESULT 1369
ID ADV15286 standard; DNA; 54779 BP.
DE Human osteoporosis related genomic DNA, seq id 27.
PN US6825336-B1.
PD 30-NOV-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.6%; Score 37.2; DB 13; Length 54779;
Best Local Similarity 43.7%; Pred. No. 2.2e+02;
RESULT 1370
ID ADV15298 standard; DNA; 54780 BP.
DE Human osteoporosis related genomic DNA, seq id 39.
PN US6825336-B1.
PD 30-NOV-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.6%; Score 37.2; DB 13; Length 54780;
Best Local Similarity 43.7%; Pred. No. 2.2e+02;
RESULT 1371
ID ACN44522 standard; DNA; 70779 BP.
DE Human genomic sequence hCG17357.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 37.2; DB 11; Length 70779;
Best Local Similarity 43.7%; Pred. No. 2.4e+02;
RESULT 1372
ID AAL40781 standard; DNA; 88421 BP.
DE 88421nt genomic DNA of ramoplanin producing Actinoplanes sp.
PN WO200231155-A2.
PD 18-APR-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 3.6%; Score 37.2; DB 6; Length 88421;
Best Local Similarity 47.9%; Pred. No. 2.5e+02;
RESULT 1373
ID ADM29048 standard; DNA; 130020 BP.
DE Human interleukin 4 receptor (IL4R) genomic DNA SEQ ID NO:88.
PN EP1405921-A1.
PD 07-APR-2004.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 3.6%; Score 37.2; DB 12; Length 130020;
Best Local Similarity 43.7%; Pred. No. 2.8e+02;
RESULT 1374
ID ACN58918 standard; cDNA; 437 BP.

DE Cotton gynoecium tissue EST Clone ID: LIB3829-013-Q6-N6-G12, SEQ:13699.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (PINC/) PINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.5%; Score 37; DB 13; Length 437;
Best Local Similarity 49.7%; Pred. No. 72;
RESULT 1375
ID ACL33144 standard; cDNA; 570 BP.
DE Rice abiotic stress response related polynucleotide SEQ ID NO:11707.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.5%; Score 37; DB 11; Length 570;
Best Local Similarity 67.5%; Pred. No. 77;
RESULT 1376
ID ADJ43507 standard; cDNA; 570 BP.
DE Plant cDNA #4507.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 3.5%; Score 37; DB 12; Length 570;
Best Local Similarity 67.5%; Pred. No. 77;
RESULT 1377
ID AEB66231 standard; DNA; 638 BP.
DE Rice genome derived DNA sequence, SEQ ID 1376.
PN JP2005185101-A.
PD 14-JUL-2005.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
Query Match 3.5%; Score 37; DB 14; Length 638;
Best Local Similarity 50.9%; Pred. No. 79;
RESULT 1378
ID ADO83861 standard; cDNA; 701 BP.
DE Plant full length insert polynucleotide seqid 2581.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.5%; Score 37; DB 13; Length 701;
Best Local Similarity 53.9%; Pred. No. 81;
RESULT 1379
ID ABD06902 standard; DNA; 726 BP.
DE Pseudomonas aeruginosa polynucleotide #5506.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.5%; Score 37; DB 11; Length 726;
Best Local Similarity 48.8%; Pred. No. 82;
RESULT 1380
ID ABK33065 standard; DNA; 852 BP.
DE DNA encoding novel secreted protein Z849065G4P.
PN WO200202621-A2.
PD 10-JAN-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 3.5%; Score 37; DB 6; Length 852;
Best Local Similarity 53.9%; Pred. No. 85;
RESULT 1381
ID ABK33138 standard; DNA; 852 BP.
DE DNA encoding novel secreted protein Z930582G14P.
PN WO200202621-A2.
PD 10-JAN-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 3.5%; Score 37; DB 6; Length 852;
Best Local Similarity 53.9%; Pred. No. 85;
RESULT 1382
ID ACD05533 standard; cDNA; 852 BP.
DE cDNA encoding novel human polypeptide #43.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 37; DB 8; Length 852;
Best Local Similarity 53.9%; Pred. No. 85;
RESULT 1383
ID ADS98477 standard; DNA; 852 BP.
DE Protein factor discovery related isolated human contig DNA, SEQ ID 741.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 3.5%; Score 37; DB 13; Length 852;
Best Local Similarity 53.9%; Pred. No. 85;
RESULT 1384
ID ACL34185 standard; cDNA; 993 BP.
DE Rice abiotic stress response related polynucleotide SEQ ID NO:12748.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.5%; Score 37; DB 11; Length 993;
Best Local Similarity 48.4%; Pred. No. 89;
RESULT 1385
ID ADJ44632 standard; cDNA; 993 BP.
DE Plant cDNA #5632.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 3.5%; Score 37; DB 12; Length 993;
Best Local Similarity 48.4%; Pred. No. 89;
RESULT 1386
ID ACL66732 standard; DNA; 1011 BP.
DE M. xanthus gene sequence, seq id 3195.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 3.5%; Score 37; DB 14; Length 1011;
Best Local Similarity 49.4%; Pred. No. 89;
RESULT 1387
ID ADX49334 standard; cDNA; 1111 BP.
DE Plant full length insert polynucleotide seqid 24074.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 3.5%; Score 37; DB 13; Length 1111;

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  Best Local Similarity   46.1%;  Pred. No. 91;
RESULT 1388
ID   AAS69387 standard; cDNA; 1117 BP.
DE   DNA encoding novel human diagnostic protein #5191.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             3.5%;  Score 37;  DB 5;  Length 1117;
  Best Local Similarity   53.9%;  Pred. No. 91;
RESULT 1389
ID   ADS98364 standard; DNA; 1117 BP.
DE   Protein factor discovery related isolated human contig DNA, SEQ ID 628.
PN   WO2004087874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
  Query Match             3.5%;  Score 37;  DB 13;  Length 1117;
  Best Local Similarity   53.9%;  Pred. No. 91;
RESULT 1390
ID   ACN39558 standard; cDNA; 1131 BP.
DE   Tumour-associated antigenic target (TAT) cDNA DNA325761, SEQ ID NO:3779.
PN   WO2004030615-A2.
PD   15-APR-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 37;  DB 13;  Length 1131;
  Best Local Similarity   53.9%;  Pred. No. 92;
RESULT 1391
ID   ADX31667 standard; cDNA; 1209 BP.
DE   Plant full length insert polynucleotide seqid 14487.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
  Query Match             3.5%;  Score 37;  DB 13;  Length 1209;
  Best Local Similarity   48.4%;  Pred. No. 93;
RESULT 1392
ID   ADX32792 standard; cDNA; 1417 BP.
DE   Plant full length insert polynucleotide seqid 15612.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
  Query Match             3.5%;  Score 37;  DB 13;  Length 1417;
  Best Local Similarity   51.5%;  Pred. No. 97;
RESULT 1393
ID   ACA42444 standard; DNA; 1533 BP.
DE   Prokaryotic essential gene #24101.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match             3.5%;  Score 37;  DB 8;  Length 1533;
  Best Local Similarity   48.8%;  Pred. No. 99;
RESULT 1394
ID   ADS97895 standard; DNA; 1750 BP.
DE   Protein factor discovery related isolated human DNA, SEQ ID No 159.
PN   WO2004087874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
  Query Match             3.5%;  Score 37;  DB 13;  Length 1750;
  Best Local Similarity   53.9%;  Pred. No. 1e+02;
RESULT 1395
ID   ADX52976 standard; cDNA; 1758 BP.
DE   Plant full length insert polynucleotide seqid 27716.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
  Query Match             3.5%;  Score 37;  DB 13;  Length 1758;
  Best Local Similarity   51.5%;  Pred. No. 1e+02;
RESULT 1396
ID   ADG10424 standard; cDNA; 1866 BP.
DE   Human STAT6-activating protein-encoding cDNA, SEQ ID NO:14.
PN   WO200296943-A1.
PD   05-DEC-2002.
PA   (ASAH ) ASAHI KASEI KOGYO KK.
  Query Match             3.5%;  Score 37;  DB 10;  Length 1866;
  Best Local Similarity   53.9%;  Pred. No. 1e+02;
RESULT 1397
ID   ADT19778 standard; cDNA; 1872 BP.
DE   Plant cDNA, Seq ID 5104.
PN   US2004216190-A1.
PD   28-OCT-2004.
PA   (KOVA/) KOVALIC D K.
  Query Match             3.5%;  Score 37;  DB 13;  Length 1872;
  Best Local Similarity   46.1%;  Pred. No. 1e+02;
RESULT 1398
ID   AAD55965 standard; DNA; 1881 BP.
DE   Human secreted protein-encoding gene 4 cDNA clone HLCMJ69, SEQ ID NO:14.
PN   WO2003014314-A2.
PD   20-FEB-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.5%;  Score 37;  DB 8;  Length 1881;
  Best Local Similarity   53.9%;  Pred. No. 1e+02;
RESULT 1399
ID   AAD55980 standard; DNA; 1881 BP.
DE   Human secreted protein-encoding gene 4 cDNA clone HLCMJ69, SEQ ID NO:29.
PN   WO2003014314-A2.
PD   20-FEB-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             3.5%;  Score 37;  DB 8;  Length 1881;
  Best Local Similarity   53.9%;  Pred. No. 1e+02;
RESULT 1400
ID   AAS46021 standard; cDNA; 1968 BP.
DE   Human DNA encoding PRO polypeptide sequence #97.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 37;  DB 4;  Length 1968;
  Best Local Similarity   53.9%;  Pred. No. 1.1e+02;
RESULT 1401
ID   AAA37035 standard; cDNA; 1969 BP.
DE   Human PRO1415 (UNQ731) cDNA sequence SEQ ID NO:49.
PN   WO200012708-A2.
PD   09-MAR-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 37;  DB 3;  Length 1969;
  Best Local Similarity   53.9%;  Pred. No. 1.1e+02;
RESULT 1402
ID   AAF54237 standard; DNA; 1969 BP.
DE   DNA encoding protein of the invention #14.
PN   WO200078961-A1.
PD   28-DEC-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 37;  DB 4;  Length 1969;
  Best Local Similarity   53.9%;  Pred. No. 1.1e+02;
RESULT 1403
ID   ABL88144 standard; cDNA; 1969 BP.
DE   Human PRO1415 cDNA sequence SEQ ID NO:145.
PN   WO200200690-A2.
PD   03-JAN-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             3.5%;  Score 37;  DB 6;  Length 1969;
  Best Local Similarity   53.9%;  Pred. No. 1.1e+02;
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RESULT 1404
ID ABL95633 standard; cDNA; 1969 BP.
DE Human angiogenesis related cDNA PRO1415 SEQ ID NO: 145.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 3.5%; Score 37; DB 6; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1405
ID ACA89471 standard; cDNA; 1969 BP.
DE cDNA encoding human PRO polypeptide #97.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1406
ID ACA73481 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1407
ID ACA05796 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1408
ID ACA66630 standard; cDNA; 1969 BP.
DE cDNA encoding human PRO protein #97.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1409
ID ACF20205 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1410
ID ACF19591 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1411
ID ACD21879 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1412
ID ACF13044 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1413
ID ACD25147 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1414
ID ACF00196 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1415
ID ACA72253 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1416
ID ACD04777 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1417
ID ACD18238 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1418
ID ACD08245 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1419
ID ACA88679 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1420
ID ACA70121 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1421
ID ACD12343 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;

RESULT 1422
ID ACC74258 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1423
ID ACD15886 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1424
ID ACD25454 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1425
ID ACD17931 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1426
ID ACC88218 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1427
ID ACD21572 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1428
ID ACD18639 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1429
ID ABX98249 standard; cDNA; 1969 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 193.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1430
ID ACD14000 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1431
ID ACD09780 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1432
ID ACC88525 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1433
ID ACD21265 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1434
ID ABX75637 standard; cDNA; 1969 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1415.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1435
ID ABX97840 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1436
ID ACA97316 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1437
ID ACA57779 standard; cDNA; 1969 BP.
DE Human PRO1415 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1438
ID ACD14307 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1439
ID ACC91090 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1440
ID ACC88832 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1441
ID ACD07029 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1442
ID ACA67480 standard; cDNA; 1969 BP.

DE Human PRO polynucleotide #97.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1443
ID ACC81535 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1444
ID ACC89139 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1445
ID ACC86495 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1446
ID ACC89753 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1447
ID ACC92932 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1448
ID ACA72560 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1449
ID ACA89078 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1450
ID ACA69814 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1451
ID ACA96957 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1452
ID ACA90953 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1453
ID ACA70735 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1454
ID ACA95245 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1455
ID ACC86188 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1456
ID ACC90060 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1457
ID ACD12668 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1458
ID ACF19898 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1459
ID ABX76842 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1460
ID ACA73174 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1461
ID ACA68717 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1462
ID ACA74561 standard; cDNA; 1969 BP.
DE cDNA encoding human PRO polypeptide #97.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;

Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1463
ID ACA70428 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1464
ID ACD14614 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1465
ID ACA68286 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1466
ID ABX98751 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1467
ID ACC81228 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1468
ID ACA95552 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1469
ID ACD04470 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1470
ID ACC87911 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1471
ID ACF12573 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1472
ID ACA96288 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1473
ID ACA65062 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1474
ID ACA73788 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1475
ID ACA74200 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1476
ID ACA96595 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1477
ID ACD10701 standard; cDNA; 1969 BP.
DE cDNA encoding human PRO polypeptide #97.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1478
ID ACC91397 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1479
ID ACD02732 standard; cDNA; 1969 BP.
DE cDNA encoding human PRO polypeptide #97.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1480
ID ACC87297 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1481
ID ACC85881 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1482
ID ACA65369 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1483
ID ACA94186 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.

PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1484
ID ACA97930 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1485
ID ACA91432 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1486
ID ACA90646 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1487
ID ACD16193 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1488
ID ACD17354 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1489
ID ACC92011 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1490
ID ACA74868 standard; cDNA; 1969 BP.
DE cDNA encoding human PRO polypeptide #97.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1491
ID ACA91739 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1492
ID ACA71383 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1493
ID ACC90783 standard; cDNA; 1969 BP.
DE Human secreted polypeptide PRO1415-encoding cDNA, SEQ ID NO:193.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1494
ID ACA65793 standard; cDNA; 1969 BP.
DE cDNA encoding human PRO protein #97.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1495
ID ACA94938 standard; cDNA; 1969 BP.
DE cDNA encoding human PRO polypeptide #97.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1496
ID ACD16500 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1497
ID ACD15579 standard; cDNA; 1969 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #97.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1498
ID ABX16682 standard; cDNA; 1969 BP.
DE Human cDNA encoding secreted/transmembrane protein #97.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 37; DB 8; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1499
ID ACA97623 standard; cDNA; 1969 BP.
DE Human PRO polynucleotide #97.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 9; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;
RESULT 1500
ID ACA99072 standard; cDNA; 1969 BP.
DE Novel human secreted and transmembrane protein PRO1415 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 3.5%; Score 37; DB 9; Length 1969;
Best Local Similarity 53.9%; Pred. No. 1.1e+02;

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2006, 21:31:31 ; Search time 5313 Seconds
(without alignments)
11201.787 Million cell updates/sec

Title: US-09-854-280-4
Perfect score: 1047
Sequence: 1 gccaggtgtgcaggccgctc.....tgatgaacacatccccaaaa 1047

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1047	100.0	1047	6	BD218877	BD218877 Factor af
	2	1047	100.0	1047	6	AR338357	AR338357 Sequence
	3	1047	100.0	1047	6	AX180766	AX180766 Sequence
	4	1047	100.0	1047	6	AX376380	AX376380 Sequence
	5	1047	100.0	1047	8	AF152099	AF152099 Homo sapi
	6	1047	100.0	1047	8	AY358471	AY358471 Homo sapi
	7	1028.4	98.2	1107	6	BD265555	BD265555 Interleuk
	8	1028.4	98.2	1107	6	CS135286	CS135286 Sequence
	9	1028.4	98.2	1107	6	AR316787	AR316787 Sequence
	10	1015.4	97.0	1078	8	AF142410	AF142410 Homo sapi
	11	1006.4	96.1	1067	6	BD211219	BD211219 Interleuk
	12	1006.4	96.1	1067	6	CQ847631	CQ847631 Sequence
	13	923.4	88.2	1177	6	AX223949	AX223949 Sequence
c	14	651	62.2	156899	14	AC103884	AC103884 Homo sapi
c	15	651	62.2	176797	8	AC116552	AC116552 Homo sapi
	16	640.4	61.2	705	6	BD211199	BD211199 Interleuk
	17	640.4	61.2	705	6	CQ847604	CQ847604 Sequence
	18	613	58.5	613	8	BC069152	BC069152 Homo sapi
	19	594	56.7	594	6	BD218885	BD218885 Factor af
	20	591	56.4	591	6	AX427978	AX427978 Sequence
	21	589	56.3	593	6	CQ714767	CQ714767 Sequence
	22	525.4	50.2	599	10	BV208612	BV208612 IL17C_185
	23	368	35.1	197192	14	AC148637	AC148637 Callithri
	24	363	34.7	585	9	AF458061	AF458061 Mus muscu
	25	274.8	26.2	521	6	BD265554	BD265554 Interleuk
	26	273.8	26.2	521	6	BD265553	BD265553 Interleuk
	27	273.8	26.2	521	6	AR316785	AR316785 Sequence
	28	273.8	26.2	521	6	AR316786	AR316786 Sequence
	29	254.4	24.3	231193	14	AC148624	AC148624 Otolemur
	30	230	22.0	230	6	BD218880	BD218880 Factor af
	31	192.8	18.4	179454	14	AC123737	AC123737 Mus muscu
	32	192.8	18.4	181442	9	AC114917	AC114917 Mus muscu
	33	192.8	18.4	221647	9	AL591003	AL591003 Mouse DNA
	34	175	16.7	267809	14	AC130171	AC130171 Rattus no
	35	143.8	13.7	332	6	BD211220	BD211220 Interleuk
	36	143.8	13.7	332	6	CQ847633	CQ847633 Sequence
	37	121.8	11.6	112467	14	AC164519	AC164519 Alligator
	38	115.8	11.1	122853	14	AC154080	AC154080 Dromaius
c	39	69.8	6.7	125020	8	AF429315	AF429315 Homo sapi
	40	61	5.8	125020	8	AF429315	AF429315 Homo sapi
	41	60	5.7	60	6	CQ545428	CQ545428 Sequence
	42	58.2	5.6	7218	6	I66494	I66494 Sequence 14
	43	56.8	5.4	454	6	BD265546	BD265546 Interleuk
	44	56.8	5.4	454	6	AR316778	AR316778 Sequence
	45	56.8	5.4	498	6	CQ724626	CQ724626 Sequence
	46	56.8	5.4	522	6	BD211221	BD211221 Interleuk
	47	56.8	5.4	522	6	CQ847634	CQ847634 Sequence
	48	56.8	5.4	609	8	AF479775	AF479775 Homo sapi
	49	56.8	5.4	609	11	AY890522	AY890522 Synthetic
	50	56.8	5.4	609	11	AY892988	AY892988 Synthetic
	51	56.8	5.4	1379	8	AF458062	AF458062 Homo sapi
	52	56.8	5.4	1385	6	BD265547	BD265547 Interleuk
	53	56.8	5.4	1385	6	AR316779	AR316779 Sequence
	54	56.8	5.4	1641	6	CQ847606	CQ847606 Sequence
	55	56.8	5.4	1642	6	BD211200	BD211200 Interleuk
	56	56.8	5.4	1754	6	CQ970522	CQ970522 Sequence
	57	56.8	5.4	1754	6	AR338359	AR338359 Sequence
	58	56.8	5.4	1754	6	AX180770	AX180770 Sequence
	59	56.8	5.4	1754	6	AX358834	AX358834 Sequence
	60	56.8	5.4	1754	6	AX362327	AX362327 Sequence
	61	56.8	5.4	1754	8	AY359113	AY359113 Homo sapi
	62	56.8	5.4	1819	6	BD229887	BD229887 Mammalian
	63	56.8	5.4	1819	6	AX648016	AX648016 Sequence
	64	56.8	5.4	1873	8	AY078238	AY078238 Homo sapi
	65	56.8	5.4	1878	8	BC036243	BC036243 Homo sapi
	66	56.8	5.4	2361	6	BD229893	BD229893 Mammalian
	67	56.8	5.4	2361	6	AX648021	AX648021 Sequence
	68	56	5.3	166401	14	CR352260	CR352260 Danio rer
	69	55.2	5.3	1013	6	AX365244	AX365244 Sequence
	70	55.2	5.3	1496	6	AX365250	AX365250 Sequence
	71	53.8	5.1	486	8	AF458059	AF458059 Homo sapi
	72	53.8	5.1	504	6	BD265550	BD265550 Interleuk
	73	53.8	5.1	504	6	AR316782	AR316782 Sequence
	74	53.8	5.1	504	6	AR451796	AR451796 Sequence
	75	53.8	5.1	504	6	AX299773	AX299773 Sequence
	76	53.8	5.1	644	6	AX253225	AX253225 Sequence
	77	53.8	5.1	644	6	AX365242	AX365242 Sequence
	78	53.8	5.1	644	8	AF461739	AF461739 Homo sapi
	79	53.6	5.1	462	9	AY034088	AY034088 Mus muscu
	80	53.6	5.1	985	6	BD265552	BD265552 Interleuk
	81	53.6	5.1	985	6	AR316784	AR316784 Sequence
	82	53.6	5.1	985	6	AR451797	AR451797 Sequence
	83	53.6	5.1	985	6	AX299775	AX299775 Sequence
	84	53.6	5.1	985	9	AF458060	AF458060 Mus muscu
c	85	53.4	5.1	114339	8	AC006409	AC006409 Homo sapi
	86	53.4	5.1	181439	8	AP003559	AP003559 Homo sapi
	87	53.4	5.1	185766	8	AP002754	AP002754 Homo sapi
c	88	53.4	5.1	209545	14	AC087848	AC087848 Homo sapi
	89	52.2	5.0	897	8	BC069565	BC069565 Homo sapi
	90	52.2	5.0	1320	6	AR338358	AR338358 Sequence
	91	52.2	5.0	1320	6	AX092424	AX092424 Sequence

	92	52.2	5.0	1320	6	AX164145 AX164145 Sequence
	93	52.2	5.0	1320	6	AX180768 AX180768 Sequence
	94	52.2	5.0	1320	8	AY359127 AY359127 Homo sapi
	95	52.2	5.0	1335	8	AF305200 AF305200 Homo sapi
	96	51.8	4.9	3156	15	AK120362 AK120362 Oryza sat
c	97	51.8	4.9	110000	15	AP008214_264 Continuation (265
c	98	51.8	4.9	138944	15	AP003920 AP003920 Oryza sat
c	99	51.8	4.9	190948	15	AP005529 AP005529 Oryza sat
	100	51.8	4.9	280558	1	AE017301 AE017301 Thermus t
	101	51.6	4.9	1392	6	BD180083 BD180083 Highly th
	102	51.6	4.9	110000	1	AP008226_05 Continuation (6 of
	103	51.6	4.9	110000	1	AP008226_06 Continuation (7 of
c	104	50.4	4.8	302176	14	AC096479 AC096479 Rattus no
c	105	50.2	4.8	135119	14	AC011578 AC011578 Homo sapi
c	106	49.8	4.8	1127	6	BD221355 BD221355 Human gen
c	107	49.8	4.8	67213	14	AC024538 AC024538 Homo sapi
	108	49.4	4.7	620	6	BD265551 BD265551 Interleuk
	109	49.4	4.7	620	6	AR316783 AR316783 Sequence
	110	49.2	4.7	1032	6	CQ737533 CQ737533 Sequence
c	111	49.2	4.7	144156	8	AL160276 AL160276 Human DNA
c	112	48.4	4.6	10842	1	AE002067 AE002067 Deinococc
	113	48.2	4.6	2205	15	AK107367 AK107367 Oryza sat
	114	48.2	4.6	2771	15	AK110310 AK110310 Oryza sat
	115	48.2	4.6	110000	15	AP008218_257 Continuation (258
	116	48.2	4.6	167131	15	CNS08C8L AL731881 Oryza sat
	117	48	4.6	176386	14	CR855271 CR855271 Danio rer
c	118	47.4	4.5	2560	4	AY453841 AY453841 Oryctolag
c	119	47.4	4.5	2561	6	AR409339 AR409339 Sequence
c	120	47.4	4.5	2561	6	AR650971 AR650971 Sequence
c	121	47.4	4.5	2561	6	AX239605 AX239605 Sequence
c	122	47.4	4.5	52701	14	AC135181 AC135181 Homo sapi
c	123	47.4	4.5	136551	14	AC048354 AC048354 Homo sapi
c	124	47.2	4.5	162363	14	AC142519 AC142519 Rattus no
	125	47.2	4.5	346362	1	BX640439 BX640439 Bordetell
	126	47	4.5	40966	14	AC034180 AC034180 Homo sapi
	127	47	4.5	64706	14	AC136358 AC136358 Homo sapi
	128	46.8	4.5	1032	6	A89638 A89638 Sequence 4
	129	46.8	4.5	1032	6	BD069804 BD069804 Microorga
	130	46.8	4.5	1032	6	CQ830823 CQ830823 Sequence
	131	46.8	4.5	1035	6	CQ898327 CQ898327 Sequence
c	132	46.8	4.5	2000	6	AX655393 AX655393 Sequence
c	133	46.8	4.5	2929	1	SCCLAVAM1 AF124928 Streptomy
c	134	46.8	4.5	7193	6	A89635 A89635 Sequence 1
c	135	46.8	4.5	7193	6	BD069801 BD069801 Microorga
c	136	46.8	4.5	7193	6	CQ830820 CQ830820 Sequence
c	137	46.8	4.5	18070	6	CQ898337 CQ898337 Sequence
c	138	46.8	4.5	98873	8	AL138837 AL138837 Human DNA
c	139	46.8	4.5	298166	14	AC087563 AC087563 Homo sapi
c	140	46.6	4.5	1319	15	AK108100 AK108100 Oryza sat
	141	46.6	4.5	110000	15	AP008208_049 Continuation (50 o
	142	46.6	4.5	113755	15	AP004046 AP004046 Oryza sat
	143	46.6	4.5	132729	15	AP005849 AP005849 Oryza sat
	144	46.6	4.5	234326	14	AC159346 AC159346 Bos tauru
	145	46.6	4.5	239784	14	AC095578 AC095578 Rattus no
	146	46.6	4.5	308050	1	SCO939124 AL939124 Streptomy
	147	46.4	4.4	1065	11	AY659127 AY659127 Synthetic
c	148	46.4	4.4	46742	14	AC100281 AC100281 Mus muscu
c	149	46.4	4.4	65542	14	AC115973 AC115973 Mus muscu
	150	46.4	4.4	162447	8	AC123886 AC123886 Homo sapi
c	151	46.4	4.4	186261	14	AC160381 AC160381 Bos tauru
	152	46.4	4.4	218902	14	AC153258 AC153258 Bos tauru
	153	46.4	4.4	292100	1	SCO939121 AL939121 Streptomy
	154	46.2	4.4	1991	15	AK100770 AK100770 Oryza sat
c	155	46.2	4.4	10732	6	E32986 E32986 Gene encodi
c	156	46.2	4.4	72511	14	AC025954 AC025954 Homo sapi
c	157	46.2	4.4	110000	15	AP008207_049 Continuation (50 o
c	158	46.2	4.4	168372	15	AP002746 AP002746 Oryza sat
c	159	46	4.4	36546	14	AC100555 AC100555 Mus muscu
c	160	46	4.4	213037	14	AC093986 AC093986 Rattus no
	161	45.8	4.4	62649	14	AC022552 AC022552 Homo sapi
	162	45.8	4.4	68330	14	AC116109 AC116109 Mus muscu
	163	45.8	4.4	152331	6	BD080413 BD080413 Novel mol
	164	45.8	4.4	156789	13	AF533768 AF533768 Cercopith
c	165	45.8	4.4	156789	13	AF533768 AF533768 Cercopith
	166	45.8	4.4	165517	14	CR774180 CR774180 Danio rer
	167	45.6	4.4	521	10	PM12B8G AL684326 Penicilli
c	168	45.6	4.4	110000	1	AP006618_20 Continuation (21 o
c	169	45.6	4.4	110000	1	AP006618_21 Continuation (22 o
	170	45.6	4.4	144979	14	AC016280 AC016280 Homo sapi
c	171	45.6	4.4	207782	14	AC074334 AC074334 Mus muscu
c	172	45.6	4.4	348525	1	BX640428 BX640428 Bordetell
	173	45.6	4.4	348642	1	BX640446 BX640446 Bordetell
	174	45.4	4.3	789	6	BD179824 BD179824 Highly th
	175	45.4	4.3	6180	1	PAMEXEFOP X99514 Pseudomonas
	176	45.4	4.3	81417	14	AC023265 AC023265 Homo sapi
c	177	45.4	4.3	102247	14	AC136251 AC136251 Rattus no
	178	45.4	4.3	110000	1	AP008226_09 Continuation (10 o
c	179	45.4	4.3	199035	1	AB088420 AB088420 Pseudomon
c	180	45.4	4.3	215050	1	AL646057 AL646057 Ralstonia
c	181	45.4	4.3	223879	8	AC008735 AC008735 Homo sapi
	182	45.2	4.3	1094	10	PM7G11B AL685196 Penicilli
	183	45.2	4.3	5760	6	AX616761 AX616761 Sequence
	184	45.2	4.3	82024	14	AC023210 AC023210 Homo sapi
c	185	45.2	4.3	90348	1	AF497482 AF497482 Micromono
	186	45.2	4.3	186856	14	BX936401 BX936401 Danio rer
	187	45.2	4.3	219502	14	CR735121 CR735121 Danio rer
c	188	45.2	4.3	300695	14	AC079431 AC079431 Mus muscu
c	189	45.2	4.3	313800	1	SCO939114 AL939114 Streptomy
	190	45	4.3	60931	14	AC105113 AC105113 Homo sapi
c	191	45	4.3	64454	14	AC022620 AC022620 Homo sapi
c	192	45	4.3	64781	14	AC102025 AC102025 Mus muscu
	193	45	4.3	110737	14	AC011105 AC011105 Homo sapi
	194	45	4.3	143666	14	CT025533 CT025533 Mus muscu
	195	44.8	4.3	2000	6	AX655393 AX655393 Sequence
	196	44.8	4.3	11064	1	AE004853 AE004853 Pseudomon
c	197	44.8	4.3	110000	1	AP006618_31 Continuation (32 o
	198	44.8	4.3	110000	1	BA000030_25 Continuation (26 o
	199	44.8	4.3	110000	1	BA000030_26 Continuation (27 o
c	200	44.8	4.3	110000	15	AP008208_051 Continuation (52 o
	201	44.8	4.3	119972	14	AP004029 AP004029 Oryza sat
c	202	44.8	4.3	133464	15	AP005785 AP005785 Oryza sat
	203	44.8	4.3	144952	14	AP005629 AP005629 Oryza sat
c	204	44.8	4.3	170173	15	AP000366 AP000366 Oryza sat
	205	44.8	4.3	208301	14	AC149657 AC149657 Bos tauru
c	206	44.8	4.3	239130	14	AC079420 AC079420 Mus muscu
	207	44.6	4.3	1578	6	A38265 A38265 Sequence 1
	208	44.6	4.3	1578	6	AR001081 AR001081 Sequence
c	209	44.6	4.3	2357	13	AY363172 AY363172 Pseudorab
c	210	44.6	4.3	3797	13	PVULSGENE X87247 Pseudorabie
c	211	44.6	4.3	9382	13	SH1ULGNS L00676 Pseudorabie
	212	44.6	4.3	57178	14	AC023776 AC023776 Homo sapi
c	213	44.6	4.3	64388	14	AC124244 AC124244 Homo sapi
c	214	44.6	4.3	64679	14	AC131251 AC131251 Homo sapi
c	215	44.6	4.3	67221	14	AC133594 AC133594 Homo sapi
	216	44.6	4.3	89878	14	AC021452 AC021452 Homo sapi
c	217	44.6	4.3	101509	14	AC027353 AC027353 Homo sapi
c	218	44.6	4.3	122272	14	AC143808 AC143808 Macaca mu
c	219	44.6	4.3	204019	14	AC090491 AC090491 Mus muscu
c	220	44.6	4.3	265537	14	AC087228 AC087228 Mus muscu
c	221	44.6	4.3	298450	1	SCO939107 AL939107 Streptomy
c	222	44.6	4.3	303091	14	AC084799 AC084799 Mus muscu
c	223	44.4	4.2	4530	10	BV177248 BV177248 sqnm93602
c	224	44.4	4.2	64634	14	AC100010 AC100010 Mus muscu
c	225	44.4	4.2	87994	14	AC022704 AC022704 Homo sapi
c	226	44.4	4.2	110000	1	CP000031_28 Continuation (29 o
	227	44.4	4.2	145667	14	AC155394 AC155394 Zea mays
	228	44.4	4.2	150399	14	AC013385 AC013385 Homo sapi
	229	44.4	4.2	177883	14	AC046159 AC046159 Homo sapi
	230	44.4	4.2	189230	14	AC120836 AC120836 Mus muscu
c	231	44.4	4.2	205691	14	AC087227 AC087227 Mus muscu
c	232	44.4	4.2	249687	14	AC015693 AC015693 Homo sapi
	233	44.2	4.2	748	10	PM12B4B AL684317 Penicilli
	234	44.2	4.2	3528	15	AK109967 AK109967 Oryza sat
	235	44.2	4.2	5208	6	CQ720332 CQ720332 Sequence
c	236	44.2	4.2	38911	8	AC005559 AC005559 Homo sapi
	237	44.2	4.2	59237	14	AC091279 AC091279 Mus muscu

	238	44.2	4.2	61363	14	AC068364 AC068364 Homo sapi
	239	44.2	4.2	67171	14	AC090703 AC090703 Homo sapi
	240	44.2	4.2	75449	14	AC016188 AC016188 Homo sapi
	241	44.2	4.2	82815	14	AC062001 AC062001 Homo sapi
	242	44.2	4.2	110000	1	BA000035_24 Continuation (25 o
	243	44.2	4.2	110000	15	AE016815_6 Continuation (7 of
	244	44.2	4.2	141892	14	AC023197 AC023197 Mus muscu
	245	44.2	4.2	216449	14	AC051616 AC051616 Mus muscu
	246	44.2	4.2	226382	14	AC097295 AC097295 Rattus no
c	247	44.2	4.2	263468	14	AC106322 AC106322 Rattus no
c	248	44.2	4.2	300800	1	SCO939112 AL939112 Streptomy
c	249	44.2	4.2	347071	1	BX640415 BX640415 Bordetell
c	250	44	4.2	732	10	BV106791 BV106791 PZA01640
c	251	44	4.2	1065	10	PM2B12B AL684695 Penicilli
	252	44	4.2	2151	15	AK102694 AK102694 Oryza sat
c	253	44	4.2	2250	6	AX840058 AX840058 Sequence
c	254	44	4.2	2753	6	BD160551 BD160551 Primer fo
c	255	44	4.2	2753	6	AX883823 AX883823 Sequence
c	256	44	4.2	2753	8	AK024284 AK024284 Homo sapi
c	257	44	4.2	2801	8	BC003555 BC003555 Homo sapi
	258	44	4.2	5504	8	HSU07802 U07802 Human Tis11
	259	44	4.2	57544	14	AC100980 AC100980 Mus muscu
	260	44	4.2	63082	14	AC022663 AC022663 Homo sapi
	261	44	4.2	75628	14	AC021793 AC021793 Homo sapi
	262	44	4.2	110000	1	BA000030_68 Continuation (69 o
	263	44	4.2	110000	1	BA000030_69 Continuation (70 o
	264	44	4.2	126667	14	AC015839 AC015839 Homo sapi
	265	44	4.2	151608	14	AC118445 AC118445 Rattus no
c	266	44	4.2	156563	14	AC079458 AC079458 Homo sapi
c	267	44	4.2	189043	14	CR847952 CR847952 Danio rer
	268	44	4.2	200578	14	AC147296 AC147296 Pan trogl
c	269	44	4.2	202083	14	AC023833 AC023833 Mus muscu
c	270	44	4.2	270403	14	AC164042 AC164042 Bos tauru
	271	44	4.2	348934	1	BX640417 BX640417 Bordetell
	272	43.8	4.2	1337	6	BD216593 BD216593 Novel hum
	273	43.8	4.2	2515	15	AK070171 AK070171 Oryza sat
c	274	43.8	4.2	10500	13	BHV1ULGNS X94677 Bovine herp
c	275	43.8	4.2	37000	13	BHT1UL Z78205 Bovine herp
	276	43.8	4.2	51274	14	AC023454 AC023454 Homo sapi
c	277	43.8	4.2	68378	14	AC113131 AC113131 Homo sapi
	278	43.8	4.2	88064	14	AC022707 AC022707 Homo sapi
	279	43.8	4.2	93559	14	AC024685 AC024685 Homo sapi
	280	43.8	4.2	110000	1	BA000030_37 Continuation (38 o
	281	43.8	4.2	110000	15	AP008217_108 Continuation (109
	282	43.8	4.2	121894	15	AC135599 AC135599 Oryza sat
c	283	43.8	4.2	124321	15	OSA245900 AJ245900 Oryza sat
	284	43.8	4.2	134940	14	AC018939 AC018939 Homo sapi
c	285	43.8	4.2	135301	13	BHV1CGEN AJ004801 Bovine he
c	286	43.8	4.2	175243	14	CR854906 CR854906 Danio rer
c	287	43.8	4.2	191867	14	CR388008 CR388008 Danio rer
c	288	43.8	4.2	222707	14	AC079425 AC079425 Mus muscu
c	289	43.8	4.2	258174	14	AC079429 AC079429 Mus muscu
	290	43.8	4.2	270418	1	AE017303 AE017303 Thermus t
	291	43.6	4.2	1080	15	CNS019XP AL112229 Botrytis
	292	43.6	4.2	1143	10	PM12A11G AL684286 Penicilli
	293	43.6	4.2	3867	1	AY033407 AY033407 Myxococcu
c	294	43.6	4.2	49558	1	AY509003 AY509003 Salmonell
	295	43.6	4.2	52804	14	AC091024 AC091024 Homo sapi
	296	43.6	4.2	60885	14	AC100962 AC100962 Mus muscu
	297	43.6	4.2	77191	14	AC023381 AC023381 Homo sapi
	298	43.6	4.2	93939	1	AE006471 AE006471 Salmonell
c	299	43.6	4.2	110000	14	AC142912_5 Continuation (6 of
c	300	43.6	4.2	110000	14	AC151898_1 Continuation (2 of
	301	43.6	4.2	142014	14	CR407553 CR407553 Danio rer
c	302	43.6	4.2	174239	14	AC073830 AC073830 Homo sapi
c	303	43.6	4.2	183049	14	CR762462 CR762462 Danio rer
	304	43.6	4.2	185950	14	AL606486 AL606486 Homo sapi
c	305	43.6	4.2	222895	14	AC084065 AC084065 Mus muscu
c	306	43.6	4.2	252689	14	AC079433 AC079433 Mus muscu
c	307	43.6	4.2	265985	14	AC087226 AC087226 Mus muscu
	308	43.4	4.1	251	10	BV197639 BV197639 sqnm19425
c	309	43.4	4.1	660	15	CNS019OG AL111896 Botrytis
c	310	43.4	4.1	3281	14	AC143602 AC143602 Macaca mu
	311	43.4	4.1	56356	14	AC090305 AC090305 Homo sapi
c	312	43.4	4.1	63822	14	AC024277 AC024277 Homo sapi
	313	43.4	4.1	72360	14	AC022984 AC022984 Homo sapi
c	314	43.4	4.1	76046	14	AC101101 AC101101 Mus muscu
	315	43.4	4.1	76052	14	AC023262 AC023262 Homo sapi
	316	43.4	4.1	84742	14	AC099937 AC099937 Mus muscu
	317	43.4	4.1	87440	14	AC021226 AC021226 Homo sapi
	318	43.4	4.1	110000	1	AP006618_48 Continuation (49 o
c	319	43.4	4.1	110000	14	AC144302_1 Continuation (2 of
	320	43.4	4.1	236007	14	AC156411 AC156411 Bos tauru
c	321	43.4	4.1	244971	9	AL662891 AL662891 Mouse DNA
c	322	43.4	4.1	348171	1	BX640412 BX640412 Bordetell
	323	43.2	4.1	1017	6	AX763608 AX763608 Sequence
c	324	43.2	4.1	1071	10	BV111241 BV111241 PZA00983
c	325	43.2	4.1	12162	1	AY034175 AY034175 Streptomy
c	326	43.2	4.1	13901	1	AY258009 AY258009 Streptomy
c	327	43.2	4.1	29870	6	AX763606 AX763606 Sequence
	328	43.2	4.1	33058	14	AC100211 AC100211 Mus muscu
c	329	43.2	4.1	49503	1	AB040415 AB040415 Salmonell
	330	43.2	4.1	53552	14	AC100796 AC100796 Homo sapi
c	331	43.2	4.1	87167	8	AC134504 AC134504 Homo sapi
	332	43.2	4.1	100511	14	AC010774 AC010774 Homo sapi
	333	43.2	4.1	110000	1	AP006618_39 Continuation (40 o
c	334	43.2	4.1	110000	14	BX548027_0 BX548027 Danio rer
	335	43.2	4.1	120091	14	AC012684 AC012684 Homo sapi
c	336	43.2	4.1	130244	14	AC013518 AC013518 Homo sapi
	337	43.2	4.1	135255	14	AC013804 AC013804 Homo sapi
	338	43.2	4.1	147124	14	AC022768 AC022768 Homo sapi
	339	43.2	4.1	194191	14	AC097332 AC097332 Pan trogl
c	340	43.2	4.1	208898	14	AC144122 AC144122 Macaca mu
c	341	43.2	4.1	213292	9	AC151718 AC151718 Mus muscu
c	342	43.2	4.1	220469	14	AC074307 AC074307 Mus muscu
c	343	43.2	4.1	225119	14	AC015894 AC015894 Homo sapi
	344	43	4.1	816	15	CNS01BK8 AL114336 Botrytis
	345	43	4.1	1143	6	BD265549 BD265549 Interleuk
	346	43	4.1	1143	6	AR316781 AR316781 Sequence
	347	43	4.1	1143	9	AF458063 AF458063 Mus muscu
	348	43	4.1	1221	6	BD229890 BD229890 Mammalian
	349	43	4.1	1221	6	AX648024 AX648024 Sequence
	350	43	4.1	2510	13	SH1UL2XA M95285 Suid herpes
	351	43	4.1	32748	1	AB070951 AB070951 Streptomy
	352	43	4.1	39360	1	AY943953 AY943953 Streptomy
	353	43	4.1	63629	14	AC091187 AC091187 Homo sapi
c	354	43	4.1	67397	14	AC113440 AC113440 Mus muscu
c	355	43	4.1	77812	14	AC016860 AC016860 Homo sapi
c	356	43	4.1	110000	1	BA000030_45 Continuation (46 o
c	357	43	4.1	110000	15	AE016820_11 Continuation (12 o
c	358	43	4.1	150074	14	AC016007 AC016007 Homo sapi
	359	43	4.1	150695	14	AC023576 AC023576 Mus muscu
	360	43	4.1	164520	14	AC020738 AC020738 Homo sapi
	361	43	4.1	186261	14	AC160381 AC160381 Bos tauru
	362	43	4.1	303550	1	SCO939118 AL939118 Streptomy
	363	42.8	4.1	819	10	CNS06EWP AL395663 T7 end of
c	364	42.8	4.1	913	10	BV115820 BV115820 PZA01219
c	365	42.8	4.1	934	10	G41997 G41997 SHGC-69049
	366	42.8	4.1	58483	14	AC100352 AC100352 Mus muscu
	367	42.8	4.1	60121	14	AC036198 AC036198 Homo sapi
	368	42.8	4.1	85434	14	AC066610 AC066610 Homo sapi
c	369	42.8	4.1	110000	15	AP008216_123 Continuation (124
c	370	42.8	4.1	110000	15	AP008216_199 Continuation (200
	371	42.8	4.1	110000	15	AP008207_231 Continuation (232
	372	42.8	4.1	110000	15	AP008207_264 Continuation (265
	373	42.8	4.1	116932	15	AC074232 AC074232 Oryza sat
	374	42.8	4.1	154821	15	AP003709 AP003709 Oryza sat
	375	42.8	4.1	157201	15	AP003048 AP003048 Oryza sat
c	376	42.8	4.1	168192	15	AC078839 AC078839 Genomic S
c	377	42.8	4.1	198344	14	AC087872 AC087872 Mus muscu
c	378	42.8	4.1	300029	15	AE017089 AE017089 Oryza sat
c	379	42.8	4.1	300029	15	AE017114 AE017114 Oryza sat
c	380	42.8	4.1	314100	1	SCO939106 AL939106 Streptomy
	381	42.6	4.1	354	4	AY664382 AY664382 Ursus arc
	382	42.6	4.1	359	4	AY664379 AY664379 Ursus ame
	383	42.6	4.1	359	4	AY664380 AY664380 Ursus mar

	384	42.6	4.1	362	4	AY664381 AY664381 Ursus arc
c	385	42.6	4.1	601	10	BV167551 BV167551 sqnm5843
c	386	42.6	4.1	660	15	CNS01C7T AL115185 Botrytis
	387	42.6	4.1	42722	14	AC015870 AC015870 Homo sapi
	388	42.6	4.1	51919	14	AC100054 AC100054 Mus muscu
	389	42.6	4.1	62557	14	AC137106 AC137106 Mus muscu
	390	42.6	4.1	78167	14	AC023422 AC023422 Homo sapi
	391	42.6	4.1	80133	14	AC021347 AC021347 Homo sapi
c	392	42.6	4.1	87483	14	AC141302_3 Continuation (4 of
c	393	42.6	4.1	110000	14	AC141302_2 Continuation (3 of
c	394	42.6	4.1	110000	15	AP008215_054 Continuation (55 o
	395	42.6	4.1	115468	14	AC011820 AC011820 Homo sapi
	396	42.6	4.1	129755	14	AC019296 AC019296 Homo sapi
c	397	42.6	4.1	130540	14	AC079417 AC079417 Mus muscu
c	398	42.6	4.1	147990	14	AC148827 AC148827 Pan trogl
c	399	42.6	4.1	150715	13	AY714813 AY714813 Cercopith
c	400	42.6	4.1	157574	15	AP005547 AP005547 Oryza sat
c	401	42.6	4.1	187546	14	AC129236 AC129236 Homo sapi
c	402	42.6	4.1	191749	14	AC074381 AC074381 Homo sapi
	403	42.6	4.1	211967	14	AC013368 AC013368 Homo sapi
c	404	42.6	4.1	230272	14	AC142671 AC142671 Macaca mu
c	405	42.6	4.1	253711	14	AC143908 AC143908 Macaca mu
c	406	42.6	4.1	257047	14	AC090879 AC090879 Mus muscu
	407	42.6	4.1	300100	1	SCO939123 AL939123 Streptomy
c	408	42.4	4.0	291	6	BD081222 BD081222 Persephin
	409	42.4	4.0	291	6	BD081223 BD081223 Persephin
c	410	42.4	4.0	291	6	AR491994 AR491994 Sequence
	411	42.4	4.0	291	6	AR491995 AR491995 Sequence
c	412	42.4	4.0	471	6	BD081226 BD081226 Persephin
	413	42.4	4.0	471	6	BD081227 BD081227 Persephin
c	414	42.4	4.0	471	6	CQ720691 CQ720691 Sequence
c	415	42.4	4.0	471	6	AR491998 AR491998 Sequence
	416	42.4	4.0	471	6	AR491999 AR491999 Sequence
	417	42.4	4.0	611	10	BV122575 BV122575 PZA01737
	418	42.4	4.0	756	10	CNS06EET AL395019 T3 end of
c	419	42.4	4.0	798	10	G40890 G40890 Z8941 Zebra
c	420	42.4	4.0	1064	10	BV111233 BV111233 PZA00983
	421	42.4	4.0	1225	8	BC039588 BC039588 Homo sapi
	422	42.4	4.0	1629	6	AX411155 AX411155 Sequence
	423	42.4	4.0	1629	8	HSERF2 X78992 H.sapiens E
	424	42.4	4.0	1685	15	AK101511 AK101511 Oryza sat
c	425	42.4	4.0	2180	6	AX713738 AX713738 Sequence
c	426	42.4	4.0	2180	8	AK055490 AK055490 Homo sapi
c	427	42.4	4.0	3133	6	AX646999 AX646999 Sequence
c	428	42.4	4.0	47434	14	AC023918 AC023918 Homo sapi
c	429	42.4	4.0	71206	14	AC027744 AC027744 Homo sapi
	430	42.4	4.0	79452	14	AC016536 AC016536 Homo sapi
	431	42.4	4.0	80291	14	AC101154 AC101154 Mus muscu
	432	42.4	4.0	110000	15	AP008207_373 Continuation (374
	433	42.4	4.0	110000	15	AP008207_374 Continuation (375
	434	42.4	4.0	110000	15	AP008213_052 Continuation (53 o
	435	42.4	4.0	118820	8	AC011491 AC011491 Homo sapi
c	436	42.4	4.0	127399	8	AL158825 AL158825 Human DNA
	437	42.4	4.0	130907	15	AP003848 AP003848 Oryza sat
	438	42.4	4.0	138416	15	AP004379 AP004379 Oryza sat
	439	42.4	4.0	146951	15	AP003270 AP003270 Oryza sat
	440	42.4	4.0	151490	15	AP003611 AP003611 Oryza sat
	441	42.4	4.0	157666	8	AC034151 AC034151 Homo sapi
	442	42.4	4.0	158087	8	AC128677 AC128677 Homo sapi
	443	42.4	4.0	160460	14	AC140516 AC140516 Homo sapi
c	444	42.4	4.0	161808	14	AC139268 AC139268 Homo sapi
c	445	42.4	4.0	163118	14	AC090973 AC090973 Oryza sat
	446	42.4	4.0	164192	8	AC074338 AC074338 Human Chr
	447	42.4	4.0	179488	8	AC083863 AC083863 Homo sapi
	448	42.4	4.0	181079	14	AC016667 AC016667 Homo sapi
	449	42.4	4.0	187393	14	AC084325 AC084325 Mus muscu
	450	42.4	4.0	204540	8	AC122710 AC122710 Homo sapi
	451	42.4	4.0	207840	14	AC142383 AC142383 Homo sapi
	452	42.4	4.0	252261	14	AC096911 AC096911 Rattus no
c	453	42.4	4.0	262256	14	CR855391 CR855391 Danio rer
c	454	42.4	4.0	267876	14	AC095156 AC095156 Rattus no
c	455	42.4	4.0	309050	1	SCO939117 AL939117 Streptomy
c	456	42.4	4.0	348934	1	BX640417 BX640417 Bordetell
	457	42.4	4.0	349442	1	BX640447 BX640447 Bordetell
	458	42.2	4.0	583	10	BV383122 BV383122 S244P6289
c	459	42.2	4.0	586	8	HSU18294 U18294 Human histo
	460	42.2	4.0	612	10	BV122572 BV122572 PZA01737
c	461	42.2	4.0	626	15	CNS018RP AL110716 Botrytis
	462	42.2	4.0	906	15	AF364542 AF364542 Larix lya
	463	42.2	4.0	971	10	PM12E5B AL684391 Penicilli
	464	42.2	4.0	1475	8	HUMRNAF L10377 Human (clon
	465	42.2	4.0	3492	6	AX226561 AX226561 Sequence
	466	42.2	4.0	3493	6	AX226562 AX226562 Sequence
	467	42.2	4.0	7406	6	CS055401 CS055401 Sequence
	468	42.2	4.0	8776	6	CQ730478 CQ730478 Sequence
	469	42.2	4.0	9045	6	AX223857 AX223857 Sequence
	470	42.2	4.0	9057	6	CS055399 CS055399 Sequence
	471	42.2	4.0	9087	6	AX226507 AX226507 Sequence
	472	42.2	4.0	11389	6	CS055397 CS055397 Sequence
	473	42.2	4.0	11389	6	AX549158 AX549158 Sequence
	474	42.2	4.0	11389	8	AF231024 AF231024 Homo sapi
	475	42.2	4.0	25681	1	SAE414559 AJ414559 Saccharot
	476	42.2	4.0	26144	1	AB090952 AB090952 Lechevali
c	477	42.2	4.0	28654	1	AF534707 AF534707 Lechevali
	478	42.2	4.0	53634	14	AC119277 AC119277 Mus muscu
c	479	42.2	4.0	65612	14	AC087452 AC087452 Homo sapi
	480	42.2	4.0	65942	14	AC036124 AC036124 Homo sapi
	481	42.2	4.0	66758	14	AC102366 AC102366 Mus muscu
c	482	42.2	4.0	69227	14	AC074060 AC074060 Homo sapi
	483	42.2	4.0	69354	14	AC069342 AC069342 Homo sapi
c	484	42.2	4.0	70511	14	AC091083 AC091083 Homo sapi
c	485	42.2	4.0	72910	14	AC023998 AC023998 Homo sapi
c	486	42.2	4.0	106590	14	AC151952 AC151952 Pan trogl
	487	42.2	4.0	106707	14	AC019314 AC019314 Homo sapi
c	488	42.2	4.0	106707	14	AC019314 AC019314 Homo sapi
	489	42.2	4.0	106950	14	AC016474 AC016474 Homo sapi
	490	42.2	4.0	120206	8	HS439F8 AL021392 Human DNA
	491	42.2	4.0	155038	14	AC013684 AC013684 Homo sapi
c	492	42.2	4.0	185822	14	AC073554 AC073554 Homo sapi
c	493	42.2	4.0	205645	14	AC093923 AC093923 Mus muscu
c	494	42.2	4.0	217412	14	AC024400 AC024400 Homo sapi
c	495	42.2	4.0	241522	14	AC137599 AC137599 Oryza sat
	496	42.2	4.0	283100	1	SCO939110 AL939110 Streptomy
c	497	42	4.0	659	15	BT018958 BT018958 Zea mays
c	498	42	4.0	803	10	BV117394 BV117394 PZA01861
c	499	42	4.0	1000	6	BD221362 BD221362 Human gen
	500	42	4.0	1080	15	CNS01A6O AL112552 Botrytis
	501	42	4.0	3065	9	AF307777 AF307777 Mus muscu
	502	42	4.0	22449	1	SPSNBCDE Y11548 S.pristinae
	503	42	4.0	22449	1	SPSNBCGEN X98690 S.pristinae
	504	42	4.0	55606	14	AC137083 AC137083 Homo sapi
	505	42	4.0	56379	14	AC023447 AC023447 Homo sapi
c	506	42	4.0	56539	14	AC083758 AC083758 Homo sapi
	507	42	4.0	60609	14	AC023519 AC023519 Homo sapi
c	508	42	4.0	65523	14	AC024266 AC024266 Homo sapi
c	509	42	4.0	71123	14	AC103643 AC103643 Mus muscu
c	510	42	4.0	71596	14	AC100877 AC100877 Mus muscu
	511	42	4.0	73948	14	AC022556 AC022556 Homo sapi
c	512	42	4.0	76557	14	AC018439 AC018439 Homo sapi
	513	42	4.0	77237	14	AC022599 AC022599 Homo sapi
c	514	42	4.0	80615	14	AC023304 AC023304 Homo sapi
c	515	42	4.0	91224	8	AC093582 AC093582 Homo sapi
c	516	42	4.0	110000	1	AP006618_49 Continuation (50 o
c	517	42	4.0	110000	1	BA000030_44 Continuation (45 o
	518	42	4.0	110000	1	CP000088_25 Continuation (26 o
c	519	42	4.0	119153	14	AC152037 AC152037 Dasypus n
	520	42	4.0	127236	14	AC155438 AC155438 Zea mays
	521	42	4.0	132415	14	AC034276 AC034276 Homo sapi
	522	42	4.0	134105	14	AC073383 AC073383 Homo sapi
c	523	42	4.0	141003	14	AC016463 AC016463 Homo sapi
c	524	42	4.0	156119	14	AC073247 AC073247 Homo sapi
c	525	42	4.0	164374	14	AC145358 AC145358 Didelphis
	526	42	4.0	166031	14	CR354375 CR354375 Danio rer
c	527	42	4.0	172090	14	AC051661 AC051661 Homo sapi
c	528	42	4.0	196311	9	AC159644 AC159644 Mus muscu
c	529	42	4.0	196965	14	AC073080 AC073080 Homo sapi

c 530	42	4.0	196978	14	AC015872	AC015872 Homo sapi
c 531	42	4.0	222973	14	AC093403	AC093403 Mus muscu
532	42	4.0	225164	14	CR855270	CR855270 Danio rer
c 533	42	4.0	227067	14	AC140391	AC140391 Mus muscu
534	41.8	4.0	885	10	PM7F8G	AL685189 Penicilli
c 535	41.8	4.0	1194	6	AR623553	AR623553 Sequence
c 536	41.8	4.0	1272	15	AY346329	AY346329 Oryza sat
c 537	41.8	4.0	4546	6	CQ722533	CQ722533 Sequence
c 538	41.8	4.0	27219	6	AR619849	AR619849 Sequence
539	41.8	4.0	48603	14	AC100169	AC100169 Mus muscu
540	41.8	4.0	52359	14	AC010772	AC010772 Homo sapi
c 541	41.8	4.0	58779	14	AC036219	AC036219 Homo sapi
542	41.8	4.0	62170	14	AC025600	AC025600 Homo sapi
c 543	41.8	4.0	65495	14	AC127501	AC127501 Homo sapi
544	41.8	4.0	74138	14	AC021272	AC021272 Homo sapi
545	41.8	4.0	76064	14	AC101191	AC101191 Mus muscu
c 546	41.8	4.0	77227	14	AC025099	AC025099 Homo sapi
547	41.8	4.0	82897	14	AC022595	AC022595 Homo sapi
c 548	41.8	4.0	95674	15	AE017086	AE017086 Oryza sat
c 549	41.8	4.0	110000	15	AP008216_097	Continuation (98 o
c 550	41.8	4.0	110000	15	AP008216_115	Continuation (116
c 551	41.8	4.0	126933	1	DQ118863	DQ118863 Streptomy
c 552	41.8	4.0	139468	15	AC090441	AC090441 Oryza sat
553	41.8	4.0	145695	14	AC015690	AC015690 Homo sapi
c 554	41.8	4.0	154025	14	AC142058	AC142058 Rattus no
c 555	41.8	4.0	156052	14	CR749776	CR749776 Danio rer
c 556	41.8	4.0	156159	15	AC079935	AC079935 Genomic s
557	41.8	4.0	169723	14	AC153257	AC153257 Bos tauru
c 558	41.8	4.0	170708	14	AC149308	AC149308 Zea mays
559	41.8	4.0	190462	8	AC092535	AC092535 Homo sapi
560	41.8	4.0	203050	1	AL646071	AL646071 Ralstonia
561	41.8	4.0	245342	14	AC130961	AC130961 Rattus no
c 562	41.8	4.0	260790	14	AC136577	AC136577 Rattus no
c 563	41.8	4.0	300029	15	AE017080	AE017080 Oryza sat
c 564	41.8	4.0	347356	1	BX640437	BX640437 Bordetell
c 565	41.8	4.0	348251	1	BX640423	BX640423 Bordetell
566	41.6	4.0	551	10	BV107389	BV107389 PZA01604
567	41.6	4.0	625	10	BV107430	BV107430 PZA01630
568	41.6	4.0	963	10	PM12H12G	AL684456 Penicilli
569	41.6	4.0	1562	15	AK109895	AK109895 Oryza sat
570	41.6	4.0	2072	15	AK072481	AK072481 Oryza sat
571	41.6	4.0	2388	15	AK121595	AK121595 Oryza sat
c 572	41.6	4.0	3163	6	AX647321	AX647321 Sequence
c 573	41.6	4.0	27825	14	AC015763	AC015763 Homo sapi
c 574	41.6	4.0	36021	14	AC087524	AC087524 Homo sapi
c 575	41.6	4.0	59050	14	AC133635	AC133635 Homo sapi
576	41.6	4.0	59520	14	AC100072	AC100072 Mus muscu
c 577	41.6	4.0	70820	14	AC139544	AC139544 Homo sapi
578	41.6	4.0	72847	14	AC023563	AC023563 Homo sapi
c 579	41.6	4.0	75101	14	AC136397	AC136397 Rattus no
c 580	41.6	4.0	77884	14	AC139551	AC139551 Homo sapi
c 581	41.6	4.0	78220	14	AC023212	AC023212 Homo sapi
c 582	41.6	4.0	79355	14	AC021280	AC021280 Homo sapi
583	41.6	4.0	84701	14	AC016122	AC016122 Homo sapi
584	41.6	4.0	88114	14	AC022906	AC022906 Homo sapi
585	41.6	4.0	104836	14	AC151619	AC151619 Medicago
c 586	41.6	4.0	110000	15	AP008216_186	Continuation (187
587	41.6	4.0	110000	15	AP008216_219	Continuation (220
588	41.6	4.0	113124	14	AC150076	AC150076 Gallus ga
c 589	41.6	4.0	114791	8	HSDJ850E9	AL121758 Human DNA
c 590	41.6	4.0	130058	15	AC078840	AC078840 Oryza sat
c 591	41.6	4.0	165191	8	HSDJ140A9	AL109917 Human DNA
592	41.6	4.0	166604	14	AC022783	AC022783 Mus muscu
c 593	41.6	4.0	177364	14	AC150041	AC150041 Gallus ga
c 594	41.6	4.0	177426	14	AC021222	AC021222 Homo sapi
c 595	41.6	4.0	181988	14	AC090552	AC090552 Homo sapi
c 596	41.6	4.0	183046	15	AC087599	AC087599 Oryza sat
c 597	41.6	4.0	190590	14	AC135045	AC135045 Homo sapi
c 598	41.6	4.0	196471	14	CR846101	CR846101 Danio rer
599	41.6	4.0	202046	14	AC151872	AC151872 Lemur cat
600	41.6	4.0	204924	14	AC015616	AC015616 Homo sapi
c 601	41.6	4.0	207790	14	AC150166	AC150166 Gallus ga
602	41.6	4.0	248550	1	SCO939120	AL939120 Streptomy
603	41.6	4.0	271402	14	AC137598	AC137598 Oryza sat
c 604	41.6	4.0	301934	15	AE017110	AE017110 Oryza sat
605	41.6	4.0	304969	15	AE017120	AE017120 Oryza sat
606	41.6	4.0	309430	14	AC012209	AC012209 Homo sapi
c 607	41.4	4.0	578	10	BV106802	BV106802 PZA01642
c 608	41.4	4.0	686	10	BV106785	BV106785 PZA01640
c 609	41.4	4.0	720	15	CNS01AGV	AL112919 Botrytis
c 610	41.4	4.0	720	15	CNS01D1X	AL116269 Botrytis
611	41.4	4.0	936	15	CNS01AYK	AL113556 Botrytis
612	41.4	4.0	1136	5	AF064608	AF064608 Gallus ga
c 613	41.4	4.0	2764	13	HSBBICP4B	L14321 Bovine herp
c 614	41.4	4.0	12425	6	AR409341	AR409341 Sequence
c 615	41.4	4.0	12425	6	AR650973	AR650973 Sequence
c 616	41.4	4.0	12425	6	AX239607	AX239607 Sequence
c 617	41.4	4.0	56133	14	AC115998	AC115998 Homo sapi
618	41.4	4.0	59219	14	AC090585	AC090585 Homo sapi
619	41.4	4.0	62709	14	AC136463	AC136463 Rattus no
620	41.4	4.0	64628	14	AC116899	AC116899 Mus muscu
c 621	41.4	4.0	65500	14	AC136897	AC136897 Homo sapi
622	41.4	4.0	65748	14	AC090187	AC090187 Homo sapi
623	41.4	4.0	71333	14	AC100716	AC100716 Mus muscu
c 624	41.4	4.0	76141	14	AC024393	AC024393 Homo sapi
625	41.4	4.0	77836	14	AC022573	AC022573 Homo sapi
626	41.4	4.0	79023	14	AC021951	AC021951 Homo sapi
c 627	41.4	4.0	89813	14	AC023660	AC023660 Homo sapi
628	41.4	4.0	108399	14	AL356736	AL356736 Homo sapi
c 629	41.4	4.0	110000	1	BX571965_16	Continuation (17 o
630	41.4	4.0	110000	1	CP000010_14	Continuation (15 o
631	41.4	4.0	110000	15	AP008211_014	Continuation (15 o
632	41.4	4.0	122262	15	AC161790	AC161790 Oryza sat
633	41.4	4.0	129049	14	AC069191	AC069191 Homo sapi
634	41.4	4.0	138537	14	AC130608	AC130608 Oryza sat
635	41.4	4.0	140176	14	AC016411	AC016411 Homo sapi
636	41.4	4.0	144455	15	AC129720	AC129720 Oryza sat
637	41.4	4.0	166931	8	AL358792	AL358792 Human DNA
638	41.4	4.0	171574	14	AC012300	AC012300 Homo sapi
c 639	41.4	4.0	179206	8	CNS01DS6	AL121656 BAC seque
640	41.4	4.0	179342	14	CR855375	CR855375 Danio rer
c 641	41.4	4.0	192736	14	AC091383	AC091383 Rattus no
642	41.4	4.0	208936	14	AC010821	AC010821 Homo sapi
643	41.4	4.0	243422	14	AC098453	AC098453 Rattus no
c 644	41.4	4.0	253148	14	AC098015	AC098015 Rattus no
645	41.4	4.0	259583	14	AC160709	AC160709 Bos tauru
646	41.2	3.9	868	15	AB119279	AB119279 Oryza sat
647	41.2	3.9	902	15	AK068407	AK068407 Oryza sat
648	41.2	3.9	902	15	AK099152	AK099152 Oryza sat
649	41.2	3.9	3216	1	SCU51332	U51332 Streptomyce
650	41.2	3.9	10444	13	PVI422133	AJ422133 Suid herp
c 651	41.2	3.9	19289	14	AC090926	AC090926 Homo sapi
652	41.2	3.9	56467	14	AC069577	AC069577 Homo sapi
c 653	41.2	3.9	57491	14	AC132847	AC132847 Homo sapi
c 654	41.2	3.9	57868	14	AC100588	AC100588 Mus muscu
c 655	41.2	3.9	63082	14	AC022663	AC022663 Homo sapi
c 656	41.2	3.9	67769	14	AC068336	AC068336 Homo sapi
657	41.2	3.9	69941	14	AC027815	AC027815 Homo sapi
658	41.2	3.9	72663	14	AC090140	AC090140 Homo sapi
659	41.2	3.9	78700	14	AC022685	AC022685 Homo sapi
c 660	41.2	3.9	84066	14	AC166463	AC166463 Bos tauru
661	41.2	3.9	84082	14	AC022676	AC022676 Homo sapi
662	41.2	3.9	87283	14	AC022856	AC022856 Homo sapi
c 663	41.2	3.9	110000	14	AC151276_2	Continuation (3 of
664	41.2	3.9	110000	15	AP008215_095	Continuation (96 o
c 665	41.2	3.9	124311	3	AY907537	AY907537 Unculture
666	41.2	3.9	126933	1	DQ118863	DQ118863 Streptomy
c 667	41.2	3.9	132445	14	AC020774	AC020774 Homo sapi
668	41.2	3.9	133997	14	AC015469	AC015469 Homo sapi
669	41.2	3.9	135110	8	AL512652	AL512652 Human DNA
c 670	41.2	3.9	140800	14	AC018392	AC018392 Homo sapi
671	41.2	3.9	141544	15	AP005593	AP005593 Oryza sat
c 672	41.2	3.9	179836	8	AL590822	AL590822 Human DNA
673	41.2	3.9	204944	14	CR354590	CR354590 Danio rer
c 674	41.2	3.9	209548	14	AC157140	AC157140 Bos tauru
675	41.2	3.9	213432	14	AC068198	AC068198 Homo sapi

c 676	41.2	3.9	233725	14	AC127048	AC127048 Rattus no
677	41.2	3.9	234946	14	AC109693	AC109693 Rattus no
c 678	41.2	3.9	235310	14	AC094274	AC094274 Rattus no
c 679	41.2	3.9	244947	14	AC127721	AC127721 Rattus no
680	41.2	3.9	249779	14	AC159220	AC159220 Bos tauru
c 681	41.2	3.9	253751	14	AC051621	AC051621 Mus muscu
682	41.2	3.9	276800	1	SCO939115	AL939115 Streptomy
c 683	41.2	3.9	294100	14	AC144093	AC144093 Macaca mu
c 684	41.2	3.9	304090	14	AC140576	AC140576 Macaca mu
685	41	3.9	401	10	BV185216	BV185216 sqnm14726
c 686	41	3.9	735	10	BV106784	BV106784 PZA01640
687	41	3.9	840	15	CNS01BNS	AL114464 Botrytis
688	41	3.9	972	10	PM12A12G	AL684288 Penicilli
c 689	41	3.9	2527	15	AY730687	AY730687 Oryza sat
c 690	41	3.9	2538	15	AY274928	AY274928 Oryza sat
c 691	41	3.9	2632	15	AK073225	AK073225 Oryza sat
c 692	41	3.9	2635	15	AY311344	AY311344 Oryza sat
c 693	41	3.9	3112	15	AY654584	AY654584 Oryza sat
694	41	3.9	11130	1	AE011684	AE011684 Xanthomon
c 695	41	3.9	13054	14	AC149986	AC149986 Strongylo
696	41	3.9	13548	8	AB017335	AB017335 Homo sapi
c 697	41	3.9	13949	8	HS745C22	AL031596 Human DNA
c 698	41	3.9	29623	14	AC133146	AC133146 Homo sapi
c 699	41	3.9	62649	14	AC022552	AC022552 Homo sapi
700	41	3.9	63409	14	AC022982	AC022982 Homo sapi
701	41	3.9	64272	14	AC023019	AC023019 Homo sapi
c 702	41	3.9	67426	14	AC118609	AC118609 Mus muscu
703	41	3.9	68328	14	AC137705	AC137705 Homo sapi
c 704	41	3.9	68999	7	AF547430	AF547430 Mycobacte
705	41	3.9	69173	14	AC025052	AC025052 Homo sapi
706	41	3.9	70394	14	AC023011	AC023011 Homo sapi
c 707	41	3.9	72533	14	AC127543	AC127543 Homo sapi
c 708	41	3.9	83276	14	AC026631	AC026631 Homo sapi
709	41	3.9	108992	15	AP003740	AP003740 Oryza sat
710	41	3.9	110000	1	BA000030_70	Continuation (71 o
711	41	3.9	110000	1	CP000076_69	Continuation (70 o
c 712	41	3.9	110000	15	AP008215_017	Continuation (18 o
713	41	3.9	110000	15	AP008216_208	Continuation (209
c 714	41	3.9	110000	15	AP008217_176	Continuation (177
c 715	41	3.9	110000	15	AP008208_238	Continuation (239
716	41	3.9	110000	15	AP008213_068	Continuation (69 o
c 717	41	3.9	118948	14	AP003226	AP003226 Oryza sat
718	41	3.9	119048	14	AP004167	AP004167 Oryza sat
719	41	3.9	136416	9	AL607032	AL607032 Mouse DNA
c 720	41	3.9	143487	14	AC141129	AC141129 Rattus no
721	41	3.9	160634	14	AC141999	AC141999 Rattus no
c 722	41	3.9	163423	15	AP006438	AP006438 Oryza sat
723	41	3.9	166341	14	AC013381	AC013381 Homo sapi
724	41	3.9	171124	14	AC161360	AC161360 Mus muscu
c 725	41	3.9	174363	8	AC009133	AC009133 Homo sapi
726	41	3.9	176378	14	CR407600	CR407600 Danio rer
c 727	41	3.9	176627	15	AP006062	AP006062 Oryza sat
728	41	3.9	178022	15	AC025783	AC025783 Oryza sat
729	41	3.9	178343	14	AC024049	AC024049 Homo sapi
c 730	41	3.9	179057	14	AF276758	AF276758 Homo sapi
731	41	3.9	179941	8	AC105118	AC105118 Homo sapi
c 732	41	3.9	187486	14	AC079840	AC079840 Homo sapi
c 733	41	3.9	190462	8	AC092535	AC092535 Homo sapi
c 734	41	3.9	197176	14	AC022763	AC022763 Homo sapi
c 735	41	3.9	209887	14	AC079424	AC079424 Mus muscu
c 736	41	3.9	276728	14	AC152092	AC152092 Bos tauru
737	41	3.9	299735	15	AE017117	AE017117 Oryza sat
738	41	3.9	301332	1	AE017237	AE017237 Mycobacte
c 739	41	3.9	302898	1	AE017238	AE017238 Mycobacte
c 740	41	3.9	303550	1	SCO939131	AL939131 Streptomy
741	41	3.9	344805	1	BX640434	BX640434 Bordetell
742	41	3.9	346359	1	BX640411	BX640411 Bordetell
743	41	3.9	348074	1	BX640449	BX640449 Bordetell
c 744	40.8	3.9	291	6	BD081220	BD081220 Persephin
745	40.8	3.9	291	6	BD081221	BD081221 Persephin
c 746	40.8	3.9	291	6	AR491992	AR491992 Sequence
747	40.8	3.9	291	6	AR491993	AR491993 Sequence
c 748	40.8	3.9	471	6	BD081224	BD081224 Persephin
749	40.8	3.9	471	6	BD081225	BD081225 Persephin
c 750	40.8	3.9	471	6	AR491996	AR491996 Sequence
751	40.8	3.9	471	6	AR491997	AR491997 Sequence
c 752	40.8	3.9	471	8	AF040962	AF040962 Homo sapi
c 753	40.8	3.9	660	15	CNS01D61	AL116417 Botrytis
754	40.8	3.9	750	10	PM12B11B	AL684309 Penicilli
755	40.8	3.9	877	8	PPY133272	AJ133272 Pongo pyg
756	40.8	3.9	890	6	BD145545	BD145545 Primer fo
757	40.8	3.9	890	6	AX865483	AX865483 Sequence
758	40.8	3.9	976	10	PM12D6G	AL684370 Penicilli
c 759	40.8	3.9	1281	6	AR621437	AR621437 Sequence
760	40.8	3.9	1494	11	AY892170	AY892170 Synthetic
761	40.8	3.9	1903	8	BC005010	BC005010 Homo sapi
762	40.8	3.9	1946	6	BD155755	BD155755 Primer fo
763	40.8	3.9	1946	6	AX875773	AX875773 Sequence
764	40.8	3.9	1946	8	AK000972	AK000972 Homo sapi
765	40.8	3.9	2177	5	AJ720530	AJ720530 Gallus ga
766	40.8	3.9	2406	8	BC052975	BC052975 Homo sapi
767	40.8	3.9	2528	6	CS030797	CS030797 Sequence
768	40.8	3.9	2528	6	CS030801	CS030801 Sequence
769	40.8	3.9	2528	6	CS039749	CS039749 Sequence
770	40.8	3.9	2528	6	CS039753	CS039753 Sequence
771	40.8	3.9	2943	8	S40369	S40369 glutamate r
772	40.8	3.9	3308	8	BC037358	BC037358 Homo sapi
773	40.8	3.9	3695	6	AR085272	AR085272 Sequence
774	40.8	3.9	3695	6	I17703	I17703 Sequence 1
775	40.8	3.9	3695	6	I38615	I38615 Sequence 1
776	40.8	3.9	5533	6	CS030799	CS030799 Sequence
777	40.8	3.9	5533	6	CS039751	CS039751 Sequence
778	40.8	3.9	16047	6	AR619741	AR619741 Sequence
779	40.8	3.9	37476	8	HS316G12	AL031709 Human DNA
c 780	40.8	3.9	39799	14	AC074056	AC074056 Homo sapi
781	40.8	3.9	45702	14	AC061982	AC061982 Homo sapi
c 782	40.8	3.9	46251	8	AD000671	AD000671 Homo sapi
c 783	40.8	3.9	49434	14	AC100924	AC100924 Mus muscu
c 784	40.8	3.9	51753	14	AC124247	AC124247 Homo sapi
c 785	40.8	3.9	53239	14	AC011971	AC011971 Homo sapi
786	40.8	3.9	55536	14	AC090310	AC090310 Homo sapi
787	40.8	3.9	56942	14	AC100571	AC100571 Mus muscu
788	40.8	3.9	58693	14	AC107875	AC107875 Homo sapi
789	40.8	3.9	60565	14	AC023852	AC023852 Homo sapi
790	40.8	3.9	61223	14	AC130347	AC130347 Homo sapi
791	40.8	3.9	61633	14	AC084075	AC084075 Homo sapi
c 792	40.8	3.9	61834	14	AC068105	AC068105 Homo sapi
c 793	40.8	3.9	65505	14	AC027799	AC027799 Homo sapi
794	40.8	3.9	65666	14	AC100399	AC100399 Mus muscu
c 795	40.8	3.9	73938	14	AC044861	AC044861 Mus muscu
796	40.8	3.9	76795	14	AC023515	AC023515 Homo sapi
c 797	40.8	3.9	105659	14	AP003961	AP003961 Oryza sat
798	40.8	3.9	110000	1	AP006840_27	Continuation (28 o
c 799	40.8	3.9	110000	15	AP008212_253	Continuation (254
800	40.8	3.9	119199	14	AP003812	AP003812 Oryza sat
c 801	40.8	3.9	136880	14	AC078787	AC078787 Homo sapi
c 802	40.8	3.9	138032	14	AC141033	AC141033 Rattus no
c 803	40.8	3.9	164483	15	AP005386	AP005386 Oryza sat
c 804	40.8	3.9	171849	8	AC010616	AC010616 Homo sapi
805	40.8	3.9	173576	14	AC073329	AC073329 Homo sapi
c 806	40.8	3.9	175152	14	AC074195	AC074195 Homo sapi
807	40.8	3.9	188721	14	RN462P8	AL603727 Rattus no
808	40.8	3.9	194835	14	AC022315	AC022315 Homo sapi
809	40.8	3.9	197093	14	CR394569	CR394569 Danio rer
c 810	40.8	3.9	215532	8	AC010883	AC010883 Homo sapi
811	40.8	3.9	237931	8	AC022098	AC022098 Homo sapi
812	40.8	3.9	244428	14	AC130959	AC130959 Rattus no
813	40.8	3.9	279011	8	AE006467	AE006467 Homo sapi
814	40.6	3.9	305	10	CNS06EXB	AL395685 T7 end of
c 815	40.6	3.9	497	10	BV123309	BV123309 PZA01113
c 816	40.6	3.9	526	10	BV106797	BV106797 PZA01642
817	40.6	3.9	594	10	BV107432	BV107432 PZA01630
c 818	40.6	3.9	660	15	CNS019KB	AL111747 Botrytis
819	40.6	3.9	942	8	PPA133270	AJ133270 Pan panis
820	40.6	3.9	1026	6	CQ737362	CQ737362 Sequence
821	40.6	3.9	1124	8	BC000912	BC000912 Homo sapi

	822	40.6	3.9	1920	1	AB018799 AB018799 Streptomy
	823	40.6	3.9	2736	1	AF160253 AF160253 Streptomy
	824	40.6	3.9	2941	6	AR380520 AR380520 Sequence
	825	40.6	3.9	2954	6	CQ842138 CQ842138 Sequence
	826	40.6	3.9	2954	8	AK125168 AK125168 Homo sapi
	827	40.6	3.9	2954	8	HUME12A M31222 Human e12 p
	828	40.6	3.9	3925	1	AF177946 AF177946 Streptomy
	829	40.6	3.9	4043	8	AK074103 AK074103 Homo sapi
	830	40.6	3.9	4211	8	BC011665 BC011665 Homo sapi
	831	40.6	3.9	4349	6	CQ824581 CQ824581 Sequence
	832	40.6	3.9	4382	8	BC051795 BC051795 Homo sapi
	833	40.6	3.9	5248	8	AB002354 AB002354 Homo sapi
	834	40.6	3.9	5277	8	BC064361 BC064361 Homo sapi
	835	40.6	3.9	5522	8	AB209345 AB209345 Homo sapi
	836	40.6	3.9	52493	14	AC099923 AC099923 Mus muscu
	837	40.6	3.9	56953	14	AC100340 AC100340 Mus muscu
	838	40.6	3.9	57075	14	AC110746 AC110746 Homo sapi
	839	40.6	3.9	61240	14	AC068578 AC068578 Homo sapi
c	840	40.6	3.9	62875	14	AC068436 AC068436 Homo sapi
c	841	40.6	3.9	63087	14	AC023446 AC023446 Homo sapi
c	842	40.6	3.9	64207	14	AC024002 AC024002 Homo sapi
c	843	40.6	3.9	64937	14	AC101492 AC101492 Mus muscu
c	844	40.6	3.9	65088	14	AC084720 AC084720 Homo sapi
	845	40.6	3.9	67736	14	AC132831 AC132831 Homo sapi
	846	40.6	3.9	68799	14	AC101328 AC101328 Mus muscu
	847	40.6	3.9	69880	14	AC099820 AC099820 Homo sapi
	848	40.6	3.9	72030	14	AC083987 AC083987 Homo sapi
	849	40.6	3.9	76734	14	AC023218 AC023218 Homo sapi
c	850	40.6	3.9	79776	14	AC139431 AC139431 Homo sapi
c	851	40.6	3.9	93663	14	AC107039 AC107039 Pan trogl
	852	40.6	3.9	95559	14	AC136067 AC136067 Rattus no
c	853	40.6	3.9	95884	14	AC068839 AC068839 Homo sapi
	854	40.6	3.9	110000	1	AP006840_04 Continuation (5 of
	855	40.6	3.9	110000	1	BA000030_01 Continuation (2 of
c	856	40.6	3.9	110000	1	BA000035_29 Continuation (30 o
	857	40.6	3.9	110000	15	AP008208_083 Continuation (84 o
	858	40.6	3.9	113196	8	HSJ697K14 AL121829 Human DNA
	859	40.6	3.9	133869	9	AC139157 AC139157 Mus muscu
c	860	40.6	3.9	143733	14	AC142786 AC142786 Macaca mu
c	861	40.6	3.9	148507	14	AC011263 AC011263 Homo sapi
	862	40.6	3.9	150715	13	AY714813 AY714813 Cercopith
c	863	40.6	3.9	152586	8	AC016968 AC016968 Homo sapi
	864	40.6	3.9	155975	8	AC006512 AC006512 Homo sapi
	865	40.6	3.9	158586	15	AP005511 AP005511 Oryza sat
	866	40.6	3.9	174842	15	AP005614 AP005614 Oryza sat
c	867	40.6	3.9	179246	14	AC142592 AC142592 Macaca mu
c	868	40.6	3.9	183683	14	BX897750 BX897750 Danio rer
c	869	40.6	3.9	185061	14	AC062024 AC062024 Homo sapi
c	870	40.6	3.9	189050	1	AL646077 AL646077 Ralstonia
	871	40.6	3.9	189389	8	CNS05TCF AL355096 Human chr
c	872	40.6	3.9	198614	14	AC073293 AC073293 Mus muscu
	873	40.6	3.9	207611	8	AC091132 AC091132 Homo sapi
c	874	40.6	3.9	207774	8	CNS0000H AL049836 Human chr
	875	40.6	3.9	207905	9	AL672013 AL672013 Mouse DNA
	876	40.6	3.9	213673	9	AC130218 AC130218 Mus muscu
	877	40.6	3.9	215287	14	AC079432 AC079432 Mus muscu
	878	40.6	3.9	222930	8	HSU47924 U47924 Human chrom
	879	40.6	3.9	247910	1	AE017307 AE017307 Thermus t
c	880	40.6	3.9	249262	14	AC079430 AC079430 Mus muscu
c	881	40.6	3.9	262980	14	AC098981 AC098981 Rattus no
	882	40.6	3.9	268644	14	AC091323 AC091323 Mus muscu
	883	40.6	3.9	273403	8	AC011498 AC011498 Homo sapi
c	884	40.6	3.9	276800	1	SCO939115 AL939115 Streptomy
	885	40.6	3.9	293050	1	SCO939116 AL939116 Streptomy
	886	40.6	3.9	299986	1	AE017240 AE017240 Mycobacte
	887	40.6	3.9	339972	15	OSA307662 AJ307662 Oryza sat
	888	40.4	3.9	403	6	BD265556 BD265556 Interleuk
	889	40.4	3.9	403	6	BD265557 BD265557 Interleuk
	890	40.4	3.9	403	6	AR316788 AR316788 Sequence
	891	40.4	3.9	403	6	AR316789 AR316789 Sequence
c	892	40.4	3.9	498	10	BV123303 BV123303 PZA01113
	893	40.4	3.9	612	10	BV122569 BV122569 PZA01737
	894	40.4	3.9	613	10	BV107435 BV107435 PZA01630
c	895	40.4	3.9	638	10	BV106807 BV106807 PZA01642
	896	40.4	3.9	674	10	PM12C11B AL684333 Penicilli
	897	40.4	3.9	888	6	CS138022 CS138022 Sequence
	898	40.4	3.9	1083	6	AR622788 AR622788 Sequence
	899	40.4	3.9	1314	1	TTHNUSG L10348 Thermus the
	900	40.4	3.9	1392	6	AX934691 AX934691 Sequence
c	901	40.4	3.9	1907	6	AX305682 AX305682 Sequence
c	902	40.4	3.9	1907	9	MMNFIC1B Y07693 M.musculus
c	903	40.4	3.9	1996	15	AK107061 AK107061 Oryza sat
c	904	40.4	3.9	4481	8	AK074045 AK074045 Homo sapi
	905	40.4	3.9	8089	1	AB186138 AB186138 Corynebac
c	906	40.4	3.9	8651	1	AY124589 AY124589 Agromyces
c	907	40.4	3.9	22301	6	AR619813 AR619813 Sequence
c	908	40.4	3.9	34175	8	CNS00YVB AL096805 Homo sapi
	909	40.4	3.9	37405	14	AC101273 AC101273 Mus muscu
c	910	40.4	3.9	37892	8	BX649323 BX649323 Human DNA
	911	40.4	3.9	38128	14	BX296528 BX296528 Homo sapi
	912	40.4	3.9	44438	8	AL732369 AL732369 Human DNA
c	913	40.4	3.9	48636	15	AC138196 AC138196 Oryza sat
c	914	40.4	3.9	52884	14	AC068018 AC068018 Homo sapi
	915	40.4	3.9	57971	14	AC101222 AC101222 Mus muscu
c	916	40.4	3.9	61021	14	AC101916 AC101916 Mus muscu
	917	40.4	3.9	63022	14	AC013681 AC013681 Homo sapi
c	918	40.4	3.9	64233	14	AC101177 AC101177 Mus muscu
	919	40.4	3.9	64272	14	AC101276 AC101276 Mus muscu
	920	40.4	3.9	64998	14	AC104992 AC104992 Homo sapi
c	921	40.4	3.9	67066	14	AC126358 AC126358 Homo sapi
	922	40.4	3.9	69861	14	AC032033 AC032033 Homo sapi
c	923	40.4	3.9	70679	14	AC026151 AC026151 Homo sapi
c	924	40.4	3.9	70730	14	AC091107 AC091107 Homo sapi
c	925	40.4	3.9	72079	14	AC027022 AC027022 Homo sapi
c	926	40.4	3.9	75678	14	AC093372 AC093372 Mus muscu
	927	40.4	3.9	78765	14	AC021584 AC021584 Homo sapi
c	928	40.4	3.9	110000	1	AP008226_02 Continuation (3 of
c	929	40.4	3.9	110000	1	BA000030_64 Continuation (65 o
c	930	40.4	3.9	110000	1	BA000030_78 Continuation (79 o
c	931	40.4	3.9	110000	14	CR936358_0 CR936358 Homo sapi
c	932	40.4	3.9	110000	15	AP008217_024 Continuation (25 o
	933	40.4	3.9	110000	15	AP008217_040 Continuation (41 o
c	934	40.4	3.9	110000	15	AP008208_218 Continuation (219
c	935	40.4	3.9	110524	14	AC138239 AC138239 Mus muscu
c	936	40.4	3.9	112159	8	AL162741 AL162741 Human DNA
	937	40.4	3.9	116899	4	AC144753 AC144753 Ornithorh
c	938	40.4	3.9	128408	14	AC016086 AC016086 Homo sapi
	939	40.4	3.9	129473	14	AC040158 AC040158 Homo sapi
	940	40.4	3.9	130151	15	AC135794 AC135794 Oryza sat
c	941	40.4	3.9	132001	14	AC142984 AC142984 Macaca mu
c	942	40.4	3.9	135803	15	AP005114 AP005114 Oryza sat
c	943	40.4	3.9	136753	14	AC149968 AC149968 Strongylo
c	944	40.4	3.9	149132	15	AC116949 AC116949 Oryza sat
	945	40.4	3.9	150074	14	AC016007 AC016007 Homo sapi
c	946	40.4	3.9	154589	8	AC006557 AC006557 Homo sapi
c	947	40.4	3.9	156856	15	AP005835 AP005835 Oryza sat
c	948	40.4	3.9	159234	14	AC069284 AC069284 Homo sapi
c	949	40.4	3.9	162560	14	AC069005 AC069005 Homo sapi
	950	40.4	3.9	163420	14	AC012576 AC012576 Homo sapi
	951	40.4	3.9	176640	14	AC107005 AC107005 Rattus no
c	952	40.4	3.9	178141	14	AC074345 AC074345 Homo sapi
	953	40.4	3.9	182424	8	AP001004 AP001004 Homo sapi
	954	40.4	3.9	182486	15	AC134044 AC134044 Oryza sat
	955	40.4	3.9	185872	14	AC068810 AC068810 Mus muscu
	956	40.4	3.9	188914	8	AC019118 AC019118 Homo sapi
	957	40.4	3.9	200019	14	AC024111 AC024111 Mus muscu
c	958	40.4	3.9	201634	14	AC119024 AC119024 Rattus no
c	959	40.4	3.9	208735	14	AC108506 AC108506 Mus muscu
	960	40.4	3.9	209173	9	AC162391 AC162391 Mus muscu
	961	40.4	3.9	220977	14	BX928743 BX928743 Danio rer
c	962	40.4	3.9	223020	8	AL162424 AL162424 Human DNA
c	963	40.4	3.9	242294	14	AC094420 AC094420 Rattus no
	964	40.4	3.9	270403	14	AC164042 AC164042 Bos tauru
	965	40.4	3.9	272572	14	AC157074 AC157074 Bos tauru
c	966	40.4	3.9	301877	14	AC096091 AC096091 Rattus no
	967	40.4	3.9	303550	1	SCO939131 AL939131 Streptomy

968	40.4	3.9	322783	14	AC133423	AC133423 Rattus no
c 969	40.2	3.8	840	15	CNS019IG	AL111680 Botrytis
c 970	40.2	3.8	1117	6	AX646949	AX646949 Sequence
c 971	40.2	3.8	1246	6	AX164174	AX164174 Sequence
c 972	40.2	3.8	1277	15	AK121989	AK121989 Oryza sat
c 973	40.2	3.8	1416	6	AX840138	AX840138 Sequence
c 974	40.2	3.8	1416	6	AX840139	AX840139 Sequence
975	40.2	3.8	1431	6	AX535310	AX535310 Sequence
c 976	40.2	3.8	1479	9	AB221693	AB221693 Mus muscu
c 977	40.2	3.8	1593	9	AF023915	AF023915 Mus muscu
978	40.2	3.8	2188	6	BD203712	BD203712 Human nuc
979	40.2	3.8	2188	6	AX014867	AX014867 Sequence
c 980	40.2	3.8	2685	8	HUMHBA1	J00182 Homo sapien
981	40.2	3.8	2728	8	BC065919	BC065919 Homo sapi
c 982	40.2	3.8	4259	8	AF042832	AF042832 Homo sapi
c 983	40.2	3.8	4349	4	AF011927	AF011927 Bos indic
c 984	40.2	3.8	4455	10	BV174812	BV174812 sqnm74427
985	40.2	3.8	7411	15	ZMA563423	AJ563423 Zea mays
c 986	40.2	3.8	9471	5	AY186728	AY186728 Gallus ga
987	40.2	3.8	50000	6	AX535264	AX535264 Sequence
c 988	40.2	3.8	50000	6	AX535266	AX535266 Sequence
989	40.2	3.8	54007	14	AC100469	AC100469 Mus muscu
990	40.2	3.8	56458	15	AC148880	AC148880 Chlamydom
991	40.2	3.8	57787	14	AC100680	AC100680 Mus muscu
992	40.2	3.8	59816	1	AF333038	AF333038 Streptomy
c 993	40.2	3.8	60016	14	AC126381	AC126381 Homo sapi
c 994	40.2	3.8	61150	14	AC100284	AC100284 Mus muscu
c 995	40.2	3.8	61954	14	AC120915	AC120915 Homo sapi
996	40.2	3.8	63994	14	AC126396	AC126396 Homo sapi
997	40.2	3.8	64551	14	AC101380	AC101380 Mus muscu
998	40.2	3.8	66791	14	AC083970	AC083970 Homo sapi
999	40.2	3.8	66867	14	AC073170	AC073170 Homo sapi
1000	40.2	3.8	69429	14	AC100015	AC100015 Mus muscu
c1001	40.2	3.8	69570	14	AC067888	AC067888 Homo sapi
c1002	40.2	3.8	75663	8	AC068987	AC068987 Homo sapi
1003	40.2	3.8	90600	1	AJ862840	AJ862840 Streptomy
c1004	40.2	3.8	106239	8	AL607122	AL607122 Human DNA
c1005	40.2	3.8	110000	14	AC098456_1	Continuation (2 of
c1006	40.2	3.8	110000	14	AC098456_2	Continuation (3 of
1007	40.2	3.8	132745	14	AC134836	AC134836 Mus muscu
1008	40.2	3.8	135119	14	AC011578	AC011578 Homo sapi
c1009	40.2	3.8	144586	8	AL354831	AL354831 Human DNA
c1010	40.2	3.8	147210	14	AC154935	AC154935 Felis cat
1011	40.2	3.8	149915	14	AC021637	AC021637 Homo sapi
1012	40.2	3.8	153604	14	AC022754	AC022754 Homo sapi
c1013	40.2	3.8	157827	14	AC027260	AC027260 Homo sapi
1014	40.2	3.8	158523	14	AC013547	AC013547 Homo sapi
1015	40.2	3.8	159028	14	AC142003	AC142003 Rattus no
1016	40.2	3.8	160197	14	AC009814	AC009814 Homo sapi
1017	40.2	3.8	164834	14	AC013505	AC013505 Homo sapi
c1018	40.2	3.8	165096	14	AC112423	AC112423 Rattus no
1019	40.2	3.8	172935	14	CR774191	CR774191 Danio rer
1020	40.2	3.8	177255	14	AC148806	AC148806 Carollia
1021	40.2	3.8	177384	14	AC091786	AC091786 Mus muscu
c1022	40.2	3.8	182703	14	AC073117	AC073117 Homo sapi
c1023	40.2	3.8	185784	9	AC069564	AC069564 Mus muscu
c1024	40.2	3.8	192089	14	AC154377	AC154377 Mus muscu
c1025	40.2	3.8	197346	8	CNS01RFZ	AL157687 Human chr
1026	40.2	3.8	198179	14	CR450745	CR450745 Danio rer
1027	40.2	3.8	201142	9	AL670035	AL670035 Mouse DNA
c1028	40.2	3.8	202337	14	CT025524	CT025524 Mus muscu
c1029	40.2	3.8	203363	8	CNS01RHB	AL161668 Human chr
1030	40.2	3.8	207918	14	AC145969	AC145969 Pan trogl
c1031	40.2	3.8	211429	14	BX324152	BX324152 Danio rer
1032	40.2	3.8	219695	9	AC122252	AC122252 Mus muscu
1033	40.2	3.8	230138	13	AF232689	AF232689 Rat cytom
1034	40.2	3.8	241133	14	AC160428	AC160428 Bos tauru
c1035	40.2	3.8	242184	14	AC015899	AC015899 Homo sapi
1036	40.2	3.8	256241	14	AC096075	AC096075 Rattus no
1037	40.2	3.8	289791	14	AC161690	AC161690 Bos tauru
1038	40.2	3.8	299050	1	SCO939104	AL939104 Streptomy
c1039	40.2	3.8	301443	1	AE017239	AE017239 Mycobacte
1040	40	3.8	40	6	BD218883	BD218883 Factor af
1041	40	3.8	40	6	AR338367	AR338367 Sequence
1042	40	3.8	40	6	AX180784	AX180784 Sequence
c1043	40	3.8	319	6	AR137499	AR137499 Sequence
c1044	40	3.8	569	10	BV106801	BV106801 PZA01642
c1045	40	3.8	631	10	BV106794	BV106794 PZA01642
c1046	40	3.8	710	10	BV117858	BV117858 PZA00815
c1047	40	3.8	736	10	BV106786	BV106786 PZA01640
c1048	40	3.8	1060	10	BV111230	BV111230 PZA00983
1049	40	3.8	1279	10	PM2H12G	AL684840 Penicilli
1050	40	3.8	1389	6	AX934671	AX934671 Sequence
c1051	40	3.8	1888	6	CQ412943	CQ412943 Sequence
c1052	40	3.8	2061	6	I09570	I09570 Sequence 1
1053	40	3.8	2084	1	AY423558	AY423558 Streptomy
c1054	40	3.8	2344	6	CQ412022	CQ412022 Sequence
c1055	40	3.8	2523	9	RRA011020	AJ011020 Rattus ra
c1056	40	3.8	3422	13	HEPVGH	X58868 Pseudorabie
c1057	40	3.8	5452	6	AX646997	AX646997 Sequence
1058	40	3.8	14006	1	AE002049	AE002049 Deinococc
1059	40	3.8	39109	14	AC025107	AC025107 Homo sapi
c1060	40	3.8	48144	14	AC069166	AC069166 Homo sapi
1061	40	3.8	50368	14	AC100931	AC100931 Mus muscu
c1062	40	3.8	56121	14	AC068076	AC068076 Homo sapi
1063	40	3.8	62567	14	AC068877	AC068877 Homo sapi
c1064	40	3.8	64211	14	AC091110	AC091110 Homo sapi
1065	40	3.8	67593	14	AC079197	AC079197 Homo sapi
1066	40	3.8	67884	14	AC090561	AC090561 Homo sapi
c1067	40	3.8	77534	1	AF235504	AF235504 Streptomy
c1068	40	3.8	77536	6	BD235937	BD235937 Polyketid
c1069	40	3.8	77536	6	AR271638	AR271638 Sequence
c1070	40	3.8	77536	6	AR564393	AR564393 Sequence
1071	40	3.8	80099	14	AC021290	AC021290 Homo sapi
1072	40	3.8	80542	14	AC020683	AC020683 Homo sapi
1073	40	3.8	84868	1	DQ013294	DQ013294 Polyangiu
c1074	40	3.8	86608	14	AC021430	AC021430 Homo sapi
c1075	40	3.8	97218	8	AC092385	AC092385 Homo sapi
1076	40	3.8	110000	1	AP006618_50	Continuation (51 o
1077	40	3.8	110000	1	AP006618_51	Continuation (52 o
c1078	40	3.8	110000	1	AP006840_14	Continuation (15 o
c1079	40	3.8	110000	1	BA000030_72	Continuation (73 o
c1080	40	3.8	110000	15	AE016814_2	Continuation (3 of
c1081	40	3.8	113193	1	AF357202	AF357202 Streptomy
c1082	40	3.8	113193	6	AX703543	AX703543 Sequence
1083	40	3.8	124090	8	AC096657	AC096657 Homo sapi
1084	40	3.8	136551	14	AC048354	AC048354 Homo sapi
1085	40	3.8	136753	14	AC149968	AC149968 Strongylo
1086	40	3.8	141895	8	HSDJ827L5	AL121910 Human DNA
c1087	40	3.8	152533	14	AC016506	AC016506 Homo sapi
c1088	40	3.8	153733	14	AC011980	AC011980 Homo sapi
c1089	40	3.8	162445	8	AL158151	AL158151 Human DNA
c1090	40	3.8	170022	8	AC024367	AC024367 Homo sapi
1091	40	3.8	175133	14	AC144393	AC144393 Rattus no
1092	40	3.8	183671	8	AC023024	AC023024 Homo sapi
1093	40	3.8	184503	8	AC079305	AC079305 Homo sapi
c1094	40	3.8	191358	8	AC012533	AC012533 Homo sapi
c1095	40	3.8	196441	9	AC118021	AC118021 Mus muscu
1096	40	3.8	203324	9	AL662780	AL662780 Mouse DNA
1097	40	3.8	206673	14	CR927368	CR927368 Danio rer
c1098	40	3.8	207212	14	AL671876	AL671876 Mus muscu
c1099	40	3.8	248754	14	AC134101	AC134101 Rattus no
c1100	40	3.8	261587	14	AC126139	AC126139 Rattus no
c1101	40	3.8	299262	14	AC136856	AC136856 Rattus no
1102	40	3.8	308147	1	AE016915	AE016915 Chromobac
1103	39.8	3.8	340	1	AB125375	AB125375 Actinopla
1104	39.8	3.8	408	8	HSA326670	AJ326670 Homo sapi
c1105	39.8	3.8	601	10	BV167536	BV167536 sqnm5800
c1106	39.8	3.8	954	6	AR622653	AR622653 Sequence
c1107	39.8	3.8	1007	10	PM3H11G	AL685749 Penicilli
1108	39.8	3.8	1407	1	AF230490	AF230490 Streptomy
1109	39.8	3.8	1515	6	AR624707	AR624707 Sequence
c1110	39.8	3.8	1519	6	AR618884	AR618884 Sequence
c1111	39.8	3.8	1640	6	AR627673	AR627673 Sequence
c1112	39.8	3.8	1877	15	AK069912	AK069912 Oryza sat
c1113	39.8	3.8	3423	10	BV177232	BV177232 sqnm93526

1114	39.8	3.8	5895	1	SOL441123	AJ441123 Streptomy
c1115	39.8	3.8	8180	6	AR619575	AR619575 Sequence
c1116	39.8	3.8	10417	1	AE004546	AE004546 Pseudomon
1117	39.8	3.8	10871	6	AR619630	AR619630 Sequence
c1118	39.8	3.8	42074	1	SGR578458	AJ578458 Streptomy
1119	39.8	3.8	50872	14	AC084140	AC084140 Homo sapi
c1120	39.8	3.8	53897	14	AC101434	AC101434 Mus muscu
c1121	39.8	3.8	59203	14	AC126350	AC126350 Homo sapi
1122	39.8	3.8	62074	14	AC101270	AC101270 Mus muscu
c1123	39.8	3.8	65162	14	AC022643	AC022643 Homo sapi
c1124	39.8	3.8	65845	14	AC101554	AC101554 Mus muscu
c1125	39.8	3.8	66801	14	AC119895	AC119895 Mus muscu
c1126	39.8	3.8	69515	14	AC099971	AC099971 Mus muscu
c1127	39.8	3.8	70389	14	AC135853	AC135853 Homo sapi
1128	39.8	3.8	72793	14	AC021727	AC021727 Homo sapi
c1129	39.8	3.8	73516	14	AC041001	AC041001 Homo sapi
c1130	39.8	3.8	77508	14	AC023005	AC023005 Homo sapi
1131	39.8	3.8	87256	14	AC013754	AC013754 Homo sapi
c1132	39.8	3.8	88064	14	AC022707	AC022707 Homo sapi
1133	39.8	3.8	89994	14	AC021263	AC021263 Homo sapi
c1134	39.8	3.8	93821	14	AC021596	AC021596 Homo sapi
1135	39.8	3.8	107044	14	AC142570	AC142570 Gallus ga
1136	39.8	3.8	110000	15	AP008214_258	Continuation (259
1137	39.8	3.8	110000	15	AP008207_077	Continuation (78 o
c1138	39.8	3.8	119531	14	AP003879	AP003879 Oryza sat
c1139	39.8	3.8	124402	14	AC155403	AC155403 Zea mays
c1140	39.8	3.8	129273	14	AC142018	AC142018 Rattus no
c1141	39.8	3.8	129984	14	AC148211	AC148211 Dasypus n
1142	39.8	3.8	137261	8	AC132825	AC132825 Homo sapi
1143	39.8	3.8	144404	15	AP003210	AP003210 Oryza sat
1144	39.8	3.8	147516	15	AP004622	AP004622 Oryza sat
1145	39.8	3.8	148061	14	CR848712	CR848712 Danio rer
1146	39.8	3.8	149101	14	AC069375	AC069375 Homo sapi
1147	39.8	3.8	150165	14	AC154402	AC154402 Mus muscu
c1148	39.8	3.8	150680	8	AC090894	AC090894 Homo sapi
1149	39.8	3.8	150755	15	AP005509	AP005509 Oryza sat
c1150	39.8	3.8	159998	14	AC074292	AC074292 Homo sapi
c1151	39.8	3.8	163807	14	AC018934	AC018934 Homo sapi
1152	39.8	3.8	164186	8	AC107940	AC107940 Homo sapi
c1153	39.8	3.8	168991	14	AC025462	AC025462 Homo sapi
c1154	39.8	3.8	169713	14	AC015919	AC015919 Homo sapi
c1155	39.8	3.8	175866	14	CR855383	CR855383 Danio rer
1156	39.8	3.8	177241	8	HS402G11	AL022328 Human DNA
c1157	39.8	3.8	177466	1	AE001826	AE001826 Deinococc
c1158	39.8	3.8	184244	14	AC073282	AC073282 Homo sapi
c1159	39.8	3.8	185724	14	AC146285	AC146285 Callicebu
1160	39.8	3.8	186540	14	AC134052	AC134052 Mus muscu
1161	39.8	3.8	186795	14	AC090492	AC090492 Mus muscu
c1162	39.8	3.8	197229	14	AC021162	AC021162 Homo sapi
1163	39.8	3.8	199375	14	AC161469	AC161469 Gallus ga
c1164	39.8	3.8	201294	14	AC128748	AC128748 Rattus no
c1165	39.8	3.8	203765	8	AC087289	AC087289 Homo sapi
c1166	39.8	3.8	213741	14	AC160126	AC160126 Mus muscu
c1167	39.8	3.8	218640	14	AC152662	AC152662 Bos tauru
c1168	39.8	3.8	228056	14	AC144061	AC144061 Macaca mu
c1169	39.8	3.8	232278	14	AC087876	AC087876 Mus muscu
1170	39.8	3.8	235660	14	CR388183	CR388183 Danio rer
c1171	39.8	3.8	253002	14	CT010439	CT010439 Mus muscu
c1172	39.8	3.8	260534	14	AC078912	AC078912 Mus muscu
c1173	39.8	3.8	300717	1	AE017229	AE017229 Mycobacte
1174	39.8	3.8	311000	1	SCO939122	AL939122 Streptomy
c1175	39.6	3.8	320	6	AR137505	AR137505 Sequence
c1176	39.6	3.8	437	10	BV121528	BV121528 PZA00958
c1177	39.6	3.8	602	10	BV106772	BV106772 PZA01639
1178	39.6	3.8	617	8	AF188738S4	AF188741 Homo sapi
1179	39.6	3.8	621	10	BV107431	BV107431 PZA01630
c1180	39.6	3.8	636	15	CNS019OT	AL111909 Botrytis
1181	39.6	3.8	1458	4	AF324409	AF324409 Oryctolag
1182	39.6	3.8	2560	15	AB070343	AB070343 Volvox ca
c1183	39.6	3.8	3856	8	BC028375	BC028375 Homo sapi
1184	39.6	3.8	4855	1	SAU03114	U03114 Streptomyce
c1185	39.6	3.8	5165	6	CQ413028	CQ413028 Sequence
1186	39.6	3.8	36687	14	AC013672	AC013672 Homo sapi
c1187	39.6	3.8	37823	1	SVPTT	X65195 Streptomyce
1188	39.6	3.8	47296	14	AC136985	AC136985 Mus muscu
1189	39.6	3.8	49052	8	AL359836	AL359836 Human DNA
c1190	39.6	3.8	50320	14	AC126373	AC126373 Homo sapi
1191	39.6	3.8	52884	14	AC068018	AC068018 Homo sapi
c1192	39.6	3.8	58595	14	AC131300	AC131300 Mus muscu
1193	39.6	3.8	59015	14	AC067811	AC067811 Homo sapi
1194	39.6	3.8	64651	14	AC101572	AC101572 Mus muscu
1195	39.6	3.8	68320	14	AC129571	AC129571 Mus muscu
c1196	39.6	3.8	70575	14	AC025103	AC025103 Homo sapi
1197	39.6	3.8	74315	14	AC023029	AC023029 Homo sapi
c1198	39.6	3.8	76828	14	AC032029	AC032029 Homo sapi
1199	39.6	3.8	77534	1	AF235504	AF235504 Streptomy
1200	39.6	3.8	77536	6	BD235937	BD235937 Polyketid
1201	39.6	3.8	77536	6	AR271638	AR271638 Sequence
1202	39.6	3.8	77536	6	AR564393	AR564393 Sequence
1203	39.6	3.8	83296	14	AC022588	AC022588 Homo sapi
1204	39.6	3.8	110000	1	BA000030_09	Continuation (10 o
c1205	39.6	3.8	110000	15	AP008208_225	Continuation (226
1206	39.6	3.8	110000	15	AP008209_127	Continuation (128
c1207	39.6	3.8	110000	15	AP008209_218	Continuation (219
c1208	39.6	3.8	120578	8	AC005887	AC005887 citb_173_
1209	39.6	3.8	132243	15	AC148339	AC148339 Oryza sat
1210	39.6	3.8	139771	15	AC135564	AC135564 Oryza sat
c1211	39.6	3.8	146608	14	AC114719	AC114719 Rattus no
c1212	39.6	3.8	147313	15	AP005800	AP005800 Oryza sat
c1213	39.6	3.8	147728	15	AP005644	AP005644 Oryza sat
1214	39.6	3.8	156782	14	AC142000	AC142000 Rattus no
1215	39.6	3.8	165000	8	AC137894	AC137894 Homo sapi
c1216	39.6	3.8	172977	14	AC141528	AC141528 Rattus no
c1217	39.6	3.8	173764	14	AC150562	AC150562 Bos tauru
c1218	39.6	3.8	178772	14	AC084745	AC084745 Mus muscu
c1219	39.6	3.8	181066	14	AC144606	AC144606 Canis fam
1220	39.6	3.8	187160	8	AC138230	AC138230 Homo sapi
1221	39.6	3.8	214206	9	AC116677	AC116677 Mus muscu
c1222	39.6	3.8	232605	1	AE017222	AE017222 Thermus t
c1223	39.6	3.8	346362	1	BX640439	BX640439 Bordetell
1224	39.4	3.8	509	10	BV122579	BV122579 PZA01737
1225	39.4	3.8	551	10	BV107384	BV107384 PZA01604
1226	39.4	3.8	614	10	BV122564	BV122564 PZA01737
c1227	39.4	3.8	641	10	BV106808	BV106808 PZA01642
1228	39.4	3.8	742	10	BV653066	BV653066 S215P6551
c1229	39.4	3.8	1614	6	AR409337	AR409337 Sequence
c1230	39.4	3.8	1614	6	AR650969	AR650969 Sequence
c1231	39.4	3.8	1614	6	AX239602	AX239602 Sequence
c1232	39.4	3.8	1617	8	AY453840	AY453840 Homo sapi
1233	39.4	3.8	1965	8	AF251041	AF251041 Homo sapi
1234	39.4	3.8	2085	6	AX402509	AX402509 Sequence
1235	39.4	3.8	2142	6	AX714099	AX714099 Sequence
1236	39.4	3.8	2142	8	AK056193	AK056193 Homo sapi
1237	39.4	3.8	2146	8	AK223611	AK223611 Homo sapi
1238	39.4	3.8	2258	6	AX405912	AX405912 Sequence
c1239	39.4	3.8	2362	8	BC038235	BC038235 Homo sapi
c1240	39.4	3.8	3260	6	CS117901	CS117901 Sequence
c1241	39.4	3.8	5128	6	CQ874022	CQ874022 Sequence
c1242	39.4	3.8	5153	8	HSYAP65	X80507 H.sapiens Y
c1243	39.4	3.8	5800	1	AF373594	AF373594 Thauera a
1244	39.4	3.8	12502	1	AE012483	AE012483 Xanthomon
c1245	39.4	3.8	33499	8	AL590548	AL590548 Human DNA
1246	39.4	3.8	50369	14	AC083990	AC083990 Homo sapi
c1247	39.4	3.8	61008	14	AC130330	AC130330 Homo sapi
c1248	39.4	3.8	61797	14	AC023094	AC023094 Homo sapi
1249	39.4	3.8	62556	14	AC125011	AC125011 Mus muscu
1250	39.4	3.8	63808	14	AC090554	AC090554 Homo sapi
1251	39.4	3.8	64976	14	AC026256	AC026256 Homo sapi
c1252	39.4	3.8	65755	14	AC011160	AC011160 Homo sapi
c1253	39.4	3.8	66369	14	AC101619	AC101619 Mus muscu
c1254	39.4	3.8	66522	14	AC122565	AC122565 Mus muscu
c1255	39.4	3.8	67416	14	AC117742	AC117742 Mus muscu
1256	39.4	3.8	69050	14	AC118657	AC118657 Homo sapi
1257	39.4	3.8	70202	14	AC101627	AC101627 Mus muscu
c1258	39.4	3.8	81417	14	AC023265	AC023265 Homo sapi
c1259	39.4	3.8	83461	14	AC155429	AC155429 Zea mays

c1260	39.4	3.8	92883	14	AC142027	AC142027 Rattus no
1261	39.4	3.8	94420	8	AC116493	AC116493 Homo sapi
1262	39.4	3.8	101799	15	AC099401	AC099401 Oryza sat
c1263	39.4	3.8	110000	1	AP006618_26	Continuation (27 o
c1264	39.4	3.8	110000	1	AP006618_27	Continuation (28 o
1265	39.4	3.8	110000	1	AP008226_17	Continuation (18 o
1266	39.4	3.8	110000	1	CP000031_35	Continuation (36 o
1267	39.4	3.8	110000	1	CP000050_06	Continuation (7 of
1268	39.4	3.8	110000	1	CP000050_07	Continuation (8 of
1269	39.4	3.8	110000	15	AP008209_030	Continuation (31 o
1270	39.4	3.8	110000	15	AP008209_031	Continuation (32 o
c1271	39.4	3.8	110000	15	AP008211_018	Continuation (19 o
c1272	39.4	3.8	115640	15	AC118288	AC118288 Oryza sat
c1273	39.4	3.8	119725	14	AC148040	AC148040 Ovis arie
1274	39.4	3.8	129506	14	AC136100	AC136100 Rattus no
c1275	39.4	3.8	132933	8	AL137002	AL137002 Human DNA
1276	39.4	3.8	144605	14	AC015618	AC015618 Homo sapi
c1277	39.4	3.8	153459	14	AC011116	AC011116 Homo sapi
1278	39.4	3.8	157910	8	CNS01DTR	AL132855 Human chr
c1279	39.4	3.8	163332	8	AC004821	AC004821 Homo sapi
c1280	39.4	3.8	166801	14	AC135842	AC135842 Felis cat
1281	39.4	3.8	167159	8	AC113403	AC113403 Homo sapi
c1282	39.4	3.8	167305	8	AP001527	AP001527 Homo sapi
c1283	39.4	3.8	168185	14	AC079805	AC079805 Homo sapi
1284	39.4	3.8	170241	14	AC016434	AC016434 Homo sapi
c1285	39.4	3.8	178637	14	CR513782	CR513782 Danio rer
1286	39.4	3.8	178815	8	AC124220	AC124220 Pan trogl
1287	39.4	3.8	179465	9	AC132307	AC132307 Mus muscu
1288	39.4	3.8	183192	14	AC149273	AC149273 Mus muscu
c1289	39.4	3.8	189637	14	AC009765	AC009765 Homo sapi
1290	39.4	3.8	196292	8	CNS0000B	AL049829 Human chr
1291	39.4	3.8	203777	8	CNS01DVH	AL135818 Human chr
1292	39.4	3.8	210063	14	AC154566	AC154566 Mus muscu
1293	39.4	3.8	212111	14	AC094482	AC094482 Rattus no
1294	39.4	3.8	217877	14	AC159775	AC159775 Bos tauru
1295	39.4	3.8	226601	9	AC122863	AC122863 Mus muscu
c1296	39.4	3.8	228193	14	AC095493	AC095493 Rattus no
1297	39.4	3.8	243982	14	AC125964	AC125964 Rattus no
c1298	39.4	3.8	254677	14	AC068494	AC068494 Mus muscu
c1299	39.4	3.8	302325	1	AE017236	AE017236 Mycobacte
c1300	39.4	3.8	310059	14	AC152075	AC152075 Mus muscu
1301	39.4	3.8	317137	15	AY664413	AY664413 Zea mays
1302	39.4	3.8	348257	1	BX640425	BX640425 Bordetell
c1303	39.2	3.7	464	10	BV106809	BV106809 PZA01644
1304	39.2	3.7	520	10	BV107438	BV107438 PZA01630
c1305	39.2	3.7	540	10	BV106795	BV106795 PZA01642
c1306	39.2	3.7	660	15	CNS019RA	AL111998 Botrytis
1307	39.2	3.7	704	6	AX259505	AX259505 Sequence
c1308	39.2	3.7	710	10	BV115816	BV115816 PZA01219
c1309	39.2	3.7	847	15	AK099127	AK099127 Oryza sat
c1310	39.2	3.7	921	10	BV111228	BV111228 PZA00983
c1311	39.2	3.7	962	15	AK069170	AK069170 Oryza sat
c1312	39.2	3.7	1001	10	PM12E6G	AL684394 Penicilli
1313	39.2	3.7	1042	10	BV110240	BV110240 PZA01003
c1314	39.2	3.7	1377	10	PM12C6G	AL684346 Penicilli
1315	39.2	3.7	1687	15	AK122074	AK122074 Oryza sat
c1316	39.2	3.7	2238	6	AX658754	AX658754 Sequence
1317	39.2	3.7	2356	8	BC009383	BC009383 Homo sapi
c1318	39.2	3.7	3536	9	MMU44942	U44942 Mus musculu
1319	39.2	3.7	4566	1	FRANIFX	L29299 Frankia aln
c1320	39.2	3.7	6125	1	AF160974	AF160974 Xanthomon
1321	39.2	3.7	11820	6	CQ797964	CQ797964 Sequence
1322	39.2	3.7	11820	8	AF135025	AF135025 Homo sapi
1323	39.2	3.7	13045	14	AC108454	AC108454 Homo sapi
1324	39.2	3.7	41523	14	AC101065	AC101065 Mus muscu
1325	39.2	3.7	45449	14	AC027546	AC027546 Homo sapi
1326	39.2	3.7	49574	14	AC100207	AC100207 Mus muscu
c1327	39.2	3.7	54298	14	AC080041	AC080041 Homo sapi
c1328	39.2	3.7	54450	14	AC080179	AC080179 Homo sapi
1329	39.2	3.7	55972	1	AF386507	AF386507 Streptomy
c1330	39.2	3.7	57051	14	AC084331	AC084331 Homo sapi
c1331	39.2	3.7	58722	14	AC100192	AC100192 Mus muscu
c1332	39.2	3.7	58990	14	AC091007	AC091007 Homo sapi
1333	39.2	3.7	62050	14	AC124823	AC124823 Mus muscu
c1334	39.2	3.7	63121	14	AC036107	AC036107 Homo sapi
c1335	39.2	3.7	64668	14	AC101190	AC101190 Mus muscu
c1336	39.2	3.7	64764	14	AC037442	AC037442 Homo sapi
1337	39.2	3.7	64866	14	AC105237	AC105237 Homo sapi
c1338	39.2	3.7	66657	14	AC118049	AC118049 Mus muscu
c1339	39.2	3.7	67161	14	AC134971	AC134971 Homo sapi
c1340	39.2	3.7	68877	14	AC103839	AC103839 Homo sapi
c1341	39.2	3.7	69217	14	AC129516	AC129516 Homo sapi
c1342	39.2	3.7	69614	14	AC115882	AC115882 Mus muscu
c1343	39.2	3.7	75144	14	AC027483	AC027483 Homo sapi
1344	39.2	3.7	75314	14	AC023378	AC023378 Homo sapi
c1345	39.2	3.7	75863	14	AC016059	AC016059 Homo sapi
1346	39.2	3.7	78690	14	AC016541	AC016541 Homo sapi
c1347	39.2	3.7	81336	14	AC100140	AC100140 Mus muscu
1348	39.2	3.7	85268	14	AC022648	AC022648 Homo sapi
c1349	39.2	3.7	95419	14	OSIG00051	AL732356 Oryza sat
c1350	39.2	3.7	96895	14	AC141768	AC141768 Apis mell
1351	39.2	3.7	99630	14	AC142060	AC142060 Rattus no
1352	39.2	3.7	99795	15	AC113332	AC113332 Oryza sat
1353	39.2	3.7	101104	1	CP000089_44	Continuation (45 o
1354	39.2	3.7	110000	1	BX571966_14	Continuation (15 o
c1355	39.2	3.7	110000	1	CP000076_03	Continuation (4 of
1356	39.2	3.7	110000	15	AP008208_032	Continuation (33 o
c1357	39.2	3.7	110000	15	AP008210_342	Continuation (343
1358	39.2	3.7	110000	15	AP008211_243	Continuation (244
1359	39.2	3.7	119242	5	AC140933	AC140933 Gallus ga
1360	39.2	3.7	122599	15	AC130605	AC130605 Oryza sat
c1361	39.2	3.7	125760	14	AC080122	AC080122 Homo sapi
1362	39.2	3.7	126543	14	AC143806	AC143806 Macaca mu
c1363	39.2	3.7	132323	8	AC011473	AC011473 Homo sapi
c1364	39.2	3.7	140596	14	RN75P15	AL603730 Rattus no
1365	39.2	3.7	141056	8	AL354836	AL354836 Human DNA
1366	39.2	3.7	141860	15	AP004126	AP004126 Oryza sat
1367	39.2	3.7	141937	14	AC011686	AC011686 Homo sapi
c1368	39.2	3.7	149162	14	AC013758	AC013758 Homo sapi
1369	39.2	3.7	152732	14	AC074204	AC074204 Mus muscu
c1370	39.2	3.7	159028	14	AC142003	AC142003 Rattus no
c1371	39.2	3.7	160204	6	CS086320	CS086320 Sequence
c1372	39.2	3.7	172533	8	AC009116	AC009116 Homo sapi
c1373	39.2	3.7	173700	6	CS086321	CS086321 Sequence
c1374	39.2	3.7	174298	14	AC152025	AC152025 Papio anu
1375	39.2	3.7	174941	8	AC102941	AC102941 Homo sapi
1376	39.2	3.7	182931	15	AP004843	AP004843 Oryza sat
1377	39.2	3.7	188172	8	AP003041	AP003041 Homo sapi
c1378	39.2	3.7	190050	1	AL646080	AL646080 Ralstonia
c1379	39.2	3.7	190432	15	OSJN00032	AL606619 Oryza sat
c1380	39.2	3.7	195100	14	AC141421	AC141421 Pan trogl
c1381	39.2	3.7	195364	6	CS086319	CS086319 Sequence
c1382	39.2	3.7	207664	8	AC157497	AC157497 Pan trogl
c1383	39.2	3.7	207918	14	AC145969	AC145969 Pan trogl
1384	39.2	3.7	219811	14	AC034123	AC034123 Mus muscu
1385	39.2	3.7	225846	14	CR848790	CR848790 Danio rer
1386	39.2	3.7	228718	14	AC103423	AC103423 Rattus no
c1387	39.2	3.7	230000	8	AF243527	AF243527 Homo sapi
1388	39.2	3.7	238472	8	AC010290	AC010290 Homo sapi
1389	39.2	3.7	239995	14	AC073154	AC073154 Mus muscu
c1390	39.2	3.7	240531	14	AC149658	AC149658 Bos tauru
1391	39.2	3.7	242870	9	AC110175	AC110175 Mus muscu
c1392	39.2	3.7	250074	14	AC156824	AC156824 Bos tauru
c1393	39.2	3.7	255261	9	AL929212	AL929212 Mouse DNA
1394	39.2	3.7	290850	1	SCO939127	AL939127 Streptomy
c1395	39.2	3.7	292200	1	SCO939129	AL939129 Streptomy
c1396	39.2	3.7	293050	1	SCO939116	AL939116 Streptomy
1397	39.2	3.7	300717	1	AE017229	AE017229 Mycobacte
1398	39.2	3.7	308015	1	AE016783	AE016783 Pseudomon
c1399	39.2	3.7	349497	1	BX640440	BX640440 Bordetell
c1400	39	3.7	720	15	CNS01BM9	AL114409 Botrytis
c1401	39	3.7	906	10	BV111239	BV111239 PZA00983
c1402	39	3.7	1286	6	AX305935	AX305935 Sequence
1403	39	3.7	1352	8	HUMIMENBPA	M24405 Homo sapien
1404	39	3.7	2064	15	AK106429	AK106429 Oryza sat
1405	39	3.7	2482	15	AK121766	AK121766 Oryza sat

1406	39	3.7	2966	1	STMAFSQ	D10654 S.coelicolo
c1407	39	3.7	3618	1	AY392421	AY392421 Streptomy
1408	39	3.7	4396	6	CQ895402	CQ895402 Sequence
1409	39	3.7	4396	6	CS117994	CS117994 Sequence
1410	39	3.7	4396	6	AX409682	AX409682 Sequence
1411	39	3.7	4396	6	AX771485	AX771485 Sequence
1412	39	3.7	4396	8	HUMTFAA	M31523 Human trans
1413	39	3.7	11332	1	AY260902	AY260902 Rhodospir
c1414	39	3.7	24728	8	AL162375	AL162375 Human DNA
1415	39	3.7	26822	14	AC011674	AC011674 Homo sapi
c1416	39	3.7	39200	8	AL954664	AL954664 Human DNA
1417	39	3.7	39709	14	AC145431	AC145431 Homo sapi
1418	39	3.7	44508	14	AC136063	AC136063 Rattus no
c1419	39	3.7	45514	14	AC102345	AC102345 Mus muscu
1420	39	3.7	46445	14	AC023941	AC023941 Homo sapi
c1421	39	3.7	55961	14	AC027765	AC027765 Homo sapi
1422	39	3.7	61893	14	AC104973	AC104973 Homo sapi
1423	39	3.7	62726	14	AC084090	AC084090 Homo sapi
1424	39	3.7	64693	14	AC105143	AC105143 Homo sapi
1425	39	3.7	66450	14	AC060821	AC060821 Homo sapi
c1426	39	3.7	66744	14	AC100116	AC100116 Mus muscu
c1427	39	3.7	67477	14	AC055848	AC055848 Homo sapi
1428	39	3.7	68730	14	AC100664	AC100664 Mus muscu
c1429	39	3.7	82558	14	AC116495	AC116495 Mus muscu
c1430	39	3.7	87478	14	AC139860	AC139860 Mus muscu
c1431	39	3.7	90250	14	AC095028	AC095028 Leishmani
1432	39	3.7	95445	14	AC016175	AC016175 Homo sapi
c1433	39	3.7	101083	14	AC139010	AC139010 Homo sapi
1434	39	3.7	110000	1	BA000040_88	Continuation (89 o
1435	39	3.7	110000	1	BA000040_89	Continuation (90 o
1436	39	3.7	110000	1	CP000010_17	Continuation (18 o
c1437	39	3.7	110000	14	AC123648_0	AC123648 Mus muscu
1438	39	3.7	110000	15	AP008207_186	Continuation (187
c1439	39	3.7	113816	14	AC004358	AC004358 Drosophil
1440	39	3.7	117409	14	AC138141	AC138141 Homo sapi
1441	39	3.7	122630	14	AC012434	AC012434 Homo sapi
c1442	39	3.7	124498	14	AC141194	AC141194 Rattus no
c1443	39	3.7	132290	14	AC026137	AC026137 Homo sapi
1444	39	3.7	134712	14	AP003891	AP003891 Oryza sat
c1445	39	3.7	134966	14	AC115983	AC115983 Homo sapi
c1446	39	3.7	138390	13	AY261359	AY261359 Bovine he
1447	39	3.7	140491	15	AP003276	AP003276 Oryza sat
1448	39	3.7	142680	15	AP004611	AP004611 Oryza sat
1449	39	3.7	149454	14	AC013648	AC013648 Homo sapi
1450	39	3.7	152309	8	AC138185	AC138185 Homo sapi
c1451	39	3.7	156328	14	AC148280	AC148280 Sorex ara
1452	39	3.7	160770	8	AC010336	AC010336 Homo sapi
c1453	39	3.7	163379	14	CR450714	CR450714 Danio rer
1454	39	3.7	172369	8	AC093123	AC093123 Papio anu
c1455	39	3.7	175483	14	AC163318	AC163318 Bos tauru
1456	39	3.7	179659	14	AC122121	AC122121 Mus muscu
c1457	39	3.7	191327	14	AC151887	AC151887 Saimiri b
1458	39	3.7	201339	14	AC155746	AC155746 Bos tauru
c1459	39	3.7	204050	1	AL646073	AL646073 Ralstonia
1460	39	3.7	226213	14	AC107064	AC107064 Bos tauru
c1461	39	3.7	245900	14	AC097727	AC097727 Rattus no
c1462	39	3.7	268597	14	AC094787	AC094787 Rattus no
1463	39	3.7	276938	14	AC073671	AC073671 Mus muscu
c1464	39	3.7	277000	1	SCO939109	AL939109 Streptomy
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1466	39	3.7	300217	1	AE016922	AE016922 Chromobac
1467	39	3.7	331409	14	AC155865	AC155865 Bos tauru
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c1469	38.8	3.7	267	6	AR492010	AR492010 Sequence
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1472	38.8	3.7	560	10	BV122577	BV122577 PZA01737
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c1474	38.8	3.7	602	8	F450120S01	AF450120 Homo sapi
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c1480	38.8	3.7	962	1	SAV320278	AJ320278 Streptomy
c1481	38.8	3.7	972	10	PM12A12G	AL684288 Penicilli
c1482	38.8	3.7	1327	6	AX414274	AX414274 Sequence
1483	38.8	3.7	1599	6	AX654063	AX654063 Sequence
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c1486	38.8	3.7	2235	6	CQ846019	CQ846019 Sequence
c1487	38.8	3.7	2235	8	AK131361	AK131361 Homo sapi
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c1496	38.8	3.7	13123	1	AB070954	AB070954 Streptomy
1497	38.8	3.7	17809	6	CQ926638	CQ926638 Sequence
1498	38.8	3.7	25306	1	AF058302	AF058302 Streptomy
c1499	38.8	3.7	26928	2	AB029444	AB029444 Leishmani
1500	38.8	3.7	36334	14	AC136981	AC136981 Mus muscu

ALIGNMENTS

RESULT 1
BD218877
LOCUS BD218877 1047 bp DNA linear PAT 17-JUL-2003
DEFINITION Factor affecting tumor necrosis factor receptor releasing enzyme.
ACCESSION BD218877
VERSION BD218877.1 GI:33028647
KEYWORDS JP 2002514402-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Gatanaga,T. and Granger,G.A.
TITLE Factor affecting tumor necrosis factor receptor releasing enzyme
JOURNAL Patent: JP 2002514402-A 2 21-MAY-2002;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT OS Homo sapiens (human)
PN JP 2002514402-A/2
PD 21-MAY-2002
PF 14-MAY-1999 JP 2000548361
PR 14-MAY-1998 US 09/081385
PI TETSUYA GATANAGA,GALE A GRANGER
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
,C12N5/10,C12Q1/68,
PC G01N33/15,G01N33/50//C07K14/715,C12N15/00,C12N5/00 CC Factor
affecting tumor necrosis factor receptor releasing CC
enzyme
FH Key Location/Qualifiers
FT source 1. .1047
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
source 1. .1047
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 1047; DB 6; Length 1047;
Best Local Similarity 100.0%; Pred. No. 5.6e-191;
Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60
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Qy         421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
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Qy         601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660
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Qy         661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720
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Qy         781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840
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Qy        1021 ATTAAACTGATGAACACATCCCCAAAA 1047
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Db        1021 ATTAAACTGATGAACACATCCCCAAAA 1047
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RESULT 2
AR338357
LOCUS AR338357 1047 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 3 from patent US 6569645.

ACCESSION AR338357
VERSION AR338357.1 GI:33725120
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Chen,J., Filvaroff,E., Fong,S., Goddard,A., Godowski,P., Grimaldi,C., Gurney,A., Li,H., Hillan,K., Tumas,D., VanLookeren,M., Vandlen,R., Watanabe,C., Williams,P.M., Wood,W.I. and Yansura,D.
TITLE IL-17 homologous polypeptides and therapeutic uses thereof
JOURNAL Patent: US 6569645-A 3 27-MAY-2003;
Genentech, Inc.; South San Francisco, CA
FEATURES Location/Qualifiers
source 1. .1047
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 1047; DB 6; Length 1047;
Best Local Similarity 100.0%; Pred. No. 5.6e-191;
Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy           1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60
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Qy         121 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180
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Qy         421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
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Db         421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480

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Db       1021 ATTAAACTGATGAACACATCCCCAAAA 1047


RESULT 3
AX180766
LOCUS       AX180766               1047 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 3 from Patent WO0146420.
ACCESSION   AX180766
VERSION     AX180766.1  GI:15132617
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Chen,J., Filvaroff,E., Fong,S., Goddard,A., Godowski,P.J.,
            Grimaldi,C.J., Gurney,A.L., Li,H., Hillan,K.J., Tumas,D., van
            Lookeren,M., Vandlen,R.L., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Yansura,D.G.
  TITLE     Il-17 and il-17r homologous polypeptides and therapeutic uses
            thereof
  JOURNAL   Patent: WO 0146420-A 3 28-JUN-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           100.0%;  Score 1047;  DB 6;  Length 1047;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-191;
  Matches 1047;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        961 TTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATT 1020

Qy       1021 ATTAAACTGATGAACACATCCCCAAAA 1047
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Db       1021 ATTAAACTGATGAACACATCCCCAAAA 1047


RESULT 4
AX376380
LOCUS       AX376380               1047 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 447 from Patent WO0168848.
ACCESSION   AX376380
VERSION     AX376380.1  GI:19170581
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
            Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
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  JOURNAL   Patent: WO 0168848-A 447 20-SEP-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1047
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 1047;  DB 6;  Length 1047;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-191;
  Matches 1047;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60
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Db          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60

Qy         61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120

Qy        121 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180

Qy        181 CGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 240
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Db        181 CGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 240

Qy        241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300

Qy        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360
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Db        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360

Qy        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
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Db        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420

Qy        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
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Qy        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540
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Db        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540

Qy        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600
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Db        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600

Qy        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660

Qy        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720
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Db        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720

Qy        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780

Qy        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840

Qy        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900
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Db        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900

Qy        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTC 960
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Db        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTC 960

Qy        961 TTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATT 1020
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Db        961 TTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATT 1020

Qy       1021 ATTAAACTGATGAACACATCCCCAAAA 1047
              |||||||||||||||||||||||||||
Db       1021 ATTAAACTGATGAACACATCCCCAAAA 1047


RESULT 5
AF152099
LOCUS       AF152099               1047 bp    mRNA    linear   PRI 27-JAN-2000
DEFINITION  Homo sapiens interleukin 17C mRNA, complete cds.
ACCESSION   AF152099
VERSION     AF152099.1  GI:6759914
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1047)
  AUTHORS   Li,H., Chen,J., Huang,A., Stinson,J., Heldens,S., Foster,J.,
            Dowd,P., Gurney,A.L. and Wood,W.I.
  TITLE     Cloning and characterization of IL-17B and IL-17C, two new members
            of the IL-17 cytokine family
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (2), 773-778 (2000)
   PUBMED   10639155
REFERENCE   2  (bases 1 to 1047)
  AUTHORS   Li,H., Chen,J., Stinson,J. and Wood,W.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-1999) Molecular Biology, Genentech, Inc., 1 DNA
            Way, S. San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1047
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="2"
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                     /clone="DNA62377"
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                     /note="IL-17C; similar to interleukin 17"
                     /codon_start=1
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                     /protein_id="AAF28105.1"
                     /db_xref="GI:6759915"
                     /translation="MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPL
                     GQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTH
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                     RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRSV"
ORIGIN

  Query Match           100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-191;
  Matches 1047;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60

Qy         61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120
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Db         61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120

Qy        121 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180
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Qy        181 CGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 240
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Qy        241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300
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Qy        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360
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Qy        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
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Qy        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
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Qy        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540
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Db        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540

Qy        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600
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Qy        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660
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Qy        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720
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Qy        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840
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Db        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840

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Qy        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTC 960
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Qy        961 TTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATT 1020
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Db        961 TTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATT 1020

Qy       1021 ATTAAACTGATGAACACATCCCCAAAA 1047
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RESULT 6
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LOCUS       AY358471               1047 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA62377 IL17C (UNQ561) mRNA, complete cds.
ACCESSION   AY358471
VERSION     AY358471.1  GI:37182064
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1047)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1047)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1047
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                     /clone="DNA62377"
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     CDS             50. .643
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                     /codon_start=1
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                     /db_xref="GI:37182065"
                     /translation="MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPL
                     GQAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTH
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                     RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRSV"
ORIGIN
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  Query Match           100.0%;  Score 1047;  DB 8;  Length 1047;
  Best Local Similarity  100.0%;  Pred. No. 5.6e-191;
  Matches 1047;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60
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Qy         61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120
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Qy        121 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180
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Qy        181 CGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 240
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Qy        241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300
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Db        241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300

Qy        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360
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Db        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360

Qy        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
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Qy        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
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Db        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540

Qy        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600
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Db        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600

Qy        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660
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Qy        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCCTATTTATGTGTATTTATTGT 720
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Qy        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780
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Qy        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840
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Db        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900

Qy        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTC 960
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Qy        961 TTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATT 1020
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Qy       1021 ATTAAACTGATGAACACATCCCCAAAA 1047
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Db       1021 ATTAAACTGATGAACACATCCCCAAAA 1047
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RESULT 7
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LOCUS       BD265555                1107 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Interleukin-17-associated mammalian cytokine, polynucleotide
            encoding the same and utilization thereof.
ACCESSION   BD265555
VERSION     BD265555.1  GI:33075323
KEYWORDS    JP 2002534122-A/12.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1107)
  AUTHORS   Gorman,D.M., Bazan,F.J. and Kastelein,R.A.
  TITLE     Interleukin-17-associated mammalian cytokine, polynucleotide
            encoding the same and utilization thereof
  JOURNAL   Patent: JP 2002534122-A 12 15-OCT-2002;
            SCHERING CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534122-A/12
            PD   15-OCT-2002
            PF   10-JAN-2000 JP 2000593745
            PR   11-JAN-1999 US    09/228822
            PI   DANIEL M GORMAN,FERNANDO J BAZAN,ROBERT A KASTELEIN PC
            C12N15/09,C07K14/54,C07K16/24,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N5/10,
            PC   C12P21/02,G01N33/53//(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   C12N5/00
            CC   Interleukin-17-associated mammalian cytokine, polynucleotide
            CC         encoding the
            CC   same and utilization thereof
            FH   Key             Location/Qualifiers
            FT   CDS             (115). .(705)
            FT   mat_peptide     (166). .(705).
FEATURES            Location/Qualifiers
     source         1. .1107
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
ORIGIN
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  Query Match           98.2%;  Score 1028.4;  DB 6;  Length 1107;
  Best Local Similarity 99.8%;  Pred. No. 2.1e-187;
  Matches 1040;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60
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Db         66 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 125

Qy         61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 185

Qy        121 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 245

Qy        181 CGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 240
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Db        246 CGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 305

Qy        241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300
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Db        306 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 365

Qy        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360
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Db        366 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 425

Qy        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
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Db        426 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 485

Qy        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
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Db        486 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 545

Qy        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540
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Db        546 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 605

Qy        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600
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Db        606 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 665

Qy        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660
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Db        666 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 725

Qy        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720
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Db        726 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGG 785

Qy        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780
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Db        786 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 845

Qy        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840
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Db        846 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 905
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Qy        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900
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Db        906 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 965

Qy        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGG-CCCCGCAGGCTGCCT 959
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Db        966 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCT 1025

Qy        960 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1019
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Db       1026 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1085

Qy       1020 TATTAAACTGATGAACACATCC 1041
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Db       1086 TATTAAACTGATGAACACATCC 1107


RESULT 8
CS135286
LOCUS       CS135286                1107 bp    DNA     linear   PAT 09-AUG-2005
DEFINITION  Sequence 23 from Patent WO2005065711.
ACCESSION   CS135286
VERSION     CS135286.1  GI:72067734
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gorman,D.M.
  TITLE     Mammalian receptor proteins; related reagents and methods
  JOURNAL   Patent: WO 2005065711-A 23 21-JUL-2005;
            Schering Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1107
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.2%;  Score 1028.4;  DB 6;  Length 1107;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-187;
  Matches 1040;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 125

Qy         61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 185

Qy        121 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180
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Db        186 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 245

Qy        181 CGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 240
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Db        246 CGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 305

Qy        241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 365

Qy        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360
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Db        366 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 425

Qy        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
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Db        426 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 485

Qy        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
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Db        486 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 545

Qy        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540
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Db        546 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 605

Qy        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600
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Db        606 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 665

Qy        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660
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Db        666 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 725

Qy        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720
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Db        726 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGG 785

Qy        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780
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Db        786 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 845

Qy        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840
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Db        846 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 905

Qy        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900
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Db        906 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 965

Qy        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGG-CCCCGCAGGCTGCCT 959
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Db        966 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCT 1025

Qy        960 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1019
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Db       1026 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1085

Qy       1020 TATTAAACTGATGAACACATCC 1041
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Db       1086 TATTAAACTGATGAACACATCC 1107


RESULT 9
AR316787
LOCUS       AR316787                1107 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 22 from patent US 6562578.
ACCESSION   AR316787
VERSION     AR316787.1  GI:33695749
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1107)
  AUTHORS   Gorman,D.M., Bazan,J.F. and Kastelein,R.A.
  TITLE     IL-17-like cytokine binding compounds and antibodies
  JOURNAL   Patent: US 6562578-A 22 13-MAY-2003;
            Schering Corporation; Kenilworth, NJ;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .1107
                     /organism="unknown"
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ORIGIN

  Query Match             98.2%;  Score 1028.4;  DB 6;  Length 1107;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-187;
  Matches 1040;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60
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Db        66 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 125

Qy        61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120

Db       126 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 185

Qy       121 CAGGGGGCACCCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180

Db       186 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 245

Qy       181 CGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 240

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Qy       241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300

Db       306 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 365

Qy       301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360

Db       366 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 425

Qy       361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420

Db       426 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 485

Qy       421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480

Db       486 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 545

Qy       481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540

Db       546 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 605

Qy       541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600

Db       606 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 665

Qy       601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660

Db       666 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 725

Qy       661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCCTATTTATGTGTATTTATTGT 720

Db       726 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCCTATTTATGTGTATTTATTGG 785

Qy       721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780

Db       786 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 845

Qy       781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840

Db       846 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 905

Qy       841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900

Db       906 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 965

Qy       901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGG-CCCCGCAGGCTGCCT 959

Db       966 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCT 1025

Qy       960 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1019

Db      1026 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1085

Qy      1020 TATTAAACTGATGAACACATCC 1041

Db      1086 TATTAAACTGATGAACACATCC 1107
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RESULT 10

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AF142410
LOCUS       AF142410               1078 bp    mRNA    linear   PRI 31-OCT-2000
DEFINITION  Homo sapiens cytokine CX2 precusor mRNA, complete cds.
ACCESSION   AF142410
VERSION     AF142410.1  GI:11055014
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1078)
  AUTHORS   Zhang,W., He,L., Wan,T., Yuan,Z. and Cao,X.
  TITLE     Novel human cytokine CX2 with homology to IL-17
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1078)
  AUTHORS   Zhang,W., He,L., Wan,T., Yuan,Z. and Cao,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-1999) Department of Immunology, Second Military
            Medical University & Shanghai Brilliance Biotechnology Institute,
            800 Xiangyin Road, Shanghai 200433, P.R. China
FEATURES             Location/Qualifiers
     source          1. .1078
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     CDS             43. .636
                     /note="similar to IL-17"
                     /codon_start=1
                     /product="cytokine CX2 precusor"
                     /protein_id="AAG27921.1"
                     /db_xref="GI:11055015"
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                     GQAPPRLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTH
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                     RPCSRDGSGLPTPGAFAPHTEFIHVPVGCTCVLPRSV"
ORIGIN

  Query Match           97.0%;  Score 1015.4;  DB 8;  Length 1078;
  Best Local Similarity 99.4%;  Pred. No. 6.5e-185;
  Matches 1027;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          8 GTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGC 67

Db          1 GTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGC 60

Qy         68 CTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGG 127

Db         61 CTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGG 120

Qy        128 CACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAG 187

Db        121 CACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAG 180

Qy        188 GCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTG 247

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Qy        248 GTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACC 307

Db        241 GTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACC 300

Qy        308 CAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATC 367

Db        301 CAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATC 360

Qy        368 TCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTC 427

Db        361 TCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTC 420

Qy        428 GCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTC 487

Db        421 GCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTC 480
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Qy        488 AACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGAC 547
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Db        481 AACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGAC 540

Qy        548 GGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCC 607
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Db        541 GGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCC 600

Qy        608 GTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGGCCCCTAG 667
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Db        601 GTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCAAGGCCGTGGGGCCCTTAG 660

Qy        668 ACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTAT 727
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Db        661 ACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTAT 720

Qy        728 ATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCC 787
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Db        721 ATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCC 780

Qy        788 CCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTT 847
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Db        781 CCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTWGAAGGAGCTCAGCACCTCTT 840

Qy        848 CCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCC 907
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Db        841 CCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGYTCCCTGTCC 900

Qy        908 TGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGG-CCCCGCAGGCTGCCTCTTCCCA 966
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Db        901 TGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCA 960

Qy        967 ACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAA 1026
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Db        961 ACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAA 1020

Qy       1027 CTGATGAACACAT 1039
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Db       1021 CTGATGAACACAT 1033
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RESULT 11
BD211219
LOCUS       BD211219               1067 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Interleukins-21 and 22.
ACCESSION   BD211219
VERSION     BD211219.1  GI:33020989
KEYWORDS    JP 2002516103-A/21.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1067)
  AUTHORS   Ruben,S.M. and Ebner,R.
  TITLE     Interleukins-21 and 22
  JOURNAL   Patent: JP 2002516103-A 21 04-JUN-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002516103-A/21
            PD   04-JUN-2002
            PF   27-MAY-1999 JP 2000551001
            PR   29-MAY-1998 US    60/087340,10-SEP-1998 US    60/099805 PR
            30-APR-1999 US    60/131965
            PI   STEVEN M RUBEN,REINHARD EBNER
            PC   C12N15/09,A61K38/00,A61P7/04,A61P9/00,A61P15/08,A61P25/00, PC
             A61P35/04,
            PC   A61P43/00,A61P43/00,C07K14/54,C07K16/24,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12Q1/68,G01N33/68,C12N15/00,A61K37/02, PC
             C12N5/00
            CC   Interleukins-21 and 22.
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            FH   Key             Location/Qualifiers
            FT   CDS             (34). .(624).
FEATURES             Location/Qualifiers
     source          1. .1067
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN
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  Query Match           96.1%;  Score 1006.4;  DB 6;  Length 1067;
  Best Local Similarity  98.9%;  Pred. No. 3.5e-183;
  Matches 1021;  Conservative    2;  Mismatches    8;  Indels    1;  Gaps    1;

Qy         17 GCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGTTT 76
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Qy         77 CTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCAC 136
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Qy        137 AGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCAGGCCCCCCCA 196
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Db        241 CTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCG 300

Qy        317 GTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCTGG 376
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Db        301 GTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCTGG 360

Qy        377 AGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGC 436
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Db        361 AGATACCGGGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGC 420

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Qy        617 ACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACAC 676
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Qy        677 GTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCC 736
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Db        901 CTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTG 960

Qy        976 GAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAAC 1035
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Db        961 GAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAAC 1020

Qy       1036 ACATCCCCAAAA 1047
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RESULT 12
CQ847631
LOCUS       CQ847631               1067 bp    DNA     linear   PAT 19-AUG-2004
DEFINITION  Sequence 28 from Patent EP1443055.
ACCESSION   CQ847631
VERSION     CQ847631.1  GI:51469191
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ruben,S.M. and Ebner,R.
  TITLE     Interleukins-21 and 22
  JOURNAL   Patent: EP 1443055-A 28 04-AUG-2004;
            Human Genome Sciences, Inc. (US)
FEATURES             Location/Qualifiers
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     CDS             34. .627
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                     RPCSRDGSGLPTPGAFAFHTEFIHVPVGCTCVLPRSV"
ORIGIN

  Query Match           96.1%;  Score 1006.4;  DB 6;  Length 1067;
  Best Local Similarity  98.9%;  Pred. No. 3.5e-183;
  Matches 1021;  Conservative    2;  Mismatches    8;  Indels    1;  Gaps    1;

Qy         17 GCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGTTT 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         77 CTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCAC 136
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Qy        197 CACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGC 256
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Db        181 CACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGC 240

Qy        257 CTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCG 316
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Db        241 CTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCG 300

Qy        317 GTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCTGG 376
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Db        541 CTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGC 600

Qy        617 ACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACAC 676
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Db        601 ACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCAAGGCCGTGGGGCCCTTAGACTGGACAC 660

Qy        677 GTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCC 736
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Db        841 AAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGYTCCCTGTCCTGCTCCCGG 900

Qy        917 CTTCCCTTACCCTATCACTGGCCTCAGG-CCCCGCAGGCTGCCTCTTCCCAACCTCCTTG 975
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Db        901 CTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTG 960

Qy        976 GAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAAC 1035
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Db        961 GAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAAC 1020

Qy       1036 ACATCCCCAAAA 1047
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Db       1021 ACAAAAAAAAAA 1032


RESULT 13
AX223949
LOCUS       AX223949               1177 bp    DNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 1 from Patent WO0159120.
ACCESSION   AX223949
VERSION     AX223949.1  GI:15551624
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jing,S. and Bass,M.B.
  TITLE     Il-17 like molecules and uses thereof
  JOURNAL   Patent: WO 0159120-A 1 16-AUG-2001;
            Amgen Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1177
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ORIGIN

  Query Match             88.2%;  Score 923.4;  DB 6;  Length 1177;
  Best Local Similarity   99.8%;  Pred. No. 3e-167;
  Matches  935;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

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Qy        113 CCCTCCCTCAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAA 172
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Qy        173 CTGCCCCTCGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCT 232
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Qy        233 TTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGG 292
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Db        416 TTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGG 475

Qy        293 CCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACC 352
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Qy        533 CCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAG 592
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Db        716 CCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAG 775

Qy        593 TTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGG 652
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Db        776 TTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGG 835

Qy        653 CCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTA 712
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Qy        893 CTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGG-CCCCGCA 951
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Db       1076 CTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCA 1135

Qy        952 GGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGT 988
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Db       1136 GGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGT 1172


RESULT 14
AC103884/c
LOCUS       AC103884              156899 bp    DNA     linear   HTG 12-DEC-2001
DEFINITION  Homo sapiens chromosome 16q24.3 clone RP11-645M1, WORKING DRAFT
            SEQUENCE, 40 unordered pieces.
ACCESSION   AC103884
VERSION     AC103884.1  GI:17155011
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 156899)
  AUTHORS   Kremmidiotis,G., Gardner,A.E., Callen,D.F. and Sutherland,G.R.
  TITLE     Large Scale Sequencing of the Chromosome 16 region q24.3
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 156899)
  AUTHORS   Kremmidiotis,G., Gardner,A.E., Callen,D.F. and Sutherland,G.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-2001) Cytogenetics & Molecular Genetics, Women's
            & Children's Hospital, 72 King William Road, North Adelaide,
            Adelaide, South Australia 5006, Australia
  REMARK    Genome Centre : Cytogenetics & Molecular Genetics
            Centre Code : CMGWCH
            Web:http://www.wch.sa.gov.au/labmedic/genetics/sequencing.html
COMMENT     ----------------------------------------------------------------
            Genome Centre :  Cytogenetics & Molecular Genetics
            Centre Code:  CMGWCH
            Website:http://www.wch.sa.gov.au/labmedic/genetics/sequencing.html
            ----------------------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 40 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *     5731     6840: contig of 1110 bp in length
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            *                   gap of unknown length
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            *    27477    29681: contig of 2205 bp in length
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            *                   gap of unknown length
            *    31514    64198: contig of 32685 bp in length
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            *    64820    65404: contig of 585 bp in length
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            *    67964    73068: contig of 5105 bp in length
            *                    gap of unknown length
            *    73069    89815: contig of 16747 bp in length
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            *    91439    92409: contig of 971 bp in length
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            *                    gap of unknown length
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            *                    gap of unknown length
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            *                    gap of unknown length
            *    95602   103877: contig of 8276 bp in length
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DEFINITION  Homo sapiens chromosome 16 clone RP11-21B21, complete sequence.
ACCESSION   AC116552 AC022554
VERSION     AC116552.2  GI:40714624
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 176797)
  AUTHORS   DOE Joint Genome Institute, Stanford Human Genome Center and Los
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  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 176797)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAR-2002) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 176797)
  AUTHORS   Stanford Human Genome Center and Los Alamos National Laboratory.
  CONSRTM   DOE Joint Genome Institute
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2004) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jan 7, 2004 this sequence version replaced gi:19807788.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center and Los Alamos
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National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.

NOTE: Shatter libraries failed to verify the repeat region 118516-119880. Unsure region 118516-119880. Forced join 119251.

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 29, 2006, 17:48:00 ; Search time 339 Seconds
(without alignments)
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Title: US-09-854-280-4
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	95	39	3.7	1535	3	US-09-668-680-12	Sequence 12, Appl
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c	110	38.6	3.7	71989	3	US-09-724-876-2	Sequence 2, Appli
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	115	38.4	3.7	13248	3	US-09-949-016-12024	Sequence 12024, A
	116	38.4	3.7	13248	3	US-09-949-016-14230	Sequence 14230, A
c	117	38.4	3.7	46253	3	US-09-949-016-11890	Sequence 11890, A
c	118	38.4	3.7	46257	3	US-09-949-016-13711	Sequence 13711, A
c	119	38.4	3.7	161607	3	US-09-949-016-12210	Sequence 12210, A
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c	121	38.2	3.6	1068	3	US-09-252-991A-438	Sequence 438, App
	122	38.2	3.6	1164	3	US-09-252-991A-363	Sequence 363, App
	123	38.2	3.6	1514	3	US-09-162-524-4	Sequence 4, Appli
c	124	38.2	3.6	1659	3	US-09-083-351-3	Sequence 3, Appli
c	125	38.2	3.6	1659	3	US-09-083-352-3	Sequence 3, Appli
c	126	38.2	3.6	1662	3	US-09-612-809B-3	Sequence 3, Appli
c	127	38.2	3.6	3946	3	US-09-083-351-1	Sequence 1, Appli
c	128	38.2	3.6	3946	3	US-09-083-352-1	Sequence 1, Appli
c	129	38.2	3.6	20103	3	US-09-949-016-17223	Sequence 17223, A
	130	38.2	3.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	131	38.2	3.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	132	38	3.6	1271	3	US-09-231-227-1	Sequence 1, Appli
	133	38	3.6	1271	3	US-09-768-585-1	Sequence 1, Appli
	134	38	3.6	2055	3	US-09-252-991A-12033	Sequence 12033, A
	135	38	3.6	2160	3	US-09-252-991A-12005	Sequence 12005, A
c	136	38	3.6	2639	3	US-10-104-047-684	Sequence 684, App
c	137	38	3.6	3366	3	US-09-252-991A-11980	Sequence 11980, A
	138	38	3.6	5773	3	US-09-566-921-112	Sequence 112, App
c	139	38	3.6	24459	3	US-09-902-540-5004	Sequence 5004, Ap
	140	38	3.6	32241	3	US-09-902-540-1247	Sequence 1247, Ap
c	141	37.8	3.6	318	3	US-09-165-264-12	Sequence 12, Appl
c	142	37.8	3.6	320	3	US-09-165-264-13	Sequence 13, Appl
	143	37.8	3.6	822	3	US-09-228-986-38	Sequence 38, Appl
	144	37.8	3.6	822	3	US-10-101-464A-38	Sequence 38, Appl
	145	37.8	3.6	939	3	US-09-252-991A-3645	Sequence 3645, Ap
	146	37.8	3.6	1881	3	US-09-252-991A-3697	Sequence 3697, Ap
c	147	37.8	3.6	1998	3	US-09-252-991A-3812	Sequence 3812, Ap
	148	37.8	3.6	2138	3	US-10-101-464A-462	Sequence 462, App
	149	37.8	3.6	3957	3	US-10-237-551-193	Sequence 193, App
	150	37.8	3.6	11003	3	US-09-949-016-13166	Sequence 13166, A
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c	152	37.8	3.6	154746	3	US-09-827-688-8	Sequence 8, Appli
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	156	37.6	3.6	1577	3	US-09-976-594-50	Sequence 50, Appl
	157	37.6	3.6	1587	3	US-09-023-655-878	Sequence 878, App
	158	37.6	3.6	1876	3	US-09-566-921-70	Sequence 70, Appl
	159	37.6	3.6	2460	3	US-09-252-991A-2998	Sequence 2998, Ap
c	160	37.6	3.6	2856	3	US-09-252-991A-2869	Sequence 2869, Ap
	161	37.6	3.6	3387	3	US-09-252-991A-3101	Sequence 3101, Ap
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c	163	37.6	3.6	5117	3	US-10-120-988-438	Sequence 438, App
c	164	37.6	3.6	14101	3	US-09-902-540-1080	Sequence 1080, Ap
c	165	37.6	3.6	26533	3	US-09-902-540-1199	Sequence 1199, Ap
c	166	37.6	3.6	27578	3	US-09-949-016-12167	Sequence 12167, A
c	167	37.6	3.6	27579	3	US-09-949-016-15005	Sequence 15005, A
c	168	37.6	3.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	169	37.4	3.6	320	3	US-09-165-264-11	Sequence 11, Appl
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	171	37.4	3.6	1212	3	US-09-170-496D-113	Sequence 113, App
	172	37.4	3.6	1212	3	US-09-170-496D-223	Sequence 223, App
	173	37.4	3.6	1212	3	US-09-743-742B-3	Sequence 3, Appli
	174	37.4	3.6	2569	3	US-10-104-047-452	Sequence 452, App
	175	37.4	3.6	25048	3	US-09-902-540-1239	Sequence 1239, Ap
	176	37.2	3.6	519	3	US-09-252-991A-3601	Sequence 3601, Ap
c	177	37.2	3.6	54779	3	US-09-949-001-27	Sequence 27, Appl
c	178	37.2	3.6	54780	3	US-09-949-001-39	Sequence 39, Appl
	179	37	3.5	601	3	US-09-949-016-176416	Sequence 176416,
c	180	37	3.5	726	3	US-09-252-991A-5506	Sequence 5506, Ap
c	181	37	3.5	852	3	US-09-893-737-151	Sequence 151, App
c	182	37	3.5	852	3	US-09-893-737-297	Sequence 297, App
c	183	37	3.5	1011	3	US-09-902-540-3195	Sequence 3195, Ap
c	184	37	3.5	1969	3	US-10-012-231A-49	Sequence 49, Appl
c	185	37	3.5	1969	3	US-10-015-389A-49	Sequence 49, Appl
c	186	37	3.5	1969	3	US-10-006-768A-49	Sequence 49, Appl
c	187	37	3.5	1969	3	US-10-015-671A-49	Sequence 49, Appl
c	188	37	3.5	1969	3	US-10-015-393A-49	Sequence 49, Appl
c	189	37	3.5	1969	3	US-10-011-833A-49	Sequence 49, Appl
c	190	37	3.5	1969	3	US-10-006-041A-49	Sequence 49, Appl
c	191	37	3.5	1969	3	US-10-012-064A-49	Sequence 49, Appl
	192	37	3.5	2436	3	US-09-252-991A-5435	Sequence 5435, Ap
c	193	37	3.5	3872	3	US-09-949-016-1709	Sequence 1709, Ap
	194	37	3.5	12001	2	US-08-458-568A-11	Sequence 11, Appl
	195	37	3.5	17262	3	US-09-902-540-1146	Sequence 1146, Ap
c	196	37	3.5	20187	3	US-09-902-540-1186	Sequence 1186, Ap
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c	202	37	3.5	68750	3	US-09-567-969-1	Sequence 1, Appli
c	203	37	3.5	68750	3	US-09-568-480-1	Sequence 1, Appli
c	204	37	3.5	68750	3	US-09-568-486-1	Sequence 1, Appli
c	205	37	3.5	68750	3	US-09-568-472-1	Sequence 1, Appli
c	206	37	3.5	68750	3	US-09-567-899-1	Sequence 1, Appli
c	207	37	3.5	68750	3	US-10-014-717-1	Sequence 1, Appli
c	208	37	3.5	139562	3	US-09-949-016-13451	Sequence 13451, A
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c	211	36.8	3.5	1173	3	US-09-902-540-9446	Sequence 9446, Ap
	212	36.8	3.5	1182	3	US-09-252-991A-3677	Sequence 3677, Ap
	213	36.8	3.5	1239	3	US-09-252-991A-3627	Sequence 3627, Ap
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c	216	36.8	3.5	1926	3	US-09-410-399-3	Sequence 3, Appli
c	217	36.8	3.5	2034	3	US-09-252-991A-3835	Sequence 3835, Ap
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c	219	36.8	3.5	2580	3	US-09-359-081-2	Sequence 2, Appli
c	220	36.8	3.5	4302	3	US-09-902-540-576	Sequence 576, App
	221	36.8	3.5	5452	2	US-09-130-114-1	Sequence 1, Appli
c	222	36.8	3.5	5695	3	US-09-949-016-13664	Sequence 13664, A
	223	36.8	3.5	8705	3	US-09-647-344A-14	Sequence 14, Appl
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c	225	36.8	3.5	9600	3	US-09-620-925-1	Sequence 1, Appli
c	226	36.8	3.5	10596	2	US-07-884-811-15	Sequence 15, Appl
c	227	36.8	3.5	10596	2	US-07-885-971-15	Sequence 15, Appl
c	228	36.8	3.5	10596	2	US-08-087-783A-15	Sequence 15, Appl
c	229	36.8	3.5	10596	2	US-08-194-088B-15	Sequence 15, Appl
c	230	36.8	3.5	10596	2	US-08-194-087-15	Sequence 15, Appl
c	231	36.8	3.5	10596	6	PCT-US93-04648-15	Sequence 15, Appl
	232	36.8	3.5	13904	3	US-09-902-540-1076	Sequence 1076, Ap
	233	36.8	3.5	16080	3	US-09-724-566A-48	Sequence 48, Appl
	234	36.8	3.5	16080	3	US-09-471-669A-48	Sequence 48, Appl
c	235	36.8	3.5	18662	3	US-09-949-016-14655	Sequence 14655, A
	236	36.8	3.5	58857	3	US-09-477-962-1	Sequence 1, Appli
	237	36.8	3.5	77626	3	US-09-949-016-12608	Sequence 12608, A
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	239	36.6	3.5	903	3	US-09-902-540-4251	Sequence 4251, Ap
c	240	36.6	3.5	909	3	US-09-252-991A-5329	Sequence 5329, Ap
	241	36.6	3.5	1164	3	US-09-252-991A-5240	Sequence 5240, Ap
	242	36.6	3.5	1974	3	US-09-902-540-8140	Sequence 8140, Ap
	243	36.6	3.5	2060	3	US-09-949-016-1169	Sequence 1169, Ap

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246	36.6	3.5	8450	3	US-09-902-540-834	Sequence 834, App
c 247	36.6	3.5	9871	3	US-09-949-016-15470	Sequence 15470, A
248	36.6	3.5	24791	3	US-09-902-540-1211	Sequence 1211, Ap
249	36.6	3.5	134008	3	US-09-949-016-13841	Sequence 13841, A
c 250	36.4	3.5	1309	3	US-08-362-495-4	Sequence 4, Appli
c 251	36.4	3.5	1309	3	US-09-408-508-4	Sequence 4, Appli
c 252	36.4	3.5	1437	3	US-09-902-540-2910	Sequence 2910, Ap
c 253	36.4	3.5	1719	3	US-10-164-595-13	Sequence 13, Appl
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255	36.4	3.5	4168	3	US-09-266-225D-17	Sequence 17, Appl
256	36.4	3.5	4279	3	US-09-041-886-22	Sequence 22, Appl
257	36.4	3.5	4600	3	US-09-702-705-1797	Sequence 1797, Ap
258	36.4	3.5	4600	3	US-09-736-457-1797	Sequence 1797, Ap
259	36.4	3.5	4600	3	US-09-671-325-1797	Sequence 1797, Ap
260	36.4	3.5	4600	3	US-10-017-754-1797	Sequence 1797, Ap
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c 262	36.2	3.5	903	3	US-09-758-759-142	Sequence 142, App
263	36.2	3.5	1083	3	US-09-902-540-6544	Sequence 6544, Ap
264	36.2	3.5	1278	3	US-09-902-540-6294	Sequence 6294, Ap
c 265	36.2	3.5	1281	3	US-09-902-540-377	Sequence 377, App
266	36.2	3.5	1533	3	US-09-807-201-14	Sequence 14, Appl
267	36.2	3.5	1566	3	US-09-902-540-7706	Sequence 7706, Ap
268	36.2	3.5	3215	3	US-09-902-540-481	Sequence 481, App
269	36.2	3.5	4257	2	US-08-690-473-1	Sequence 1, Appli
270	36.2	3.5	4257	3	US-09-259-821A-1	Sequence 1, Appli
271	36.2	3.5	4257	3	US-08-843-659-1	Sequence 1, Appli
272	36.2	3.5	4257	3	US-09-825-288A-1	Sequence 1, Appli
273	36.2	3.5	6611	3	US-09-902-540-762	Sequence 762, App
c 274	36.2	3.5	12001	2	US-08-458-568A-11	Sequence 11, Appl
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276	36.2	3.5	16007	3	US-09-949-016-17496	Sequence 17496, A
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c 278	36.2	3.5	109519	3	US-09-758-759-1	Sequence 1, Appli
c 279	36	3.4	927	3	US-09-902-540-9087	Sequence 9087, Ap
280	36	3.4	993	3	US-09-724-797-27	Sequence 27, Appl
281	36	3.4	999	3	US-09-724-797-17	Sequence 17, Appl
282	36	3.4	1926	3	US-09-249-585A-4	Sequence 4, Appli
283	36	3.4	1931	2	US-09-130-114-2	Sequence 2, Appli
284	36	3.4	2097	3	US-09-252-991A-885	Sequence 885, App
285	36	3.4	2487	3	US-09-902-540-3591	Sequence 3591, Ap
286	36	3.4	4563	3	US-10-012-231A-259	Sequence 259, App
287	36	3.4	4563	3	US-10-015-389A-259	Sequence 259, App
288	36	3.4	4563	3	US-10-006-768A-259	Sequence 259, App
289	36	3.4	4563	3	US-10-015-671A-259	Sequence 259, App
290	36	3.4	4563	3	US-10-015-393A-259	Sequence 259, App
291	36	3.4	4563	3	US-10-011-833A-259	Sequence 259, App
292	36	3.4	4563	3	US-10-006-041A-259	Sequence 259, App
293	36	3.4	4563	3	US-10-012-064A-259	Sequence 259, App
c 294	36	3.4	4829	3	US-09-902-540-592	Sequence 592, App
295	36	3.4	11963	3	US-09-902-540-1072	Sequence 1072, Ap
296	36	3.4	20113	3	US-09-902-540-1173	Sequence 1173, Ap
c 297	36	3.4	40586	3	US-09-949-016-16965	Sequence 16965, A
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299	35.8	3.4	429	3	US-09-902-540-8669	Sequence 8669, Ap
300	35.8	3.4	430	3	US-09-621-976-16656	Sequence 16656, A
301	35.8	3.4	1074	3	US-09-758-759-170	Sequence 170, App
302	35.8	3.4	1188	3	US-09-252-991A-14807	Sequence 14807, A
303	35.8	3.4	1200	2	US-08-040-548-32	Sequence 32, Appl
304	35.8	3.4	1200	2	US-08-466-344-32	Sequence 32, Appl
305	35.8	3.4	1200	3	US-09-701-749A-1	Sequence 1, Appli
306	35.8	3.4	1200	9	5206152-8	Patent No. 5206152
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c 308	35.8	3.4	1935	3	US-09-252-991A-8513	Sequence 8513, Ap
309	35.8	3.4	1944	3	US-09-252-991A-8364	Sequence 8364, Ap
310	35.8	3.4	2073	3	US-09-252-991A-8332	Sequence 8332, Ap
311	35.8	3.4	2445	3	US-09-252-991A-14949	Sequence 14949, A
312	35.8	3.4	3068	2	US-08-224-482-1	Sequence 1, Appli
313	35.8	3.4	3086	2	US-08-040-548-15	Sequence 15, Appl
314	35.8	3.4	3086	2	US-08-466-344-15	Sequence 15, Appl
315	35.8	3.4	3086	9	5206152-1	Patent No. 5206152
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317	35.8	3.4	7811	3	US-09-902-540-824	Sequence 824, App
318	35.8	3.4	9191	3	US-09-902-540-918	Sequence 918, App
319	35.8	3.4	9992	3	US-09-902-540-952	Sequence 952, App
c 320	35.8	3.4	109690	3	US-09-949-016-13525	Sequence 13525, A
c 321	35.8	3.4	670689	3	US-09-949-016-12505	Sequence 12505, A
c 322	35.8	3.4	670690	3	US-09-949-016-14207	Sequence 14207, A
323	35.6	3.4	559	3	US-09-747-259-9	Sequence 9, Appli
324	35.6	3.4	717	3	US-09-252-991A-3190	Sequence 3190, Ap
325	35.6	3.4	813	2	US-08-514-014-11	Sequence 11, Appl
326	35.6	3.4	813	2	US-08-833-823-11	Sequence 11, Appl
327	35.6	3.4	813	3	US-09-034-810-1	Sequence 1, Appli
328	35.6	3.4	813	3	US-08-685-239-1	Sequence 1, Appli
329	35.6	3.4	813	3	US-10-102-080-1	Sequence 1, Appli
330	35.6	3.4	840	3	US-09-902-540-3440	Sequence 3440, Ap
331	35.6	3.4	2150	3	US-09-263-023-1	Sequence 1, Appli
332	35.6	3.4	2150	3	US-09-471-867-1	Sequence 1, Appli
333	35.6	3.4	2511	3	US-09-919-497-36	Sequence 36, Appl
334	35.6	3.4	2799	3	US-09-495-050A-291	Sequence 291, App
c 335	35.6	3.4	7258	3	US-09-949-016-4832	Sequence 4832, Ap
c 336	35.6	3.4	8519	3	US-09-261-907-1	Sequence 1, Appli
337	35.6	3.4	19726	3	US-09-902-540-1164	Sequence 1164, Ap
c 338	35.6	3.4	24986	3	US-09-902-540-1200	Sequence 1200, Ap
339	35.4	3.4	600	3	US-09-252-991A-10860	Sequence 10860, A
340	35.4	3.4	618	3	US-09-252-991A-8449	Sequence 8449, Ap
c 341	35.4	3.4	951	3	US-09-252-991A-14310	Sequence 14310, A
c 342	35.4	3.4	1245	3	US-09-758-759-22	Sequence 22, Appl
c 343	35.4	3.4	1248	3	US-09-252-991A-8391	Sequence 8391, Ap
344	35.4	3.4	1446	3	US-09-902-540-5188	Sequence 5188, Ap
345	35.4	3.4	1503	3	US-09-252-991A-8482	Sequence 8482, Ap
346	35.4	3.4	1590	3	US-09-252-991A-14397	Sequence 14397, A
347	35.4	3.4	1743	3	US-09-949-016-945	Sequence 945, App
348	35.4	3.4	1743	3	US-09-949-016-2709	Sequence 2709, Ap
c 349	35.4	3.4	2721	9	5215881-2	Patent No. 5215881
350	35.4	3.4	2973	3	US-09-902-540-9566	Sequence 9566, Ap
351	35.4	3.4	3624	3	US-09-252-991A-10899	Sequence 10899, A
c 352	35.4	3.4	3801	3	US-09-252-991A-14280	Sequence 14280, A
353	35.4	3.4	5743	3	US-09-949-016-12687	Sequence 12687, A
354	35.4	3.4	5743	3	US-09-949-016-14451	Sequence 14451, A
c 355	35.4	3.4	9867	3	US-09-902-540-1008	Sequence 1008, Ap
c 356	35.4	3.4	23109	3	US-09-949-002-648	Sequence 648, App
c 357	35.4	3.4	23116	3	US-09-949-002-791	Sequence 791, App
c 358	35.4	3.4	34199	3	US-09-902-540-1255	Sequence 1255, Ap
359	35.4	3.4	194889	3	US-09-949-016-15654	Sequence 15654, A
c 360	35.4	3.4	767677	3	US-09-949-016-12147	Sequence 12147, A
c 361	35.4	3.4	767677	3	US-09-949-016-17361	Sequence 17361, A
c 362	35.2	3.4	639	3	US-09-252-991A-10430	Sequence 10430, A
c 363	35.2	3.4	744	3	US-09-252-991A-10328	Sequence 10328, A
364	35.2	3.4	792	3	US-09-252-991A-7724	Sequence 7724, Ap
365	35.2	3.4	870	3	US-09-252-991A-10645	Sequence 10645, A
366	35.2	3.4	957	3	US-09-902-540-4213	Sequence 4213, Ap
367	35.2	3.4	1110	3	US-09-902-540-4933	Sequence 4933, Ap
c 368	35.2	3.4	1227	3	US-09-252-991A-10523	Sequence 10523, A
369	35.2	3.4	1404	3	US-09-252-991A-10317	Sequence 10317, A
c 370	35.2	3.4	1404	3	US-09-252-991A-10743	Sequence 10743, A
371	35.2	3.4	1410	3	US-09-252-991A-10420	Sequence 10420, A
372	35.2	3.4	1431	3	US-09-489-039A-3032	Sequence 3032, Ap
373	35.2	3.4	1512	3	US-09-902-540-3874	Sequence 3874, Ap
c 374	35.2	3.4	1866	3	US-08-909-742-1	Sequence 1, Appli
c 375	35.2	3.4	1866	3	US-09-412-289-1	Sequence 1, Appli
376	35.2	3.4	2612	3	US-10-104-047-1320	Sequence 1320, Ap
377	35.2	3.4	2807	3	US-09-302-769-11	Sequence 11, Appl
378	35.2	3.4	2807	3	US-08-962-560C-11	Sequence 11, Appl
379	35.2	3.4	4406	3	US-10-104-047-979	Sequence 979, App
380	35.2	3.4	4615	3	US-09-949-016-15282	Sequence 15282, A
c 381	35.2	3.4	7142	3	US-09-949-016-11997	Sequence 11997, A
c 382	35.2	3.4	7143	3	US-09-949-016-16913	Sequence 16913, A
383	35.2	3.4	21143	3	US-09-902-540-1191	Sequence 1191, Ap
c 384	35.2	3.4	21330	3	US-09-902-540-1209	Sequence 1209, Ap
385	35.2	3.4	30780	3	US-09-902-540-1243	Sequence 1243, Ap
c 386	35.2	3.4	103987	3	US-09-949-016-12513	Sequence 12513, A
c 387	35.2	3.4	103988	3	US-09-949-016-17050	Sequence 17050, A
c 388	35	3.3	411	3	US-09-252-991A-16270	Sequence 16270, A
389	35	3.3	645	3	US-09-252-991A-16112	Sequence 16112, A

390	35	3.3	669	3	US-09-461-688-3	Sequence 3, Appli
c 391	35	3.3	700	3	US-09-236-097-7	Sequence 7, Appli
c 392	35	3.3	785	3	US-10-017-754-1868	Sequence 1868, Ap
393	35	3.3	1242	3	US-09-266-965-72	Sequence 72, Appl
c 394	35	3.3	1518	3	US-09-252-991A-7354	Sequence 7354, Ap
c 395	35	3.3	1521	3	US-09-252-991A-7437	Sequence 7437, Ap
396	35	3.3	1719	3	US-09-252-991A-7265	Sequence 7265, Ap
397	35	3.3	2075	2	US-08-167-628-1	Sequence 1, Appli
398	35	3.3	2075	2	US-08-386-680-1	Sequence 1, Appli
399	35	3.3	2075	2	US-08-459-717-1	Sequence 1, Appli
400	35	3.3	2075	2	US-08-712-302-1	Sequence 1, Appli
401	35	3.3	2075	2	US-08-880-031-1	Sequence 1, Appli
402	35	3.3	2075	3	US-09-097-179-1	Sequence 1, Appli
403	35	3.3	2075	3	US-09-080-715-1	Sequence 1, Appli
404	35	3.3	2075	3	US-09-142-569-7	Sequence 7, Appli
405	35	3.3	2075	3	US-09-461-688-1	Sequence 1, Appli
406	35	3.3	2075	3	US-09-023-655-1044	Sequence 1044, Ap
407	35	3.3	2075	3	US-09-495-448A-7	Sequence 7, Appli
408	35	3.3	2075	6	PCT-US96-08140-1	Sequence 1, Appli
409	35	3.3	2133	3	US-09-252-991A-16218	Sequence 16218, A
410	35	3.3	2312	3	US-09-949-016-270	Sequence 270, App
c 411	35	3.3	2358	3	US-09-252-991A-16381	Sequence 16381, A
412	35	3.3	2397	3	US-09-252-991A-7203	Sequence 7203, Ap
413	35	3.3	2585	3	US-09-902-540-424	Sequence 424, App
414	35	3.3	2998	3	US-09-054-368-1	Sequence 1, Appli
415	35	3.3	2998	3	US-09-054-274-1	Sequence 1, Appli
416	35	3.3	2998	3	US-09-056-704-1	Sequence 1, Appli
c 417	35	3.3	3235	3	US-09-949-016-1392	Sequence 1392, Ap
c 418	35	3.3	3372	3	US-09-949-016-165	Sequence 165, App
c 419	35	3.3	4176	3	US-09-990-613A-32	Sequence 32, Appl
420	35	3.3	4659	3	US-08-264-578-10	Sequence 10, Appl
421	35	3.3	4659	3	US-08-217-704C-9	Sequence 9, Appli
422	35	3.3	4659	3	US-08-164-487A-1	Sequence 1, Appli
423	35	3.3	6698	3	US-09-902-540-852	Sequence 852, App
424	35	3.3	7280	3	US-09-902-540-827	Sequence 827, App
425	35	3.3	20235	2	US-07-642-734C-3	Sequence 3, Appli
426	35	3.3	20235	3	US-08-439-009A-3	Sequence 3, Appli
c 427	35	3.3	22773	3	US-09-990-613A-6	Sequence 6, Appli
c 428	35	3.3	43117	3	US-09-949-016-17589	Sequence 17589, A
429	35	3.3	53500	3	US-09-266-965-76	Sequence 76, Appl
c 430	35	3.3	87205	3	US-09-949-016-13430	Sequence 13430, A
431	34.8	3.3	270	3	US-09-902-540-9415	Sequence 9415, Ap
c 432	34.8	3.3	272	3	US-09-902-540-1742	Sequence 1742, Ap
433	34.8	3.3	279	3	US-09-252-991A-11763	Sequence 11763, A
434	34.8	3.3	369	3	US-09-621-976-9326	Sequence 9326, Ap
c 435	34.8	3.3	706	3	US-09-280-116-173	Sequence 173, App
436	34.8	3.3	747	3	US-09-902-540-9574	Sequence 9574, Ap
437	34.8	3.3	1560	3	US-09-902-540-5165	Sequence 5165, Ap
c 438	34.8	3.3	1611	3	US-10-104-047-1094	Sequence 1094, Ap
439	34.8	3.3	1654	2	US-07-914-281-13	Sequence 13, Appl
440	34.8	3.3	1654	2	US-08-393-246-13	Sequence 13, Appl
441	34.8	3.3	1654	2	US-08-525-058A-13	Sequence 13, Appl
442	34.8	3.3	1654	2	US-08-696-731-13	Sequence 13, Appl
443	34.8	3.3	1654	3	US-09-042-531-13	Sequence 13, Appl
444	34.8	3.3	2100	3	US-09-902-540-4182	Sequence 4182, Ap
c 445	34.8	3.3	2714	3	US-09-949-016-5551	Sequence 5551, Ap
c 446	34.8	3.3	3390	3	US-09-902-540-6647	Sequence 6647, Ap
447	34.8	3.3	3393	3	US-09-902-540-514	Sequence 514, App
c 448	34.8	3.3	3470	3	US-09-486-147-2	Sequence 2, Appli
c 449	34.8	3.3	3511	3	US-09-949-016-37	Sequence 37, Appl
450	34.8	3.3	3531	3	US-09-991-181-32	Sequence 32, Appl
451	34.8	3.3	3531	3	US-09-990-444-32	Sequence 32, Appl
452	34.8	3.3	3531	3	US-09-997-333-32	Sequence 32, Appl
453	34.8	3.3	3531	3	US-09-992-598-32	Sequence 32, Appl
454	34.8	3.3	7898	3	US-08-984-709A-49	Sequence 49, Appl
455	34.8	3.3	14823	3	US-09-902-540-1087	Sequence 1087, Ap
456	34.8	3.3	16427	3	US-09-902-540-1160	Sequence 1160, Ap
c 457	34.8	3.3	16891	3	US-09-486-147-1	Sequence 1, Appli
c 458	34.8	3.3	17743	3	US-09-949-016-17293	Sequence 17293, A
c 459	34.8	3.3	18595	3	US-09-949-016-11779	Sequence 11779, A
460	34.8	3.3	22301	3	US-09-902-540-1208	Sequence 1208, Ap
461	34.8	3.3	29433	3	US-09-949-016-15740	Sequence 15740, A
c 462	34.8	3.3	29559	3	US-09-902-540-1254	Sequence 1254, Ap
c 463	34.8	3.3	29614	3	US-09-949-016-12390	Sequence 12390, A
464	34.8	3.3	32655	3	US-09-949-016-13947	Sequence 13947, A
c 465	34.8	3.3	48996	3	US-09-949-016-12744	Sequence 12744, A
c 466	34.8	3.3	48997	3	US-09-949-016-17373	Sequence 17373, A
467	34.6	3.3	364	3	US-09-621-976-17202	Sequence 17202, A
468	34.6	3.3	415	3	US-09-674-741-15	Sequence 15, Appl
469	34.6	3.3	415	3	US-10-379-010-15	Sequence 15, Appl
470	34.6	3.3	564	3	US-09-252-991A-1538	Sequence 1538, Ap
c 471	34.6	3.3	699	3	US-09-902-540-8069	Sequence 8069, Ap
472	34.6	3.3	729	3	US-09-902-540-3133	Sequence 3133, Ap
c 473	34.6	3.3	864	3	US-09-252-991A-2337	Sequence 2337, Ap
474	34.6	3.3	891	3	US-09-902-540-8312	Sequence 8312, Ap
c 475	34.6	3.3	960	3	US-09-252-991A-1579	Sequence 1579, Ap
476	34.6	3.3	1305	3	US-09-252-991A-1440	Sequence 1440, Ap
477	34.6	3.3	1341	3	US-09-252-991A-10539	Sequence 10539, A
478	34.6	3.3	1887	3	US-09-902-540-7442	Sequence 7442, Ap
479	34.6	3.3	2088	3	US-09-252-991A-2576	Sequence 2576, Ap
480	34.6	3.3	2153	3	US-10-117-604A-12	Sequence 12, Appl
c 481	34.6	3.3	2829	3	US-09-252-991A-14110	Sequence 14110, A
482	34.6	3.3	2854	3	US-08-971-089-3	Sequence 3, Appli
483	34.6	3.3	2854	3	US-10-117-604A-3	Sequence 3, Appli
484	34.6	3.3	4287	3	US-09-252-991A-14160	Sequence 14160, A
485	34.6	3.3	4891	3	US-10-144-198-9	Sequence 9, Appli
486	34.6	3.3	5859	3	US-09-902-540-823	Sequence 823, App
c 487	34.6	3.3	6330	3	US-09-902-540-718	Sequence 718, App
488	34.6	3.3	8048	3	US-09-902-540-867	Sequence 867, App
489	34.6	3.3	8147	3	US-09-514-247A-9	Sequence 9, Appli
490	34.6	3.3	19598	3	US-09-902-540-1143	Sequence 1143, Ap
491	34.6	3.3	33152	3	US-09-949-016-16719	Sequence 16719, A
492	34.6	3.3	38653	3	US-09-949-016-15987	Sequence 15987, A
c 493	34.6	3.3	141115	3	US-09-949-016-17490	Sequence 17490, A
c 494	34.4	3.3	314	3	US-09-513-999C-12560	Sequence 12560, A
c 495	34.4	3.3	364	3	US-09-621-976-17202	Sequence 17202, A
496	34.4	3.3	684	3	US-09-252-991A-406	Sequence 406, App
c 497	34.4	3.3	784	3	US-10-017-754-1866	Sequence 1866, Ap
c 498	34.4	3.3	789	3	US-10-017-754-1867	Sequence 1867, Ap
c 499	34.4	3.3	790	3	US-10-017-754-1865	Sequence 1865, Ap
c 500	34.4	3.3	1047	3	US-09-747-259-3	Sequence 3, Appli
c 501	34.4	3.3	1047	3	US-09-949-016-5387	Sequence 5387, Ap
c 502	34.4	3.3	1107	3	US-09-480-297A-22	Sequence 22, Appl
503	34.4	3.3	1203	3	US-09-902-540-3733	Sequence 3733, Ap
c 504	34.4	3.3	1635	3	US-09-234-332-4	Sequence 4, Appli
c 505	34.4	3.3	1635	3	US-09-702-705-1798	Sequence 1798, Ap
c 506	34.4	3.3	1635	3	US-09-736-457-1798	Sequence 1798, Ap
c 507	34.4	3.3	1635	3	US-09-671-325-1798	Sequence 1798, Ap
c 508	34.4	3.3	1635	3	US-10-017-754-1798	Sequence 1798, Ap
509	34.4	3.3	1806	3	US-09-902-540-7677	Sequence 7677, Ap
510	34.4	3.3	2232	3	US-09-252-991A-11756	Sequence 11756, A
c 511	34.4	3.3	2274	3	US-09-252-991A-11609	Sequence 11609, A
512	34.4	3.3	2499	3	US-09-252-991A-2681	Sequence 2681, Ap
513	34.4	3.3	2544	3	US-09-252-991A-2775	Sequence 2775, Ap
514	34.4	3.3	2568	3	US-09-799-451-282	Sequence 282, App
515	34.4	3.3	2613	3	US-09-252-991A-11836	Sequence 11836, A
c 516	34.4	3.3	2691	3	US-09-252-991A-3187	Sequence 3187, Ap
517	34.4	3.3	2889	2	US-08-537-002A-4	Sequence 4, Appli
518	34.4	3.3	2889	3	US-08-863-010-4	Sequence 4, Appli
519	34.4	3.3	2889	3	US-09-024-429-4	Sequence 4, Appli
520	34.4	3.3	3597	3	US-09-902-540-5402	Sequence 5402, Ap
521	34.4	3.3	3600	2	US-08-537-002A-5	Sequence 5, Appli
522	34.4	3.3	3600	3	US-08-863-010-5	Sequence 5, Appli
523	34.4	3.3	3600	3	US-09-024-429-5	Sequence 5, Appli
c 524	34.4	3.3	5884	3	US-09-949-016-17129	Sequence 17129, A
c 525	34.4	3.3	6351	3	US-09-902-540-757	Sequence 757, App
c 526	34.4	3.3	8798	3	US-09-949-016-14609	Sequence 14609, A
c 527	34.4	3.3	10096	3	US-09-902-540-935	Sequence 935, App
528	34.4	3.3	10903	3	US-09-949-016-15530	Sequence 15530, A
c 529	34.4	3.3	19112	3	US-09-902-540-1181	Sequence 1181, Ap
c 530	34.4	3.3	20235	2	US-07-642-734C-3	Sequence 3, Appli
c 531	34.4	3.3	20235	3	US-08-439-009A-3	Sequence 3, Appli
c 532	34.4	3.3	28558	3	US-09-902-540-1231	Sequence 1231, Ap
c 533	34.4	3.3	34552	3	US-09-902-540-1262	Sequence 1262, Ap
534	34.4	3.3	36223	3	US-09-949-016-14417	Sequence 14417, A
c 535	34.4	3.3	84425	3	US-09-949-016-17402	Sequence 17402, A

c 536	34.2	3.3	243	3	US-09-894-844-94	Sequence 94, Appl
c 537	34.2	3.3	426	3	US-09-252-991A-5785	Sequence 5785, Ap
c 538	34.2	3.3	507	3	US-09-902-540-3722	Sequence 3722, Ap
539	34.2	3.3	543	3	US-09-480-297A-1	Sequence 1, Appli
c 540	34.2	3.3	543	3	US-09-724-797-29	Sequence 29, Appl
541	34.2	3.3	546	3	US-09-902-540-8130	Sequence 8130, Ap
c 542	34.2	3.3	601	3	US-09-949-016-34637	Sequence 34637, A
c 543	34.2	3.3	601	3	US-09-949-016-90191	Sequence 90191, A
c 544	34.2	3.3	601	3	US-09-949-016-122743	Sequence 122743,
545	34.2	3.3	687	3	US-09-747-259-1	Sequence 1, Appli
546	34.2	3.3	687	3	US-09-999-833A-469	Sequence 469, App
547	34.2	3.3	687	3	US-10-020-445A-469	Sequence 469, App
548	34.2	3.3	688	3	US-09-949-016-4320	Sequence 4320, Ap
549	34.2	3.3	705	3	US-09-231-788-1	Sequence 1, Appli
550	34.2	3.3	705	3	US-09-796-844-34	Sequence 34, Appl
551	34.2	3.3	736	3	US-09-620-956-1	Sequence 1, Appli
552	34.2	3.3	736	3	US-09-611-152-1	Sequence 1, Appli
553	34.2	3.3	736	3	US-09-794-705A-1	Sequence 1, Appli
554	34.2	3.3	736	3	US-09-631-531-1	Sequence 1, Appli
c 555	34.2	3.3	746	3	US-09-775-398-81	Sequence 81, Appl
556	34.2	3.3	927	3	US-10-029-180-97	Sequence 97, Appl
557	34.2	3.3	981	3	US-09-902-540-4810	Sequence 4810, Ap
558	34.2	3.3	1224	3	US-09-252-991A-9489	Sequence 9489, Ap
559	34.2	3.3	1476	3	US-09-252-991A-5823	Sequence 5823, Ap
560	34.2	3.3	1524	2	US-08-716-942-24	Sequence 24, Appl
561	34.2	3.3	1524	3	US-09-130-337A-24	Sequence 24, Appl
c 562	34.2	3.3	1578	3	US-09-902-540-3677	Sequence 3677, Ap
563	34.2	3.3	1599	3	US-09-252-991A-5850	Sequence 5850, Ap
c 564	34.2	3.3	1863	3	US-09-252-991A-5819	Sequence 5819, Ap
565	34.2	3.3	1932	3	US-09-640-198D-1	Sequence 1, Appli
566	34.2	3.3	1998	3	US-09-938-901A-3	Sequence 3, Appli
567	34.2	3.3	2005	2	US-07-916-901-5	Sequence 5, Appli
568	34.2	3.3	2078	3	US-09-949-016-2102	Sequence 2102, Ap
569	34.2	3.3	2112	3	US-09-252-991A-9429	Sequence 9429, Ap
c 570	34.2	3.3	2454	3	US-09-252-991A-9316	Sequence 9316, Ap
571	34.2	3.3	2490	3	US-09-949-016-4217	Sequence 4217, Ap
572	34.2	3.3	2865	2	US-08-749-169A-2	Sequence 2, Appli
573	34.2	3.3	2865	2	US-09-130-032A-2	Sequence 2, Appli
574	34.2	3.3	3037	2	US-08-938-365-1	Sequence 1, Appli
575	34.2	3.3	3441	3	US-09-866-028-6	Sequence 6, Appli
576	34.2	3.3	3441	3	US-09-944-457-6	Sequence 6, Appli
577	34.2	3.3	3441	3	US-09-945-584-6	Sequence 6, Appli
578	34.2	3.3	3441	3	US-09-944-944-6	Sequence 6, Appli
579	34.2	3.3	3441	3	US-09-945-587-6	Sequence 6, Appli
580	34.2	3.3	4214	3	US-09-122-135-1	Sequence 1, Appli
581	34.2	3.3	4308	3	US-09-999-833A-527	Sequence 527, App
582	34.2	3.3	4308	3	US-10-020-445A-527	Sequence 527, App
583	34.2	3.3	4425	2	US-08-749-169A-1	Sequence 1, Appli
584	34.2	3.3	4425	2	US-09-130-032A-1	Sequence 1, Appli
c 585	34.2	3.3	5418	3	US-09-949-016-14328	Sequence 14328, A
586	34.2	3.3	5784	3	US-10-152-886-64	Sequence 64, Appl
c 587	34.2	3.3	7011	2	US-08-306-691B-42	Sequence 42, Appl
c 588	34.2	3.3	8352	3	US-09-902-540-832	Sequence 832, App
589	34.2	3.3	15840	3	US-09-902-540-1134	Sequence 1134, Ap
c 590	34.2	3.3	16924	3	US-09-902-540-1178	Sequence 1178, Ap
591	34.2	3.3	18197	3	US-09-949-016-12597	Sequence 12597, A
592	34.2	3.3	18197	3	US-09-949-016-15205	Sequence 15205, A
c 593	34.2	3.3	29103	3	US-09-902-540-1236	Sequence 1236, Ap
594	34.2	3.3	46902	3	US-09-949-016-13844	Sequence 13844, A
595	34.2	3.3	56832	3	US-09-949-016-12976	Sequence 12976, A
596	34.2	3.3	81433	3	US-09-949-016-11941	Sequence 11941, A
597	34.2	3.3	84227	3	US-09-949-016-17374	Sequence 17374, A
c 598	34.2	3.3	132871	3	US-09-949-016-13863	Sequence 13863, A
c 599	34	3.2	289	3	US-09-007-005-17	Sequence 17, Appl
c 600	34	3.2	289	3	US-09-244-796-17	Sequence 17, Appl
c 601	34	3.2	465	3	US-09-252-991A-9344	Sequence 9344, Ap
602	34	3.2	601	3	US-09-949-016-30791	Sequence 30791, A
603	34	3.2	601	3	US-09-949-016-187001	Sequence 187001,
604	34	3.2	789	3	US-09-902-540-7266	Sequence 7266, Ap
605	34	3.2	807	3	US-09-270-767-11520	Sequence 11520, A
c 606	34	3.2	807	3	US-09-902-540-6012	Sequence 6012, Ap
607	34	3.2	809	3	US-09-902-540-23	Sequence 23, Appl
608	34	3.2	891	3	US-09-489-039A-360	Sequence 360, App
609	34	3.2	945	3	US-09-902-540-7231	Sequence 7231, Ap
610	34	3.2	1164	2	US-08-087-772A-3	Sequence 3, Appli
611	34	3.2	1200	3	US-09-252-991A-5426	Sequence 5426, Ap
c 612	34	3.2	1287	3	US-09-489-039A-394	Sequence 394, App
613	34	3.2	1360	2	US-08-087-772A-4	Sequence 4, Appli
614	34	3.2	1416	3	US-09-902-540-7221	Sequence 7221, Ap
615	34	3.2	1470	3	US-09-252-991A-9286	Sequence 9286, Ap
616	34	3.2	1581	3	US-09-758-759-122	Sequence 122, App
617	34	3.2	1746	3	US-09-758-759-92	Sequence 92, Appl
618	34	3.2	1920	2	US-08-087-772A-1	Sequence 1, Appli
c 619	34	3.2	1977	3	US-09-252-991A-9290	Sequence 9290, Ap
620	34	3.2	1995	3	US-09-252-991A-9265	Sequence 9265, Ap
621	34	3.2	2151	3	US-10-104-047-1105	Sequence 1105, Ap
c 622	34	3.2	2253	3	US-09-902-540-8302	Sequence 8302, Ap
c 623	34	3.2	2565	3	US-09-949-016-4203	Sequence 4203, Ap
624	34	3.2	2943	2	US-08-042-747A-7	Sequence 7, Appli
625	34	3.2	3390	3	US-09-902-540-6647	Sequence 6647, Ap
c 626	34	3.2	3393	3	US-09-902-540-514	Sequence 514, App
627	34	3.2	3437	3	US-08-450-962-3	Sequence 3, Appli
628	34	3.2	3437	3	US-08-848-631-3	Sequence 3, Appli
629	34	3.2	3437	3	US-09-895-211-3	Sequence 3, Appli
630	34	3.2	4324	3	US-09-902-540-684	Sequence 684, App
631	34	3.2	4486	3	US-09-902-540-677	Sequence 677, App
632	34	3.2	4632	3	US-09-902-540-8368	Sequence 8368, Ap
c 633	34	3.2	5418	3	US-09-902-540-675	Sequence 675, App
c 634	34	3.2	6339	3	US-09-902-540-866	Sequence 866, App
c 635	34	3.2	8460	2	US-08-469-005A-9	Sequence 9, Appli
636	34	3.2	10183	3	US-09-949-016-13111	Sequence 13111, A
c 637	34	3.2	10318	3	US-09-949-002-631	Sequence 631, App
c 638	34	3.2	10319	3	US-09-949-002-701	Sequence 701, App
639	34	3.2	12462	3	US-09-949-016-15730	Sequence 15730, A
640	34	3.2	15482	3	US-09-902-540-1067	Sequence 1067, Ap
641	34	3.2	19857	3	US-09-949-016-13114	Sequence 13114, A
642	34	3.2	19998	3	US-09-949-016-12657	Sequence 12657, A
643	34	3.2	22459	3	US-09-973-278-883	Sequence 883, App
c 644	34	3.2	23901	3	US-09-949-016-16773	Sequence 16773, A
c 645	34	3.2	25497	3	US-09-902-540-1224	Sequence 1224, Ap
646	34	3.2	27908	3	US-09-949-016-12397	Sequence 12397, A
647	34	3.2	27909	3	US-09-949-016-17082	Sequence 17082, A
c 648	34	3.2	30773	3	US-09-949-016-12332	Sequence 12332, A
c 649	34	3.2	30773	3	US-09-949-016-17206	Sequence 17206, A
650	34	3.2	30922	3	US-09-949-016-16700	Sequence 16700, A
c 651	34	3.2	31623	3	US-09-949-016-15945	Sequence 15945, A
c 652	34	3.2	31713	3	US-09-949-016-16960	Sequence 16960, A
c 653	34	3.2	44120	3	US-09-949-016-14151	Sequence 14151, A
c 654	34	3.2	44120	3	US-09-949-016-14152	Sequence 14152, A
c 655	34	3.2	44120	3	US-09-949-016-14153	Sequence 14153, A
c 656	34	3.2	44120	3	US-09-949-016-14154	Sequence 14154, A
c 657	34	3.2	44120	3	US-09-949-016-14155	Sequence 14155, A
c 658	34	3.2	44120	3	US-09-949-016-14156	Sequence 14156, A
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c 660	33.8	3.2	601	3	US-09-949-016-34638	Sequence 34638, A
c 661	33.8	3.2	601	3	US-09-949-016-38975	Sequence 38975, A
c 662	33.8	3.2	601	3	US-09-949-016-78094	Sequence 78094, A
c 663	33.8	3.2	601	3	US-09-949-016-122744	Sequence 122744,
c 664	33.8	3.2	675	3	US-09-252-991A-7176	Sequence 7176, Ap
c 665	33.8	3.2	792	3	US-09-252-991A-335	Sequence 335, App
c 666	33.8	3.2	798	3	US-09-902-540-6875	Sequence 6875, Ap
667	33.8	3.2	825	3	US-10-321-188-41	Sequence 41, Appl
668	33.8	3.2	915	3	US-09-252-991A-323	Sequence 323, App
c 669	33.8	3.2	933	3	US-09-252-991A-343	Sequence 343, App
670	33.8	3.2	1008	3	US-09-252-991A-311	Sequence 311, App
671	33.8	3.2	1083	3	US-09-252-991A-7327	Sequence 7327, Ap
672	33.8	3.2	1083	3	US-09-902-540-5440	Sequence 5440, Ap
c 673	33.8	3.2	1086	3	US-09-949-016-3715	Sequence 3715, Ap
c 674	33.8	3.2	1095	3	US-09-902-540-7050	Sequence 7050, Ap
675	33.8	3.2	1152	3	US-09-252-991A-5237	Sequence 5237, Ap
676	33.8	3.2	1209	3	US-09-902-540-147	Sequence 147, App
677	33.8	3.2	1254	3	US-09-252-991A-7470	Sequence 7470, Ap
678	33.8	3.2	1458	3	US-09-902-540-3540	Sequence 3540, Ap
679	33.8	3.2	1545	3	US-09-902-540-3077	Sequence 3077, Ap
680	33.8	3.2	1675	3	US-09-679-686B-1	Sequence 1, Appli
c 681	33.8	3.2	1956	3	US-09-724-797-57	Sequence 57, Appl

c 682	33.8	3.2	1956	3	US-10-152-886-20	Sequence 20, Appl
683	33.8	3.2	2046	3	US-09-252-991A-5266	Sequence 5266, Ap
684	33.8	3.2	2165	3	US-09-799-451-926	Sequence 926, App
c 685	33.8	3.2	2449	3	US-09-949-016-1248	Sequence 1248, Ap
c 686	33.8	3.2	2553	3	US-09-902-540-2867	Sequence 2867, Ap
687	33.8	3.2	3748	3	US-09-799-451-115	Sequence 115, App
688	33.8	3.2	4019	3	US-09-902-540-583	Sequence 583, App
c 689	33.8	3.2	4772	3	US-09-484-970B-133	Sequence 133, App
c 690	33.8	3.2	4835	3	US-09-902-540-627	Sequence 627, App
c 691	33.8	3.2	5703	3	US-09-280-590A-36	Sequence 36, Appl
c 692	33.8	3.2	5703	3	US-09-892-398-36	Sequence 36, Appl
693	33.8	3.2	5811	3	US-10-152-886-2	Sequence 2, Appli
c 694	33.8	3.2	5993	3	US-09-383-630-1	Sequence 1, Appli
c 695	33.8	3.2	5993	3	US-09-383-630-2	Sequence 2, Appli
c 696	33.8	3.2	7261	3	US-09-949-016-14780	Sequence 14780, A
697	33.8	3.2	7826	3	US-09-902-540-860	Sequence 860, App
c 698	33.8	3.2	8264	3	US-09-949-016-15457	Sequence 15457, A
c 699	33.8	3.2	8438	2	US-07-945-283-1	Sequence 1, Appli
700	33.8	3.2	17228	3	US-09-902-540-1170	Sequence 1170, Ap
701	33.8	3.2	17592	3	US-09-902-540-1138	Sequence 1138, Ap
c 702	33.8	3.2	18469	3	US-09-902-540-1205	Sequence 1205, Ap
703	33.8	3.2	41310	3	US-09-902-540-1264	Sequence 1264, Ap
704	33.8	3.2	53799	3	US-10-042-665A-3	Sequence 3, Appli
c 705	33.8	3.2	346112	3	US-09-949-016-13165	Sequence 13165, A
c 706	33.6	3.2	510	2	US-07-745-206A-3	Sequence 3, Appli
c 707	33.6	3.2	510	2	US-08-311-363-3	Sequence 3, Appli
c 708	33.6	3.2	558	3	US-09-902-540-1969	Sequence 1969, Ap
c 709	33.6	3.2	579	3	US-09-902-540-5469	Sequence 5469, Ap
710	33.6	3.2	673	3	US-09-949-016-5304	Sequence 5304, Ap
c 711	33.6	3.2	717	3	US-09-252-991A-3190	Sequence 3190, Ap
c 712	33.6	3.2	912	3	US-09-252-991A-395	Sequence 395, App
713	33.6	3.2	1086	3	US-09-724-797-77	Sequence 77, Appl
714	33.6	3.2	1095	3	US-09-902-540-3906	Sequence 3906, Ap
715	33.6	3.2	1161	3	US-09-902-540-3673	Sequence 3673, Ap
716	33.6	3.2	1176	3	US-09-902-540-6887	Sequence 6887, Ap
717	33.6	3.2	1251	3	US-09-252-991A-2647	Sequence 2647, Ap
718	33.6	3.2	1254	3	US-09-902-540-3469	Sequence 3469, Ap
c 719	33.6	3.2	1323	3	US-09-252-991A-3022	Sequence 3022, Ap
c 720	33.6	3.2	1347	3	US-09-252-991A-367	Sequence 367, App
721	33.6	3.2	1383	3	US-09-530-219B-7	Sequence 7, Appli
722	33.6	3.2	1407	3	US-09-902-540-3532	Sequence 3532, Ap
c 723	33.6	3.2	1623	3	US-09-252-991A-3226	Sequence 3226, Ap
c 724	33.6	3.2	1638	3	US-09-902-540-6292	Sequence 6292, Ap
725	33.6	3.2	1740	3	US-09-252-991A-554	Sequence 554, App
c 726	33.6	3.2	2100	3	US-09-252-991A-502	Sequence 502, App
727	33.6	3.2	2322	3	US-09-252-991A-3345	Sequence 3345, Ap
728	33.6	3.2	2364	3	US-09-252-991A-3420	Sequence 3420, Ap
c 729	33.6	3.2	2460	3	US-09-252-991A-2998	Sequence 2998, Ap
730	33.6	3.2	2592	3	US-09-902-540-2500	Sequence 2500, Ap
731	33.6	3.2	2695	3	US-09-902-540-443	Sequence 443, App
732	33.6	3.2	2856	3	US-09-252-991A-2869	Sequence 2869, Ap
c 733	33.6	3.2	3387	3	US-09-252-991A-3101	Sequence 3101, Ap
734	33.6	3.2	3503	3	US-09-771-161A-72	Sequence 72, Appl
c 735	33.6	3.2	7635	2	US-08-455-543A-1	Sequence 1, Appli
c 736	33.6	3.2	7635	2	US-08-455-543A-23	Sequence 23, Appl
c 737	33.6	3.2	7635	2	US-08-193-078B-1	Sequence 1, Appli
c 738	33.6	3.2	7635	2	US-08-193-078B-29	Sequence 29, Appl
c 739	33.6	3.2	7635	2	US-08-223-305C-1	Sequence 1, Appli
c 740	33.6	3.2	7635	2	US-08-223-305C-23	Sequence 23, Appl
c 741	33.6	3.2	7635	2	US-08-149-097D-1	Sequence 1, Appli
c 742	33.6	3.2	7635	3	US-08-949-386-1	Sequence 1, Appli
c 743	33.6	3.2	7635	3	US-08-450-562-1	Sequence 1, Appli
c 744	33.6	3.2	7635	3	US-08-984-709A-1	Sequence 1, Appli
c 745	33.6	3.2	7635	3	US-08-450-272-1	Sequence 1, Appli
c 746	33.6	3.2	7635	3	US-08-450-273-1	Sequence 1, Appli
747	33.6	3.2	8625	3	US-09-949-016-16566	Sequence 16566, A
748	33.6	3.2	11563	3	US-09-902-540-1019	Sequence 1019, Ap
c 749	33.6	3.2	11579	3	US-09-902-540-1052	Sequence 1052, Ap
750	33.6	3.2	13332	3	US-09-902-540-1047	Sequence 1047, Ap
c 751	33.6	3.2	14367	3	US-09-902-540-1113	Sequence 1113, Ap
752	33.6	3.2	15632	3	US-09-949-016-15119	Sequence 15119, A
c 753	33.6	3.2	15644	3	US-09-902-540-1133	Sequence 1133, Ap
c 754	33.6	3.2	16541	3	US-09-902-540-1165	Sequence 1165, Ap
c 755	33.6	3.2	16833	3	US-09-902-540-1112	Sequence 1112, Ap
756	33.6	3.2	16924	3	US-09-902-540-1178	Sequence 1178, Ap
757	33.6	3.2	21375	3	US-09-902-540-1193	Sequence 1193, Ap
758	33.6	3.2	22156	3	US-09-902-540-1195	Sequence 1195, Ap
759	33.6	3.2	22287	3	US-09-949-016-16820	Sequence 16820, A
c 760	33.6	3.2	28493	3	US-09-902-540-1241	Sequence 1241, Ap
c 761	33.6	3.2	29899	3	US-09-902-540-1265	Sequence 1265, Ap
c 762	33.6	3.2	33478	3	US-09-949-016-13615	Sequence 13615, A
c 763	33.6	3.2	34953	3	US-09-902-540-1263	Sequence 1263, Ap
764	33.6	3.2	53526	3	US-08-658-136-2	Sequence 2, Appli
765	33.6	3.2	53577	3	US-08-658-136-1	Sequence 1, Appli
766	33.6	3.2	53577	3	US-08-460-215A-1	Sequence 1, Appli
c 767	33.6	3.2	60990	3	US-09-949-016-14080	Sequence 14080, A
c 768	33.6	3.2	65902	3	US-09-949-002-609	Sequence 609, App
c 769	33.6	3.2	118923	3	US-09-949-016-13227	Sequence 13227, A
770	33.4	3.2	594	3	US-09-252-991A-7647	Sequence 7647, Ap
771	33.4	3.2	816	3	US-09-902-540-8461	Sequence 8461, Ap
c 772	33.4	3.2	927	3	US-09-902-540-7767	Sequence 7767, Ap
c 773	33.4	3.2	945	3	US-09-489-039A-2459	Sequence 2459, Ap
774	33.4	3.2	954	3	US-09-489-039A-3440	Sequence 3440, Ap
775	33.4	3.2	1080	3	US-09-252-991A-3284	Sequence 3284, Ap
776	33.4	3.2	1173	3	US-09-252-991A-5197	Sequence 5197, Ap
c 777	33.4	3.2	1227	3	US-09-252-991A-5278	Sequence 5278, Ap
778	33.4	3.2	1308	3	US-09-252-991A-6649	Sequence 6649, Ap
779	33.4	3.2	1350	3	US-09-891-053-11	Sequence 11, Appl
780	33.4	3.2	1611	3	US-09-902-540-7324	Sequence 7324, Ap
781	33.4	3.2	1782	3	US-09-252-991A-6680	Sequence 6680, Ap
c 782	33.4	3.2	1818	3	US-09-902-540-7054	Sequence 7054, Ap
783	33.4	3.2	1920	3	US-09-902-540-4811	Sequence 4811, Ap
784	33.4	3.2	2592	3	US-09-252-991A-5260	Sequence 5260, Ap
785	33.4	3.2	2665	3	US-09-949-016-5059	Sequence 5059, Ap
786	33.4	3.2	2689	2	US-08-985-090-1	Sequence 1, Appli
787	33.4	3.2	2689	3	US-09-165-543-1	Sequence 1, Appli
788	33.4	3.2	3731	2	US-08-231-193A-31	Sequence 31, Appl
789	33.4	3.2	3731	2	US-08-486-273A-31	Sequence 31, Appl
790	33.4	3.2	3731	3	US-08-480-474-31	Sequence 31, Appl
791	33.4	3.2	3731	3	US-08-940-086A-31	Sequence 31, Appl
792	33.4	3.2	3731	3	US-08-940-035A-31	Sequence 31, Appl
793	33.4	3.2	3731	3	US-08-935-105A-31	Sequence 31, Appl
794	33.4	3.2	3731	3	US-09-648-797-31	Sequence 31, Appl
795	33.4	3.2	3731	3	US-09-386-123-31	Sequence 31, Appl
796	33.4	3.2	3731	3	US-10-038-937-31	Sequence 31, Appl
797	33.4	3.2	3731	3	US-10-007-747-31	Sequence 31, Appl
798	33.4	3.2	3731	3	US-09-945-901-31	Sequence 31, Appl
c 799	33.4	3.2	3741	3	US-09-252-991A-6569	Sequence 6569, Ap
800	33.4	3.2	3783	3	US-09-902-540-4846	Sequence 4846, Ap
801	33.4	3.2	3794	2	US-08-231-193A-27	Sequence 27, Appl
802	33.4	3.2	3794	2	US-08-486-273A-27	Sequence 27, Appl
803	33.4	3.2	3794	3	US-08-480-474-27	Sequence 27, Appl
804	33.4	3.2	3794	3	US-08-940-086A-27	Sequence 27, Appl
805	33.4	3.2	3794	3	US-08-940-035A-27	Sequence 27, Appl
806	33.4	3.2	3794	3	US-08-935-105A-27	Sequence 27, Appl
807	33.4	3.2	3794	3	US-09-648-797-27	Sequence 27, Appl
808	33.4	3.2	3794	3	US-09-386-123-27	Sequence 27, Appl
809	33.4	3.2	3794	3	US-10-038-937-27	Sequence 27, Appl
810	33.4	3.2	3794	3	US-10-007-747-27	Sequence 27, Appl
811	33.4	3.2	3794	3	US-09-945-901-27	Sequence 27, Appl
812	33.4	3.2	3935	2	US-08-231-193A-19	Sequence 19, Appl
813	33.4	3.2	3935	2	US-08-486-273A-19	Sequence 19, Appl
814	33.4	3.2	3935	3	US-08-480-474-19	Sequence 19, Appl
815	33.4	3.2	3935	3	US-08-940-086A-19	Sequence 19, Appl
816	33.4	3.2	3935	3	US-08-940-035A-19	Sequence 19, Appl
817	33.4	3.2	3935	3	US-08-935-105A-19	Sequence 19, Appl
818	33.4	3.2	3935	3	US-09-648-797-19	Sequence 19, Appl
819	33.4	3.2	3935	3	US-09-386-123-19	Sequence 19, Appl
820	33.4	3.2	3935	3	US-10-038-937-19	Sequence 19, Appl
821	33.4	3.2	3935	3	US-10-007-747-19	Sequence 19, Appl
822	33.4	3.2	3935	3	US-09-945-901-19	Sequence 19, Appl
823	33.4	3.2	3998	2	US-08-231-193A-35	Sequence 35, Appl
824	33.4	3.2	3998	2	US-08-486-273A-35	Sequence 35, Appl
825	33.4	3.2	3998	3	US-08-480-474-35	Sequence 35, Appl
826	33.4	3.2	3998	3	US-08-940-086A-35	Sequence 35, Appl
827	33.4	3.2	3998	3	US-08-940-035A-35	Sequence 35, Appl

	828	33.4	3.2	3998	3	US-08-935-105A-35	Sequence 35, Appl
	829	33.4	3.2	3998	3	US-09-648-797-35	Sequence 35, Appl
	830	33.4	3.2	3998	3	US-09-386-123-35	Sequence 35, Appl
	831	33.4	3.2	3998	3	US-10-038-937-35	Sequence 35, Appl
	832	33.4	3.2	3998	3	US-10-007-747-35	Sequence 35, Appl
	833	33.4	3.2	3998	3	US-09-945-901-35	Sequence 35, Appl
	834	33.4	3.2	4094	2	US-08-231-193A-29	Sequence 29, Appl
	835	33.4	3.2	4094	2	US-08-486-273A-29	Sequence 29, Appl
	836	33.4	3.2	4094	3	US-08-480-474-29	Sequence 29, Appl
	837	33.4	3.2	4094	3	US-08-940-086A-29	Sequence 29, Appl
	838	33.4	3.2	4094	3	US-08-940-035A-29	Sequence 29, Appl
	839	33.4	3.2	4094	3	US-08-935-105A-29	Sequence 29, Appl
	840	33.4	3.2	4094	3	US-09-648-797-29	Sequence 29, Appl
	841	33.4	3.2	4094	3	US-09-386-123-29	Sequence 29, Appl
	842	33.4	3.2	4094	3	US-10-038-937-29	Sequence 29, Appl
	843	33.4	3.2	4094	3	US-10-007-747-29	Sequence 29, Appl
	844	33.4	3.2	4094	3	US-09-945-901-29	Sequence 29, Appl
	845	33.4	3.2	4157	2	US-08-231-193A-25	Sequence 25, Appl
	846	33.4	3.2	4157	2	US-08-486-273A-25	Sequence 25, Appl
	847	33.4	3.2	4157	3	US-08-480-474-25	Sequence 25, Appl
	848	33.4	3.2	4157	3	US-08-940-086A-25	Sequence 25, Appl
	849	33.4	3.2	4157	3	US-08-940-035A-25	Sequence 25, Appl
	850	33.4	3.2	4157	3	US-08-935-105A-25	Sequence 25, Appl
	851	33.4	3.2	4157	3	US-09-648-797-25	Sequence 25, Appl
	852	33.4	3.2	4157	3	US-09-386-123-25	Sequence 25, Appl
	853	33.4	3.2	4157	3	US-10-038-937-25	Sequence 25, Appl
	854	33.4	3.2	4157	3	US-10-007-747-25	Sequence 25, Appl
	855	33.4	3.2	4157	3	US-09-945-901-25	Sequence 25, Appl
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	858	33.4	3.2	4298	2	US-08-486-273A-1	Sequence 1, Appli
	859	33.4	3.2	4298	3	US-08-480-474-1	Sequence 1, Appli
	860	33.4	3.2	4298	3	US-08-940-086A-1	Sequence 1, Appli
	861	33.4	3.2	4298	3	US-08-940-035A-1	Sequence 1, Appli
	862	33.4	3.2	4298	3	US-08-935-105A-1	Sequence 1, Appli
	863	33.4	3.2	4298	3	US-09-648-797-1	Sequence 1, Appli
	864	33.4	3.2	4298	3	US-09-386-123-1	Sequence 1, Appli
	865	33.4	3.2	4298	3	US-10-038-937-1	Sequence 1, Appli
	866	33.4	3.2	4298	3	US-10-007-747-1	Sequence 1, Appli
	867	33.4	3.2	4298	3	US-09-945-901-1	Sequence 1, Appli
	868	33.4	3.2	4361	2	US-08-231-193A-23	Sequence 23, Appl
	869	33.4	3.2	4361	2	US-08-486-273A-23	Sequence 23, Appl
	870	33.4	3.2	4361	3	US-08-480-474-23	Sequence 23, Appl
	871	33.4	3.2	4361	3	US-08-940-086A-23	Sequence 23, Appl
	872	33.4	3.2	4361	3	US-08-940-035A-23	Sequence 23, Appl
	873	33.4	3.2	4361	3	US-08-935-105A-23	Sequence 23, Appl
	874	33.4	3.2	4361	3	US-09-648-797-23	Sequence 23, Appl
	875	33.4	3.2	4361	3	US-09-386-123-23	Sequence 23, Appl
	876	33.4	3.2	4361	3	US-10-038-937-23	Sequence 23, Appl
	877	33.4	3.2	4361	3	US-10-007-747-23	Sequence 23, Appl
	878	33.4	3.2	4361	3	US-09-945-901-23	Sequence 23, Appl
	879	33.4	3.2	4376	3	US-09-407-605-1	Sequence 1, Appli
	880	33.4	3.2	4384	3	US-09-407-605-2	Sequence 2, Appli
c	881	33.4	3.2	4523	3	US-09-473-716-1	Sequence 1, Appli
c	882	33.4	3.2	4523	3	US-10-175-158-1	Sequence 1, Appli
c	883	33.4	3.2	5051	3	US-09-902-540-628	Sequence 628, App
	884	33.4	3.2	5316	3	US-10-037-417-17	Sequence 17, Appl
	885	33.4	3.2	7012	3	US-09-902-540-890	Sequence 890, App
	886	33.4	3.2	8604	3	US-09-902-540-5331	Sequence 5331, Ap
	887	33.4	3.2	9293	3	US-09-949-016-16801	Sequence 16801, A
	888	33.4	3.2	12253	3	US-09-902-540-1060	Sequence 1060, Ap
	889	33.4	3.2	13821	3	US-09-949-016-13690	Sequence 13690, A
	890	33.4	3.2	14027	3	US-09-902-540-1023	Sequence 1023, Ap
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	892	33.4	3.2	21296	3	US-09-949-016-14504	Sequence 14504, A
	893	33.4	3.2	21296	3	US-09-949-016-14505	Sequence 14505, A
	894	33.4	3.2	21296	3	US-09-949-016-15701	Sequence 15701, A
	895	33.4	3.2	21296	3	US-09-949-016-15702	Sequence 15702, A
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	897	33.4	3.2	25621	3	US-09-902-540-1253	Sequence 1253, Ap
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	899	33.4	3.2	35399	3	US-09-902-540-1260	Sequence 1260, Ap
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	902	33.4	3.2	51723	3	US-09-949-016-12152	Sequence 12152, A
	903	33.4	3.2	51723	3	US-09-949-016-16991	Sequence 16991, A
	904	33.4	3.2	52314	3	US-09-949-016-14622	Sequence 14622, A
	905	33.4	3.2	136058	3	US-09-949-016-12565	Sequence 12565, A
	906	33.4	3.2	136480	3	US-09-949-016-17064	Sequence 17064, A
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c	909	33.2	3.2	477	3	US-09-684-843A-1	Sequence 1, Appli
	910	33.2	3.2	601	3	US-09-949-016-61829	Sequence 61829, A
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	912	33.2	3.2	668	9	5498529-5	Patent No. 5498529
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c	914	33.2	3.2	711	3	US-09-799-451-103	Sequence 103, App
c	915	33.2	3.2	792	3	US-09-252-991A-15292	Sequence 15292, A
	916	33.2	3.2	804	3	US-09-902-540-3773	Sequence 3773, Ap
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	922	33.2	3.2	972	3	US-09-252-991A-6718	Sequence 6718, Ap
	923	33.2	3.2	1005	3	US-09-902-540-6578	Sequence 6578, Ap
	924	33.2	3.2	1029	3	US-09-252-991A-10644	Sequence 10644, A
	925	33.2	3.2	1086	3	US-09-902-540-7871	Sequence 7871, Ap
	926	33.2	3.2	1095	3	US-09-252-991A-3310	Sequence 3310, Ap
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c	930	33.2	3.2	1368	3	US-09-252-991A-3365	Sequence 3365, Ap
	931	33.2	3.2	1371	3	US-09-252-991A-2846	Sequence 2846, Ap
	932	33.2	3.2	1419	3	US-09-252-991A-15497	Sequence 15497, A
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	934	33.2	3.2	1521	3	US-09-252-991A-6686	Sequence 6686, Ap
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c	936	33.2	3.2	1689	3	US-09-712-363-108	Sequence 108, App
	937	33.2	3.2	1758	3	US-10-237-551-192	Sequence 192, App
c	938	33.2	3.2	1815	3	US-09-902-540-2953	Sequence 2953, Ap
c	939	33.2	3.2	1896	3	US-09-252-991A-1429	Sequence 1429, Ap
	940	33.2	3.2	2151	3	US-09-949-016-2314	Sequence 2314, Ap
	941	33.2	3.2	2373	3	US-09-902-540-8027	Sequence 8027, Ap
	942	33.2	3.2	2508	3	US-09-252-991A-15550	Sequence 15550, A
	943	33.2	3.2	2580	3	US-09-902-540-7003	Sequence 7003, Ap
	944	33.2	3.2	2751	3	US-09-252-991A-7066	Sequence 7066, Ap
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c	946	33.2	3.2	3292	3	US-09-141-908-15	Sequence 15, Appl
c	947	33.2	3.2	3292	3	US-09-657-440-22	Sequence 22, Appl
c	948	33.2	3.2	3292	3	US-09-793-708-22	Sequence 22, Appl
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	950	33.2	3.2	3411	3	US-09-949-016-3960	Sequence 3960, Ap
	951	33.2	3.2	3482	3	US-09-949-016-2762	Sequence 2762, Ap
	952	33.2	3.2	3482	3	US-09-949-016-2763	Sequence 2763, Ap
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c	954	33.2	3.2	4075	3	US-09-902-540-614	Sequence 614, App
c	955	33.2	3.2	4401	3	US-09-614-034-192	Sequence 192, App
	956	33.2	3.2	5337	3	US-09-252-991A-1588	Sequence 1588, Ap
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c	958	33.2	3.2	6196	3	US-09-902-540-788	Sequence 788, App
	959	33.2	3.2	6368	3	US-09-902-540-817	Sequence 817, App
	960	33.2	3.2	7928	3	US-09-548-473B-5	Sequence 5, Appli
	961	33.2	3.2	7965	3	US-09-949-016-13537	Sequence 13537, A
	962	33.2	3.2	9125	3	US-09-902-540-959	Sequence 959, App
c	963	33.2	3.2	12955	3	US-09-902-540-1068	Sequence 1068, Ap
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c	967	33.2	3.2	18079	3	US-09-949-016-13344	Sequence 13344, A
	968	33.2	3.2	18228	3	US-09-949-016-11964	Sequence 11964, A
	969	33.2	3.2	18229	3	US-09-949-016-14056	Sequence 14056, A
	970	33.2	3.2	18238	3	US-09-949-016-13557	Sequence 13557, A
	971	33.2	3.2	18472	3	US-09-949-016-12891	Sequence 12891, A
	972	33.2	3.2	18478	3	US-09-949-016-15925	Sequence 15925, A
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c 976	33.2	3.2	28054	3	US-09-902-540-1248	Sequence 1248, Ap
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978	33.2	3.2	80161	3	US-09-036-987A-1	Sequence 1, Appli
979	33.2	3.2	80161	3	US-09-370-700-1	Sequence 1, Appli
980	33.2	3.2	80161	3	US-09-603-207-1	Sequence 1, Appli
981	33.2	3.2	100928	3	US-09-949-016-16926	Sequence 16926, A
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984	33.2	3.2	150597	3	US-09-949-016-15379	Sequence 15379, A
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986	33	3.2	457	3	US-09-060-756-591	Sequence 591, App
987	33	3.2	457	3	US-09-670-314-591	Sequence 591, App
c 988	33	3.2	543	3	US-09-252-991A-13063	Sequence 13063, A
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993	33	3.2	1020	3	US-09-758-759-16	Sequence 16, Appl
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995	33	3.2	1102	3	US-10-037-417-45	Sequence 45, Appl
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997	33	3.2	1169	3	US-09-386-642-7	Sequence 7, Appli
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1004	33	3.2	1614	3	US-09-976-740-45	Sequence 45, Appl
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1013	33	3.2	1908	3	US-09-046-992-1	Sequence 1, Appli
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1015	33	3.2	2127	3	US-09-252-991A-1503	Sequence 1503, Ap
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c1017	33	3.2	2231	3	US-09-968-415-24	Sequence 24, Appl
1018	33	3.2	2238	3	US-09-902-540-2944	Sequence 2944, Ap
1019	33	3.2	2304	3	US-09-252-991A-2790	Sequence 2790, Ap
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c1023	33	3.2	4094	2	US-08-909-984A-5	Sequence 5, Appli
c1024	33	3.2	4094	2	US-08-909-983-5	Sequence 5, Appli
c1025	33	3.2	4787	3	US-09-949-016-14085	Sequence 14085, A
c1026	33	3.2	4787	3	US-09-949-016-14086	Sequence 14086, A
c1027	33	3.2	4854	3	US-09-902-540-768	Sequence 768, App
1028	33	3.2	5499	3	US-09-902-540-2892	Sequence 2892, Ap
c1029	33	3.2	9521	3	US-09-902-540-953	Sequence 953, App
1030	33	3.2	10733	3	US-09-902-540-1021	Sequence 1021, Ap
c1031	33	3.2	10851	3	US-09-888-233C-2	Sequence 2, Appli
1032	33	3.2	12425	3	US-09-616-289-50	Sequence 50, Appl
1033	33	3.2	12425	3	US-09-976-740-50	Sequence 50, Appl
1034	33	3.2	12898	3	US-09-902-540-1000	Sequence 1000, Ap
c1035	33	3.2	16782	3	US-09-949-016-17291	Sequence 17291, A
c1036	33	3.2	19157	3	US-09-949-016-13142	Sequence 13142, A
c1037	33	3.2	23233	3	US-09-902-540-1184	Sequence 1184, Ap
c1038	33	3.2	23417	3	US-09-902-540-1207	Sequence 1207, Ap
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1043	33	3.2	46447	3	US-09-949-016-15071	Sequence 15071, A
1044	33	3.2	46447	3	US-09-949-016-15072	Sequence 15072, A
1045	33	3.2	46447	3	US-09-949-016-15073	Sequence 15073, A
1046	33	3.2	46447	3	US-09-949-016-15074	Sequence 15074, A
1047	33	3.2	46447	3	US-09-949-016-15075	Sequence 15075, A
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1061	33	3.2	59853	3	US-09-949-016-13619	Sequence 13619, A
1062	33	3.2	59853	3	US-09-949-016-13620	Sequence 13620, A
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1067	33	3.2	59853	3	US-09-949-016-13625	Sequence 13625, A
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c1069	33	3.2	152132	3	US-09-949-016-13845	Sequence 13845, A
c1070	33	3.2	152145	3	US-09-949-016-12371	Sequence 12371, A
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1072	33	3.2	275110	3	US-09-949-016-12706	Sequence 12706, A
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1077	32.8	3.1	591	3	US-09-902-540-8060	Sequence 8060, Ap
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1079	32.8	3.1	621	3	US-09-252-991A-4261	Sequence 4261, Ap
1080	32.8	3.1	692	3	US-09-620-956-11	Sequence 11, Appl
1081	32.8	3.1	692	3	US-09-611-152-11	Sequence 11, Appl
1082	32.8	3.1	692	3	US-09-794-705A-6	Sequence 6, Appli
1083	32.8	3.1	692	3	US-09-631-531-11	Sequence 11, Appl
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1085	32.8	3.1	939	3	US-09-105-390-45	Sequence 45, Appl
1086	32.8	3.1	1020	3	US-09-105-390-61	Sequence 61, Appl
1087	32.8	3.1	1118	3	US-09-452-239-37	Sequence 37, Appl
1088	32.8	3.1	1146	3	US-09-452-239-3	Sequence 3, Appli
1089	32.8	3.1	1203	3	US-09-902-540-9122	Sequence 9122, Ap
1090	32.8	3.1	1248	3	US-09-252-991A-4192	Sequence 4192, Ap
1091	32.8	3.1	1311	3	US-09-902-540-3069	Sequence 3069, Ap
1092	32.8	3.1	1380	3	US-09-902-540-9575	Sequence 9575, Ap
1093	32.8	3.1	1401	4	US-09-605-703B-543	Sequence 543, App
1094	32.8	3.1	1488	3	US-09-902-540-7192	Sequence 7192, Ap
1095	32.8	3.1	1736	3	US-09-162-524-2	Sequence 2, Appli
1096	32.8	3.1	1779	3	US-09-902-540-9167	Sequence 9167, Ap
1097	32.8	3.1	1956	3	US-09-902-540-2389	Sequence 2389, Ap
1098	32.8	3.1	1959	3	US-09-774-528-375	Sequence 375, App
1099	32.8	3.1	1959	3	US-10-120-988-375	Sequence 375, App
1100	32.8	3.1	2040	2	US-08-031-538-10	Sequence 10, Appl
c1101	32.8	3.1	2130	3	US-09-909-962A-6	Sequence 6, Appli
c1102	32.8	3.1	2130	3	US-09-909-962A-7	Sequence 7, Appli
1103	32.8	3.1	2135	3	US-10-104-047-1181	Sequence 1181, Ap
1104	32.8	3.1	2284	3	US-09-193-792-1	Sequence 1, Appli
1105	32.8	3.1	2526	3	US-10-104-047-270	Sequence 270, App
1106	32.8	3.1	2612	3	US-09-105-390-7	Sequence 7, Appli
1107	32.8	3.1	2932	3	US-09-016-434-1419	Sequence 1419, Ap
1108	32.8	3.1	2932	3	US-09-054-272-5	Sequence 5, Appli
c1109	32.8	3.1	3147	2	US-08-781-802-7	Sequence 7, Appli
c1110	32.8	3.1	3147	3	US-08-694-078-7	Sequence 7, Appli
c1111	32.8	3.1	3147	3	US-09-058-260-7	Sequence 7, Appli
c1112	32.8	3.1	3237	3	US-09-566-921-40	Sequence 40, Appl
c1113	32.8	3.1	5872	3	US-09-902-540-859	Sequence 859, App
c1114	32.8	3.1	6360	3	US-10-212-962-2	Sequence 2, Appli
c1115	32.8	3.1	7160	3	US-09-902-540-821	Sequence 821, App
c1116	32.8	3.1	10276	3	US-09-902-540-975	Sequence 975, App
1117	32.8	3.1	11612	3	US-09-902-540-981	Sequence 981, App
1118	32.8	3.1	12299	3	US-09-902-540-1056	Sequence 1056, Ap
c1119	32.8	3.1	14823	3	US-09-902-540-1087	Sequence 1087, Ap

1120	32.8	3.1	15209	3	US-09-902-540-1104	Sequence 1104, Ap
1121	32.8	3.1	15775	3	US-09-949-016-16550	Sequence 16550, A
c1122	32.8	3.1	26852	3	US-09-949-016-12736	Sequence 12736, A
c1123	32.8	3.1	26852	3	US-09-949-016-15823	Sequence 15823, A
1124	32.8	3.1	28320	3	US-09-902-540-1222	Sequence 1222, Ap
1125	32.8	3.1	31571	2	US-08-323-443B-1	Sequence 1, Appli
c1126	32.8	3.1	39243	3	US-09-949-016-12316	Sequence 12316, A
c1127	32.8	3.1	39243	3	US-09-949-016-15443	Sequence 15443, A
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c1129	32.8	3.1	58857	3	US-09-477-962-1	Sequence 1, Appli
1130	32.8	3.1	128470	3	US-09-949-016-13765	Sequence 13765, A
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c1132	32.8	3.1	153643	3	US-09-949-016-15635	Sequence 15635, A
1133	32.8	3.1	331814	3	US-09-949-016-12008	Sequence 12008, A
1134	32.8	3.1	331814	3	US-09-949-016-17056	Sequence 17056, A
c1135	32.6	3.1	426	3	US-09-397-787-134	Sequence 134, App
1136	32.6	3.1	486	3	US-09-252-991A-2552	Sequence 2552, Ap
c1137	32.6	3.1	497	3	US-09-847-960-13	Sequence 13, Appl
1138	32.6	3.1	576	3	US-09-252-991A-7331	Sequence 7331, Ap
c1139	32.6	3.1	601	3	US-09-949-016-140427	Sequence 140427,
c1140	32.6	3.1	601	3	US-09-949-016-161524	Sequence 161524,
c1141	32.6	3.1	601	3	US-09-949-016-161525	Sequence 161525,
c1142	32.6	3.1	601	3	US-09-949-016-161526	Sequence 161526,
c1143	32.6	3.1	663	3	US-09-252-991A-4047	Sequence 4047, Ap
c1144	32.6	3.1	702	3	US-09-252-991A-6945	Sequence 6945, Ap
c1145	32.6	3.1	705	3	US-09-902-540-6333	Sequence 6333, Ap
c1146	32.6	3.1	705	3	US-09-847-960-6	Sequence 6, Appli
c1147	32.6	3.1	759	3	US-09-902-540-5421	Sequence 5421, Ap
c1148	32.6	3.1	788	3	US-09-861-893-38	Sequence 38, Appl
1149	32.6	3.1	865	3	US-09-270-767-11042	Sequence 11042, A
c1150	32.6	3.1	1050	3	US-09-482-273-58	Sequence 58, Appl
1151	32.6	3.1	1082	3	US-09-881-165-4	Sequence 4, Appli
1152	32.6	3.1	1119	3	US-08-987-943-2	Sequence 2, Appli
1153	32.6	3.1	1119	3	US-09-902-540-5911	Sequence 5911, Ap
c1154	32.6	3.1	1302	3	US-09-252-991A-7221	Sequence 7221, Ap
1155	32.6	3.1	1347	3	US-09-902-540-9063	Sequence 9063, Ap
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1157	32.6	3.1	1443	3	US-09-252-991A-2631	Sequence 2631, Ap
1158	32.6	3.1	1485	3	US-09-252-991A-6749	Sequence 6749, Ap
1159	32.6	3.1	1551	3	US-09-252-991A-7473	Sequence 7473, Ap
c1160	32.6	3.1	1560	3	US-09-252-991A-14244	Sequence 14244, A
1161	32.6	3.1	1577	3	US-09-902-540-173	Sequence 173, App
1162	32.6	3.1	1578	3	US-09-252-991A-7410	Sequence 7410, Ap
1163	32.6	3.1	1587	3	US-09-252-991A-6797	Sequence 6797, Ap
1164	32.6	3.1	1701	3	US-09-902-540-9608	Sequence 9608, Ap
1165	32.6	3.1	1707	3	US-09-023-655-449	Sequence 449, App
1166	32.6	3.1	1755	3	US-08-987-943-1	Sequence 1, Appli
1167	32.6	3.1	1811	3	US-09-902-540-396	Sequence 396, App
c1168	32.6	3.1	1932	3	US-09-252-991A-5919	Sequence 5919, Ap
1169	32.6	3.1	2046	3	US-09-252-991A-5948	Sequence 5948, Ap
c1170	32.6	3.1	2109	3	US-09-370-838-153	Sequence 153, App
c1171	32.6	3.1	2109	3	US-09-854-133-153	Sequence 153, App
1172	32.6	3.1	2139	3	US-09-252-991A-3900	Sequence 3900, Ap
1173	32.6	3.1	2214	3	US-09-252-991A-5968	Sequence 5968, Ap
1174	32.6	3.1	2337	3	US-09-252-991A-14021	Sequence 14021, A
c1175	32.6	3.1	2365	3	US-09-774-528-144	Sequence 144, App
c1176	32.6	3.1	2365	3	US-10-120-988-144	Sequence 144, App
1177	32.6	3.1	2565	3	US-09-799-451-477	Sequence 477, App
1178	32.6	3.1	2598	3	US-09-816-094-1	Sequence 1, Appli
1179	32.6	3.1	2598	3	US-10-233-613-1	Sequence 1, Appli
1180	32.6	3.1	2598	3	US-10-639-429-1	Sequence 1, Appli
c1181	32.6	3.1	2668	3	US-09-370-838-156	Sequence 156, App
c1182	32.6	3.1	2668	3	US-09-854-133-156	Sequence 156, App
c1183	32.6	3.1	2814	3	US-10-104-047-991	Sequence 991, App
c1184	32.6	3.1	2843	3	US-09-902-540-5195	Sequence 5195, Ap
c1185	32.6	3.1	3144	3	US-09-711-681-3	Sequence 3, Appli
c1186	32.6	3.1	3144	3	US-10-274-266-3	Sequence 3, Appli
c1187	32.6	3.1	3213	3	US-09-902-540-8187	Sequence 8187, Ap
1188	32.6	3.1	4455	3	US-09-902-540-7119	Sequence 7119, Ap
c1189	32.6	3.1	4458	3	US-09-902-540-650	Sequence 650, App
1190	32.6	3.1	4465	3	US-09-799-451-142	Sequence 142, App
c1191	32.6	3.1	4683	3	US-09-902-540-9346	Sequence 9346, Ap
1192	32.6	3.1	6301	3	US-09-902-540-842	Sequence 842, App
1193	32.6	3.1	7301	3	US-09-816-094-3	Sequence 3, Appli
1194	32.6	3.1	7301	3	US-10-233-613-3	Sequence 3, Appli
1195	32.6	3.1	7301	3	US-10-639-429-3	Sequence 3, Appli
c1196	32.6	3.1	9905	3	US-09-902-540-998	Sequence 998, App
c1197	32.6	3.1	12194	3	US-09-902-540-1091	Sequence 1091, Ap
1198	32.6	3.1	12250	3	US-09-949-016-17580	Sequence 17580, A
c1199	32.6	3.1	13299	3	US-09-902-540-968	Sequence 968, App
c1200	32.6	3.1	16742	3	US-09-949-016-12782	Sequence 12782, A
1201	32.6	3.1	19009	3	US-09-949-016-12522	Sequence 12522, A
1202	32.6	3.1	19012	3	US-09-949-016-16999	Sequence 16999, A
1203	32.6	3.1	22874	3	US-09-949-016-11976	Sequence 11976, A
1204	32.6	3.1	22875	3	US-09-949-016-16363	Sequence 16363, A
c1205	32.6	3.1	24207	3	US-09-949-016-14364	Sequence 14364, A
1206	32.6	3.1	34199	3	US-09-902-540-1255	Sequence 1255, Ap
1207	32.6	3.1	34662	3	US-09-902-540-1261	Sequence 1261, Ap
1208	32.6	3.1	34953	3	US-09-902-540-1263	Sequence 1263, Ap
1209	32.6	3.1	38506	3	US-09-320-878-19	Sequence 19, Appl
1210	32.6	3.1	38506	3	US-09-141-908-1	Sequence 1, Appli
1211	32.6	3.1	38506	3	US-09-657-440-19	Sequence 19, Appl
1212	32.6	3.1	38506	3	US-09-793-708-19	Sequence 19, Appl
1213	32.6	3.1	48318	3	US-09-949-016-15717	Sequence 15717, A
1214	32.6	3.1	49301	3	US-09-949-016-16296	Sequence 16296, A
1215	32.6	3.1	49377	2	US-08-764-233A-1	Sequence 1, Appli
1216	32.6	3.1	76610	3	US-09-949-016-15521	Sequence 15521, A
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c1218	32.6	3.1	80161	3	US-09-370-700-1	Sequence 1, Appli
c1219	32.6	3.1	80161	3	US-09-603-207-1	Sequence 1, Appli
c1220	32.6	3.1	88758	3	US-09-949-016-13502	Sequence 13502, A
1221	32.6	3.1	240157	3	US-09-949-016-16264	Sequence 16264, A
c1222	32.6	3.1	312957	3	US-09-949-001-31	Sequence 31, Appl
c1223	32.6	3.1	312972	3	US-09-949-001-34	Sequence 34, Appl
1224	32.4	3.1	424	3	US-09-370-838-137	Sequence 137, App
1225	32.4	3.1	424	3	US-09-854-133-137	Sequence 137, App
c1226	32.4	3.1	430	3	US-09-621-976-16656	Sequence 16656, A
1227	32.4	3.1	501	3	US-09-252-991A-11947	Sequence 11947, A
c1228	32.4	3.1	510	3	US-09-252-991A-9622	Sequence 9622, Ap
1229	32.4	3.1	549	3	US-09-370-838-167	Sequence 167, App
1230	32.4	3.1	549	3	US-09-854-133-167	Sequence 167, App
c1231	32.4	3.1	601	3	US-09-949-016-104084	Sequence 104084,
1232	32.4	3.1	603	3	US-09-252-991A-464	Sequence 464, App
1233	32.4	3.1	699	3	US-09-252-991A-9676	Sequence 9676, Ap
c1234	32.4	3.1	708	3	US-09-252-991A-7951	Sequence 7951, Ap
1235	32.4	3.1	720	3	US-09-902-540-9651	Sequence 9651, Ap
c1236	32.4	3.1	742	3	US-09-510-543-16	Sequence 16, Appl
c1237	32.4	3.1	771	3	US-09-902-540-8384	Sequence 8384, Ap
1238	32.4	3.1	891	3	US-09-902-540-5678	Sequence 5678, Ap
1239	32.4	3.1	1032	3	US-09-949-016-4945	Sequence 4945, Ap
1240	32.4	3.1	1095	3	US-09-774-639-60	Sequence 60, Appl
c1241	32.4	3.1	1144	2	US-08-014-943A-1	Sequence 1, Appli
c1242	32.4	3.1	1144	2	US-08-486-421-2	Sequence 2, Appli
c1243	32.4	3.1	1144	2	US-08-470-911-2	Sequence 2, Appli
c1244	32.4	3.1	1144	2	US-08-486-809-2	Sequence 2, Appli
1245	32.4	3.1	1182	3	US-09-252-991A-7600	Sequence 7600, Ap
c1246	32.4	3.1	1266	3	US-09-902-540-3571	Sequence 3571, Ap
1247	32.4	3.1	1371	3	US-09-252-991A-9717	Sequence 9717, Ap
1248	32.4	3.1	1377	3	US-09-377-557-17	Sequence 17, Appl
1249	32.4	3.1	1392	3	US-09-489-039A-5663	Sequence 5663, Ap
c1250	32.4	3.1	1422	3	US-09-902-540-7548	Sequence 7548, Ap
1251	32.4	3.1	1461	3	US-09-398-522-113	Sequence 113, App
1252	32.4	3.1	1500	3	US-09-252-991A-11907	Sequence 11907, A
1253	32.4	3.1	1527	3	US-09-252-991A-7679	Sequence 7679, Ap
1254	32.4	3.1	1560	3	US-09-598-747-26	Sequence 26, Appl
c1255	32.4	3.1	1671	3	US-09-902-540-6752	Sequence 6752, Ap
1256	32.4	3.1	1872	3	US-09-291-922-27	Sequence 27, Appl
1257	32.4	3.1	1889	3	US-09-902-540-7346	Sequence 7346, Ap
1258	32.4	3.1	1956	3	US-09-724-797-57	Sequence 57, Appl
1259	32.4	3.1	1956	3	US-10-152-886-20	Sequence 20, Appl
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1261	32.4	3.1	1995	3	US-09-902-540-9209	Sequence 9209, Ap
1262	32.4	3.1	2029	3	US-09-664-958-27	Sequence 27, Appl
1263	32.4	3.1	2032	3	US-09-949-016-5636	Sequence 5636, Ap
1264	32.4	3.1	2087	3	US-09-461-325-99	Sequence 99, Appl
1265	32.4	3.1	2087	3	US-10-012-542-99	Sequence 99, Appl

1266	32.4	3.1	2087	3	US-10-115-123-99	Sequence 99, Appl
1267	32.4	3.1	2113	3	US-10-104-047-477	Sequence 477, App
1268	32.4	3.1	2162	3	US-09-991-181-339	Sequence 339, App
1269	32.4	3.1	2162	3	US-09-990-444-339	Sequence 339, App
1270	32.4	3.1	2162	3	US-09-997-333-339	Sequence 339, App
1271	32.4	3.1	2162	3	US-09-992-598-339	Sequence 339, App
1272	32.4	3.1	2196	3	US-09-902-540-4673	Sequence 4673, Ap
1273	32.4	3.1	2366	3	US-09-949-016-1254	Sequence 1254, Ap
1274	32.4	3.1	2366	3	US-09-949-016-1255	Sequence 1255, Ap
1275	32.4	3.1	2366	3	US-09-949-016-1256	Sequence 1256, Ap
1276	32.4	3.1	2366	3	US-09-949-016-1257	Sequence 1257, Ap
1277	32.4	3.1	2366	3	US-09-949-016-1258	Sequence 1258, Ap
c1278	32.4	3.1	3345	3	US-10-104-047-533	Sequence 533, App
1279	32.4	3.1	3346	3	US-09-902-540-548	Sequence 548, App
c1280	32.4	3.1	3446	3	US-09-620-312D-653	Sequence 653, App
c1281	32.4	3.1	3488	3	US-09-105-470B-8	Sequence 8, Appli
1282	32.4	3.1	3508	3	US-09-902-540-8762	Sequence 8762, Ap
1283	32.4	3.1	3601	3	US-09-017-631-23	Sequence 23, Appl
1284	32.4	3.1	3602	2	US-08-358-918-33	Sequence 33, Appl
1285	32.4	3.1	3602	2	US-08-883-795A-33	Sequence 33, Appl
1286	32.4	3.1	3602	3	US-09-018-138-1	Sequence 1, Appli
c1287	32.4	3.1	3763	3	US-10-012-070A-43	Sequence 43, Appl
c1288	32.4	3.1	3763	3	US-10-012-070A-44	Sequence 44, Appl
1289	32.4	3.1	4125	3	US-10-237-551-76	Sequence 76, Appl
1290	32.4	3.1	4125	3	US-10-237-551-149	Sequence 149, App
1291	32.4	3.1	4125	3	US-10-237-551-210	Sequence 210, App
c1292	32.4	3.1	4200	3	US-09-949-016-5718	Sequence 5718, Ap
c1293	32.4	3.1	4201	3	US-09-949-016-445	Sequence 445, App
c1294	32.4	3.1	4488	3	US-08-406-030A-3	Sequence 3, Appli
1295	32.4	3.1	6108	3	US-09-949-016-12213	Sequence 12213, A
1296	32.4	3.1	7017	3	US-09-949-016-67	Sequence 67, Appl
1297	32.4	3.1	7035	3	US-09-902-540-878	Sequence 878, App
1298	32.4	3.1	9333	3	US-09-902-540-930	Sequence 930, App
1299	32.4	3.1	10301	3	US-09-902-540-985	Sequence 985, App
c1300	32.4	3.1	10916	3	US-09-902-540-1057	Sequence 1057, Ap
1301	32.4	3.1	11604	3	US-09-385-028-13	Sequence 13, Appl
1302	32.4	3.1	11604	3	US-09-726-614-13	Sequence 13, Appl
1303	32.4	3.1	11604	3	US-09-385-040-13	Sequence 13, Appl
c1304	32.4	3.1	12323	3	US-09-949-016-16703	Sequence 16703, A
1305	32.4	3.1	13518	3	US-09-949-016-16687	Sequence 16687, A
c1306	32.4	3.1	14207	3	US-09-949-016-12187	Sequence 12187, A
c1307	32.4	3.1	14207	3	US-09-949-016-17460	Sequence 17460, A
1308	32.4	3.1	14467	3	US-09-902-540-1058	Sequence 1058, Ap
1309	32.4	3.1	15079	3	US-09-385-028-1	Sequence 1, Appli
1310	32.4	3.1	15079	3	US-09-726-614-1	Sequence 1, Appli
1311	32.4	3.1	15120	3	US-09-385-040-1	Sequence 1, Appli
1312	32.4	3.1	15923	3	US-09-902-540-1095	Sequence 1095, Ap
c1313	32.4	3.1	16139	3	US-09-949-016-13278	Sequence 13278, A
1314	32.4	3.1	16448	3	US-09-902-540-9686	Sequence 9686, Ap
c1315	32.4	3.1	16450	3	US-09-902-540-1098	Sequence 1098, Ap
c1316	32.4	3.1	19394	3	US-09-902-540-1172	Sequence 1172, Ap
1317	32.4	3.1	24754	3	US-09-902-540-1230	Sequence 1230, Ap
1318	32.4	3.1	26167	3	US-09-454-466-1	Sequence 1, Appli
1319	32.4	3.1	26729	3	US-10-283-247-6	Sequence 6, Appli
1320	32.4	3.1	27160	3	US-09-949-016-17378	Sequence 17378, A
1321	32.4	3.1	36242	3	US-09-949-016-12996	Sequence 12996, A
1322	32.4	3.1	36242	3	US-09-949-016-12997	Sequence 12997, A
1323	32.4	3.1	36242	3	US-09-949-016-12998	Sequence 12998, A
1324	32.4	3.1	36242	3	US-09-949-016-12999	Sequence 12999, A
1325	32.4	3.1	36242	3	US-09-949-016-13000	Sequence 13000, A
c1326	32.4	3.1	36954	3	US-09-949-016-15304	Sequence 15304, A
c1327	32.4	3.1	40546	3	US-09-949-016-12847	Sequence 12847, A
c1328	32.4	3.1	40546	3	US-09-949-016-12915	Sequence 12915, A
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ALIGNMENTS

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RESULT 1
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; Sequence 3, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Chen, Jian
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Li,Hanzhong
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  VanLookeren,Menno
;  APPLICANT:  Vandlen,Richard
;  APPLICANT:  Watanabe,Colin
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William
;  APPLICANT:  Yansura,Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P1(US)
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;  PRIOR FILING DATE: 2000-12-01
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US-09-747-259-3

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Qy        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780
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Db        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780

Qy        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840

Qy        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900

Qy        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTC 960

Qy        961 TTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATT 1020

Qy       1021 ATTAAACTGATGAACACATCCCCAAAA 1047
              ||||||||||||||||||||||||||
Db       1021 ATTAAACTGATGAACACATCCCCAAAA 1047


RESULT 2
US-09-949-016-5387
; Sequence 5387, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5387
;   LENGTH: 1047
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5387

  Query Match            98.7%;  Score 1033.4;  DB 3;  Length 1047;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-250;
  Matches 1045;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60

Qy         61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120

Qy        121 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180

Qy        181 CGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 240

Qy        241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300

Qy        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360

Qy        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
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Qy        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480

Qy        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540

Qy        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600

Qy        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660

Qy        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720

Qy        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780

Qy        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840

Qy        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900

Qy        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGG-CCCCGCAGGCTGCCT 959
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCT 960

Qy        960 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1020

Qy       1020 TATTAAACTGATGAACACATCCCCAAA 1046
              |||||||||||||||||||||||||| |
Db       1021 TATTAAACTGATGAACACATCCCCAGA 1047
```

RESULT 3
US-09-480-297A-22
; Sequence 22, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)..(705)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (166)..()
; OTHER INFORMATION:

US-09-480-297A-22

Query Match 98.2%; Score 1028.4; DB 3; Length 1107;
Best Local Similarity 99.8%; Pred. No. 2.4e-249;
Matches 1040; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCT 125

Qy         61 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCCCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT 185

Qy        121 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CAGGGGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT 245

Qy        181 CGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CGGCCAGGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT 305

Qy        241 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGC 365

Qy        301 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCG 425

Qy        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 485

Qy        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 545

Qy        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 605

Qy        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 665

Qy        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 725

Qy        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGG 785

Qy        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 845

Qy        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 905

Qy        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 965

Qy        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGG-CCCCGCAGGCTGCCT 959
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        966 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCT 1025

Qy        960 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1085
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Qy       1020 TATTAAACTGATGAACACATCC 1041
              |||||||||||||||||||||
Db       1086 TATTAAACTGATGAACACATCC 1107
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RESULT 4
US-09-949-016-17129
; Sequence 17129, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17129
; LENGTH: 5884
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17129

Query Match 62.2%; Score 651; DB 3; Length 5884;
Best Local Similarity 97.7%; Pred. No. 5e-154;
Matches 671; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

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Qy        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
              |||  | |   ||  |     | ||||||||||||||||||||||||||||||||||||
Db       3198 CTCACTGTGCACCCCGTCCCGCAGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 3257

Qy        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3258 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 3317

Qy        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3318 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 3377

Qy        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3378 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 3437

Qy        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3438 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 3497

Qy        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3498 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 3557

Qy        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3558 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 3617

Qy        781 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3618 CAGCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGC 3677

Qy        841 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3678 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTC 3737

Qy        901 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGG-CCCCGCAGGCTGCCT 959
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       3738 CCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCT 3797

Qy        960 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3798 CTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTAT 3857

Qy       1020 TATTAAACTGATGAACACATCCCCAAA 1046
              |||||||||||||||||||||||||| |
Db       3858 TATTAAACTGATGAACACATCCCCAGA 3884
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RESULT 5
US-09-949-016-188268/c
; Sequence 188268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188268
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-188268

Query Match 39.2%; Score 410.2; DB 3; Length 601;
Best Local Similarity 96.5%; Pred. No. 1.1e-93;
Matches 418; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

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Qy        361 CTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 420
              |||  | |   ||  |     | ||||||||||||||||||||||||||||||||||||
Db        433 CTCACTGTGCACCCCGTCCCGCAGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCT 374

Qy        421 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 GGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGC 314

Qy        481 TGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 540
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        313 TGCGCTCAACTCYGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTC 254

Qy        541 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 CCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCA 194

Qy        601 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 CGTCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGG 134

Qy        661 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 CCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGT 74

Qy        721 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 TATTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGA 14

Qy        781 CAGCCCCCCACTG 793
              |||||||||||||
Db         13 CAGCCCCCCACTG 1
```

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RESULT 6
US-09-480-297A-19
; Sequence 19, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 521
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (281)..(281)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (367)..(367)
;   OTHER INFORMATION: unkonwn amino
;   NAME/KEY: misc_feature
;   LOCATION: (437)..(437)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (462)..(462)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (468)..(468)
;   OTHER INFORMATION: unknown amino
US-09-480-297A-19

  Query Match           26.2%;  Score 273.8;  DB 3;  Length 521;
  Best Local Similarity   95.3%;  Pred. No. 2.4e-59;
  Matches  303;  Conservative    0;  Mismatches   13;  Indels    2;  Gaps    2;

Qy        389 GACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGC 448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGC 60

Qy        449 TGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAG 508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAG 120

Qy        509 AGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCT 568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCT 180

Qy        569 GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTG 628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTG 240

Qy        629 CCCCGTTC-AGTGTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCC 687
              |||||||| |||||||||||| |||||||||||||| ||| ||    ||||||||||||
Db        241 CCCCGTTCAAGTGTGACCGCCAAGGCCGTGGGGCCCTTAG-NTGACACCGTGTGCTCCCC 299

Qy        688 AGAGGGCACCCCCTATTT 705
              ||||||  |||  | | |
Db        300 AGAGGGACCCCTATTTAT 317


RESULT 7
US-09-480-297A-20
; Sequence 20, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 521
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(369)
;   OTHER INFORMATION:
;   NAME/KEY: misc_feature
;   LOCATION: (281)..(281)
;   OTHER INFORMATION: unkown amino
;   NAME/KEY: misc_feature
;   LOCATION: (367)..(367)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (437)..(437)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (462)..(462)
;   OTHER INFORMATION: unknown amino
;   NAME/KEY: misc_feature
;   LOCATION: (468)..(468)
;   OTHER INFORMATION: unknown amino
US-09-480-297A-20

  Query Match           26.2%;  Score 273.8;  DB 3;  Length 521;
  Best Local Similarity   95.3%;  Pred. No. 2.4e-59;
  Matches  303;  Conservative    0;  Mismatches   13;  Indels    2;  Gaps    2;

Qy        389 GACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGC 448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGC 60

Qy        449 TGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAG 508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAG 120

Qy        509 AGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCT 568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCT 180

Qy        569 GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTG 628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTG 240

Qy        629 CCCCGTTC-AGTGTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCC 687
              |||||||| |||||||||||| |||||||||||||| ||| ||    ||||||||||||
Db        241 CCCCGTTCAAGTGTGACCGCCAAGGCCGTGGGGCCCTTAG-NTGACACCGTGTGCTCCCC 299

Qy        688 AGAGGGCACCCCCTATTT 705
              ||||||  |||  | | |
Db        300 AGAGGGACCCCTATTTAT 317


RESULT 8
US-09-949-016-188267/c
; Sequence 188267, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
```

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;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188267
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-188267

  Query Match             10.6%;  Score 111;  DB 3;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-18;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        274 CAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGA 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGA 542

Qy        334 GGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCTGGAGATACCG 384
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCTGGAGATACCG 491


RESULT 9
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             5.6%;  Score 58.2;  DB 2;  Length 7218;
  Best Local Similarity   4.5%;  Pred. No. 0.00012;
  Matches   18;  Conservative  224;  Mismatches  157;  Indels    0;  Gaps    0;

Qy        603 TCCCCGTCGGCTGCACCTGCGTGCTGCCCCGTTCAGTGTGACCGCCGAGGCCGTGGGGCC 662
              |:::: ::  :: : ::: : : :: :::: :::  : :  :: ::    :: :    ::
Db       1066 TYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1125

Qy        663 CCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTA 722
              :::   ::   : : : : ::::::      : :::::: ::: : : : ::: :: ::
Db       1126 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1185

Qy        723 TTTATATGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACA 782
              ::: : : :::::::  : :: :::::    :::   : ::::::: : :::      :
Db       1186 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1245

Qy        783 GCCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCAC 842
               :::::: :: :::::::: :::::  ::::  :  ::     :         ::: : :
Db       1246 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1305

Qy        843 CTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTCCC 902
              :::::::  :::::    :: :        : :: : :  :: ::: : ::::  :::::
Db       1306 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1365

Qy        903 TGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTCTT 962
              : :::: :::::  :::::::: :::: :: ::  ::::   :::: :   :: ::::::
Db       1366 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1425

Qy        963 CCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATT 1001
              :::  :::: |   || | |  || | |||| ||| | |
Db       1426 YYYYYYYYYGTACCAAATTCTTCTATCTCTTTAACTACT 1464


RESULT 10
US-09-480-297A-5
; Sequence 5, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 454
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(453)
;   OTHER INFORMATION:
US-09-480-297A-5

  Query Match             5.4%;  Score 56.8;  DB 3;  Length 454;
  Best Local Similarity   51.2%;  Pred. No. 0.00011;
  Matches  133;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy        349 CACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTA 408
              |||| ||| ||||  | | || ||||||   ||| |  |   |  ||   ||   | ||
Db        165 CACCAACCTGCGCAGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGGTA 224

Qy        409 TCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGG 468
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Db        225 CCCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCGG 284

Qy        469 CCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCG 528

Db        285 CGAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCGCCG 344

Qy        529 CCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACAC 588

Db        345 CACCCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCACCATCCCCGT 404

Qy        589 CGAGTTCATCCACGTCCCCG 608

Db        405 GGGCTGCACCTGCGTCCCCG 424


RESULT 11
US-09-480-297A-7
; Sequence 7, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 1385
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (59)..(664)
;   OTHER INFORMATION:
;   NAME/KEY: mat_peptide
;   LOCATION: (110)..()
;   OTHER INFORMATION:
US-09-480-297A-7

  Query Match             5.4%;  Score 56.8;  DB 3;  Length 1385;
  Best Local Similarity   51.2%;  Pred. No. 0.00016;
  Matches  133;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy        349 CACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTA 408

Db        313 CACCAACCTGCGCAGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGGTA 372

Qy        409 TCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGG 468

Db        373 CCCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCGG 432

Qy        469 CCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCG 528

Db        433 CGAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCGCCG 492

Qy        529 CCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACAC 588

Db        493 CACCCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCACCATCCCCGT 552

Qy        589 CGAGTTCATCCACGTCCCCG 608

Db        553 GGGCTGCACCTGCGTCCCCG 572


RESULT 12
US-09-747-259-7
; Sequence 7, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Chen, Jian
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Li,Hanzhong
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  VanLookeren,Menno
;  APPLICANT:  Vandlen,Richard
;  APPLICANT:  Watanabe,Colin
;  APPLICANT:  Williams,P.Mickey
;  APPLICANT:  Wood,William
;  APPLICANT:  Yansura,Daniel
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C1P1(US)
;  CURRENT APPLICATION NUMBER: US/09/747,259
;  CURRENT FILING DATE:  2000-12-20
;  PRIOR APPLICATION NUMBER: US 09/311,832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US 60/172,096
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: PCT/US99/31274
;  PRIOR FILING DATE: 1999-12-30
;  PRIOR APPLICATION NUMBER: US 60/175,481
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: PCT/US00/04341
;  PRIOR FILING DATE: 2000-02-18
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 60/191,007
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/07532
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/US00/15264
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: US 60/213,087
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: US 09/644,848
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/242,837
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: PCT/US00/30873
;  PRIOR FILING DATE: 2000-11-10
;  PRIOR APPLICATION NUMBER: US 60/253,646
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 7
;   LENGTH: 1754
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-747-259-7

  Query Match             5.4%;  Score 56.8;  DB 3;  Length 1754;
  Best Local Similarity   51.2%;  Pred. No. 0.00017;
  Matches  133;  Conservative    0;  Mismatches  127;  Indels    0;  Gaps    0;

Qy        349 CACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTA 408

Db        255 CACCAACCTGCGCAGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGGTA 314

Qy        409 TCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGG 468

Db        315 CCCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCGG 374
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Qy        469 CCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCG 528
              |   |||   |       ||  |  ||  |    |   | |  |     | || ||||||||
Db        375 CGAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCGCCG 434

Qy        529 CCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCTGGGGCCTTTGCCTTCCACAC 588
              |   |||  || |  || ||||       ||  |||    |    | |  || ||| |
Db        435 CACCCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCACCATCCCCGT 494

Qy        589 CGAGTTCATCCACGTCCCCG 608
              |  | || |  ||||||||
Db        495 GGGCTGCACCTGCGTCCCCG 514


RESULT 13
US-09-480-297A-13
; Sequence 13, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
;  APPLICANT: Gorman, Daniel M.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
;  FILE REFERENCE: DX0917K
;  CURRENT APPLICATION NUMBER: US/09/480,297A
;  CURRENT FILING DATE:  2000-01-10
;  PRIOR APPLICATION NUMBER: 60/115,506
;  PRIOR FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 504
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (19)..(501)
;   OTHER INFORMATION:
;   NAME/KEY: mat_peptide
;   LOCATION: (67)..()
;   OTHER INFORMATION:
US-09-480-297A-13

  Query Match             5.1%;  Score 53.8;  DB 3;  Length 504;
  Best Local Similarity   56.9%;  Pred. No. 0.00063;
  Matches  119;  Conservative    0;  Mismatches   87;  Indels    3;  Gaps    1;

Qy        341 GAGGCAGACACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAG 400
              || | |  |  | ||    |  |||||||||||||     ||||||  ||   |
Db        205 GATGGACCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTG 264

Qy        401 GACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCA 460
               ||||    || ||| | |||  |  ||||   |||||||||     ||| ||      |
Db        265 AACCGGCTCCCCCAGGACCTGTACCACGCCCGTTGCCTGTGCCCGCACTGCGTCAGCCTA 324

Qy        461 CGGACGGGCCGCGAGACAGCTGCGCT---CAACTCCGTGCGGCTGCTCCAGAGCCTGCTG 517
              | ||| |||  | | |  |   | |    |||||| | || |||    ||| | || |
Db        325 CAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGAGCTGCTCTACCACAACCAGACT 384

Qy        518 GTGCTGCGCCGCCGGCCCTGCTCCCGCGA 546
              ||  |   ||| ||||| |||    ||||
Db        385 GTCTTCTACCGGCGGCCATGCCATGGCGA 413


RESULT 14
US-09-836-385-1
; Sequence 1, Application US/09836385
; Patent No. 6676939
; GENERAL INFORMATION:
;  APPLICANT: Hurst, Stephen D.
;  APPLICANT:  Zurawski, Sandra M.
;  APPLICANT:  Rennick, Donna M.
;  TITLE OF INVENTION: Cytokine Uses; Compositions; Methods
;  FILE REFERENCE: DX01088K
;  CURRENT APPLICATION NUMBER: US/09/836,385
;  CURRENT FILING DATE:  2001-04-17
;  PRIOR APPLICATION NUMBER: US 60/198,488
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 504
;   TYPE: DNA
;   ORGANISM: primate
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (19)..(501)
;   NAME/KEY: mat_peptide
;   LOCATION: (67)..(501)
US-09-836-385-1

  Query Match             5.1%;  Score 53.8;  DB 3;  Length 504;
  Best Local Similarity   56.9%;  Pred. No. 0.00063;
  Matches  119;  Conservative    0;  Mismatches   87;  Indels    3;  Gaps    1;

Qy        341 GAGGCAGACACCCACCAGCGCTCCATCTCACCCTGGAGATACCGTGTGGACACGGATGAG 400
              || | |  |  | ||    |  |||||||||||||     ||||||  ||   |
Db        205 GATGGACCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTG 264

Qy        401 GACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCA 460
               ||||    || ||| | |||  |  ||||   |||||||||     ||| ||      |
Db        265 AACCGGCTCCCCCAGGACCTGTACCACGCCCGTTGCCTGTGCCCGCACTGCGTCAGCCTA 324

Qy        461 CGGACGGGCCGCGAGACAGCTGCGCT---CAACTCCGTGCGGCTGCTCCAGAGCCTGCTG 517
              | ||| |||  | | |  |   | |    |||||| | || |||    ||| | || |
Db        325 CAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGAGCTGCTCTACCACAACCAGACT 384

Qy        518 GTGCTGCGCCGCCGGCCCTGCTCCCGCGA 546
              ||  |   ||| ||||| |||    ||||
Db        385 GTCTTCTACCGGCGGCCATGCCATGGCGA 413


RESULT 15
US-09-949-016-3137
; Sequence 3137, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3137
;   LENGTH: 1317
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-3137

  Query Match             5.1%;  Score 53.8;  DB 3;  Length 1317;
  Best Local Similarity   56.9%;  Pred. No. 0.00087;
  Matches  119;  Conservative    0;  Mismatches   87;  Indels    3;  Gaps    1;

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OM nucleic - nucleic search, using sw model

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	1003	42.8	4.1	7967	7	US-10-437-963-68611	Sequence 68611, A
	1004	42.6	4.1	580	7	US-10-424-599-2320	Sequence 2320, Ap
	1005	42.6	4.1	606	7	US-10-424-599-95310	Sequence 95310, A
	1006	42.6	4.1	2919	6	US-10-369-493-39075	Sequence 39075, A
	1007	42.6	4.1	2919	6	US-10-369-493-39443	Sequence 39443, A
	1008	42.6	4.1	2919	6	US-10-369-493-39826	Sequence 39826, A
c	1009	42.4	4.0	291	10	US-11-037-782-201	Sequence 201, App
	1010	42.4	4.0	291	10	US-11-037-782-202	Sequence 202, App
c	1011	42.4	4.0	471	10	US-11-037-782-205	Sequence 205, App
	1012	42.4	4.0	471	10	US-11-037-782-206	Sequence 206, App
c	1013	42.4	4.0	741	7	US-10-437-963-61403	Sequence 61403, A
	1014	42.4	4.0	956	5	US-10-027-632-31508	Sequence 31508, A
	1015	42.4	4.0	956	6	US-10-027-632-31508	Sequence 31508, A
	1016	42.4	4.0	1056	3	US-09-906-179A-121	Sequence 121, App
	1017	42.4	4.0	1056	3	US-09-906-179A-122	Sequence 122, App
c	1018	42.4	4.0	1211	8	US-10-425-115-93385	Sequence 93385, A
	1019	42.4	4.0	1629	3	US-09-880-107-3799	Sequence 3799, Ap
	1020	42.4	4.0	1629	5	US-10-146-473-12	Sequence 12, Appl
c	1021	42.4	4.0	2180	6	US-10-094-749-422	Sequence 422, App
c	1022	42.4	4.0	3133	6	US-10-017-161-1483	Sequence 1483, Ap
c	1023	42.4	4.0	3133	6	US-10-292-798-1191	Sequence 1191, Ap
c	1024	42.2	4.0	985	8	US-10-425-115-91623	Sequence 91623, A
	1025	42.2	4.0	1475	3	US-09-795-651-72	Sequence 72, Appl
c	1026	42.2	4.0	3233	5	US-10-027-632-113126	Sequence 113126,
c	1027	42.2	4.0	3233	5	US-10-027-632-113127	Sequence 113127,
c	1028	42.2	4.0	3233	5	US-10-027-632-113128	Sequence 113128,
c	1029	42.2	4.0	3233	6	US-10-027-632-113126	Sequence 113126,
c	1030	42.2	4.0	3233	6	US-10-027-632-113127	Sequence 113127,
c	1031	42.2	4.0	3233	6	US-10-027-632-113128	Sequence 113128,
	1032	42.2	4.0	3492	6	US-10-131-409-67	Sequence 67, Appl
	1033	42.2	4.0	3492	6	US-10-139-854-67	Sequence 67, Appl
	1034	42.2	4.0	3492	6	US-10-150-813-67	Sequence 67, Appl
	1035	42.2	4.0	3492	6	US-10-150-811-67	Sequence 67, Appl
	1036	42.2	4.0	3493	6	US-10-131-409-68	Sequence 68, Appl
	1037	42.2	4.0	3493	6	US-10-139-854-68	Sequence 68, Appl

1038	42.2	4.0	3493	6	US-10-150-813-68	Sequence 68, Appl
1039	42.2	4.0	3493	6	US-10-150-811-68	Sequence 68, Appl
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1042	42.2	4.0	9087	6	US-10-131-409-13	Sequence 13, Appl
1043	42.2	4.0	9087	6	US-10-139-854-13	Sequence 13, Appl
1044	42.2	4.0	9087	6	US-10-150-813-13	Sequence 13, Appl
1045	42.2	4.0	9087	6	US-10-150-811-13	Sequence 13, Appl
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1048	42.2	4.0	11389	6	US-10-241-220-51	Sequence 51, Appl
1049	42.2	4.0	11389	6	US-10-172-118-1465	Sequence 1465, Ap
1050	42.2	4.0	11389	6	US-10-295-027-749	Sequence 749, App
1051	42.2	4.0	11389	6	US-10-240-145-20	Sequence 20, Appl
1052	42.2	4.0	11389	7	US-10-342-887-1465	Sequence 1465, Ap
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1054	42.2	4.0	11389	8	US-10-775-920-25	Sequence 25, Appl
1055	42.2	4.0	11389	8	US-10-872-972-51	Sequence 51, Appl
1056	42.2	4.0	11389	8	US-10-872-991-51	Sequence 51, Appl
1057	42.2	4.0	11389	9	US-10-291-128-20	Sequence 20, Appl
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1061	42	4.0	1131	8	US-10-723-860-6627	Sequence 6627, Ap
1062	42	4.0	11058	6	US-10-156-761-3629	Sequence 3629, Ap
1065	41.8	4.0	697	8	US-10-425-115-72220	Sequence 72220, A
1066	41.8	4.0	1173	6	US-10-214-446-9	Sequence 9, Appli
c1067	41.8	4.0	1286	7	US-10-437-963-49695	Sequence 49695, A
c1068	41.8	4.0	1755	7	US-10-437-963-28113	Sequence 28113, A
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c1071	41.6	4.0	653	8	US-10-363-345A-25629	Sequence 25629, A
1072	41.6	4.0	653	8	US-10-363-345A-25630	Sequence 25630, A
c1073	41.6	4.0	653	9	US-10-363-483A-25629	Sequence 25629, A
1074	41.6	4.0	653	9	US-10-363-483A-25630	Sequence 25630, A
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c1076	41.6	4.0	765	7	US-10-437-963-8013	Sequence 8013, Ap
c1077	41.6	4.0	805	7	US-10-424-599-61903	Sequence 61903, A
1078	41.6	4.0	1065	7	US-10-437-963-50018	Sequence 50018, A
1079	41.6	4.0	1397	8	US-10-425-115-155311	Sequence 155311,
c1080	41.6	4.0	3163	6	US-10-017-161-1857	Sequence 1857, Ap
c1081	41.6	4.0	3163	6	US-10-292-798-1513	Sequence 1513, Ap
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1084	41.4	4.0	600	8	US-10-363-345A-39088	Sequence 39088, A
c1085	41.4	4.0	600	9	US-10-363-483A-39087	Sequence 39087, A
1086	41.4	4.0	600	9	US-10-363-483A-39088	Sequence 39088, A
1087	41.4	4.0	700	8	US-10-425-115-14077	Sequence 14077, A
1088	41.4	4.0	746	8	US-10-425-115-38689	Sequence 38689, A
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1090	41.4	4.0	822	8	US-10-425-115-102047	Sequence 102047,
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1092	41.4	4.0	2961	7	US-10-437-963-56840	Sequence 56840, A
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c1094	41.4	4.0	12425	3	US-09-976-740-50	Sequence 50, Appl
c1095	41.4	4.0	12425	5	US-10-023-529-50	Sequence 50, Appl
c1096	41.4	4.0	12425	5	US-10-023-523-50	Sequence 50, Appl
c1097	41.4	4.0	12425	7	US-10-616-187-50	Sequence 50, Appl
c1098	41.4	4.0	12425	7	US-10-671-242-50	Sequence 50, Appl
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1104	41	3.9	417	7	US-10-437-963-61582	Sequence 61582, A
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1106	41	3.9	503	8	US-10-425-115-13601	Sequence 13601, A
c1107	41	3.9	638	7	US-10-437-963-1432	Sequence 1432, Ap
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1113	41	3.9	2432	7	US-10-437-963-64501	Sequence 64501, A
1114	41	3.9	2466	6	US-10-156-761-5788	Sequence 5788, Ap
c1115	41	3.9	2703	7	US-10-437-963-48228	Sequence 48228, A
1116	41	3.9	3040	7	US-10-282-122A-14876	Sequence 14876, A
1117	41	3.9	24525	5	US-10-087-192-1180	Sequence 1180, Ap
c1118	40.8	3.9	291	10	US-11-037-782-199	Sequence 199, App
1119	40.8	3.9	291	10	US-11-037-782-200	Sequence 200, App
c1120	40.8	3.9	471	9	US-10-491-997-91	Sequence 91, Appl
c1121	40.8	3.9	471	10	US-11-037-782-203	Sequence 203, App
1122	40.8	3.9	471	10	US-11-037-782-204	Sequence 204, App
1123	40.8	3.9	600	10	US-11-060-756-3921	Sequence 3921, Ap
1124	40.8	3.9	600	10	US-11-060-756-8193	Sequence 8193, Ap
c1125	40.8	3.9	607	9	US-10-487-901-5694	Sequence 5694, Ap
1126	40.8	3.9	673	8	US-10-425-115-11145	Sequence 11145, A
c1127	40.8	3.9	771	7	US-10-424-599-107958	Sequence 107958,
c1128	40.8	3.9	873	9	US-10-487-901-5695	Sequence 5695, Ap
1129	40.8	3.9	891	6	US-10-156-761-3573	Sequence 3573, Ap
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1131	40.8	3.9	1635	5	US-10-087-192-509	Sequence 509, App
c1132	40.8	3.9	1863	7	US-10-437-963-86389	Sequence 86389, A
c1133	40.8	3.9	2156	7	US-10-437-963-614	Sequence 614, App
1134	40.8	3.9	2164	7	US-10-437-963-59826	Sequence 59826, A
1135	40.8	3.9	2528	9	US-10-489-740-45	Sequence 45, Appl
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1137	40.8	3.9	2943	6	US-10-320-351-8	Sequence 8, Appli
1138	40.8	3.9	4707	9	US-10-499-353A-471	Sequence 471, App
1139	40.8	3.9	22147	5	US-10-087-192-508	Sequence 508, App
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1143	40.6	3.9	751	6	US-10-027-632-21996	Sequence 21996, A
1144	40.6	3.9	751	6	US-10-027-632-21997	Sequence 21997, A
c1145	40.6	3.9	809	7	US-10-424-599-26988	Sequence 26988, A
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1147	40.6	3.9	1026	6	US-10-029-386-20398	Sequence 20398, A
1148	40.6	3.9	1026	6	US-10-094-886-147	Sequence 147, App
1149	40.6	3.9	1026	6	US-10-094-886-149	Sequence 149, App
c1150	40.6	3.9	1117	9	US-10-450-763-13998	Sequence 13998, A
c1151	40.6	3.9	1164	6	US-10-156-761-149	Sequence 149, App
1152	40.6	3.9	1215	7	US-10-260-238-1432	Sequence 1432, Ap
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1154	40.6	3.9	2941	7	US-10-641-643-1065	Sequence 1065, Ap
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1156	40.6	3.9	4349	7	US-10-721-693-8	Sequence 8, Appli
1157	40.6	3.9	4349	8	US-10-852-997-8	Sequence 8, Appli
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1160	40.4	3.9	403	6	US-10-366-791-25	Sequence 25, Appl
1161	40.4	3.9	403	7	US-10-742-220-24	Sequence 24, Appl
1162	40.4	3.9	403	7	US-10-742-220-25	Sequence 25, Appl
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c1167	40.4	3.9	805	7	US-10-437-963-99490	Sequence 99490, A
1168	40.4	3.9	821	8	US-10-425-115-131043	Sequence 131043,
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1172	40.4	3.9	1167	7	US-10-437-963-54786	Sequence 54786, A
1173	40.4	3.9	1168	3	US-09-443-704-23	Sequence 23, Appl
1174	40.4	3.9	1168	5	US-10-008-118A-23	Sequence 23, Appl
1175	40.4	3.9	1200	7	US-10-374-780A-1054	Sequence 1054, Ap
1176	40.4	3.9	1200	7	US-10-412-699B-1305	Sequence 1305, Ap
1177	40.4	3.9	1239	6	US-10-156-761-5343	Sequence 5343, Ap
1178	40.4	3.9	1392	7	US-10-417-700A-122	Sequence 122, App
c1179	40.4	3.9	1767	8	US-10-739-930-1720	Sequence 1720, Ap
1180	40.4	3.9	38146	8	US-10-719-993-6860	Sequence 6860, Ap
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1182	40.2	3.8	613	8	US-10-425-115-177644	Sequence 177644,
1183	40.2	3.8	630	7	US-10-437-963-18774	Sequence 18774, A
c1184	40.2	3.8	675	7	US-10-767-701-15502	Sequence 15502, A
c1185	40.2	3.8	740	8	US-10-425-115-131885	Sequence 131885,

1186	40.2	3.8	756	8	US-10-425-115-87665	Sequence 87665, A
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1190	40.2	3.8	855	6	US-10-369-493-31623	Sequence 31623, A
c1191	40.2	3.8	1117	6	US-10-017-161-1403	Sequence 1403, Ap
c1192	40.2	3.8	1117	6	US-10-292-798-1141	Sequence 1141, Ap
1193	40.2	3.8	1431	6	US-10-084-846A-45	Sequence 45, Appl
1194	40.2	3.8	59816	6	US-10-084-846A-1	Sequence 1, Appli
c1195	40.2	3.8	59816	6	US-10-084-846A-2	Sequence 2, Appli
1196	40	3.8	40	3	US-09-854-280-10	Sequence 10, Appl
1197	40	3.8	40	3	US-09-854-208-10	Sequence 10, Appl
1198	40	3.8	40	3	US-09-874-503-21	Sequence 21, Appl
1199	40	3.8	40	3	US-09-747-259-21	Sequence 21, Appl
1201	40	3.8	40	3	US-09-908-827-21	Sequence 21, Appl
1203	40	3.8	40	5	US-10-000-157-21	Sequence 21, Appl
1208	40	3.8	40	5	US-10-036-160-14	Sequence 14, Appl
1213	40	3.8	40	6	US-10-410-927-21	Sequence 21, Appl
1214	40	3.8	40	6	US-10-410-374-21	Sequence 21, Appl
1215	40	3.8	40	6	US-10-410-552-21	Sequence 21, Appl
1216	40	3.8	40	6	US-10-458-442-21	Sequence 21, Appl
1217	40	3.8	40	7	US-10-408-385-21	Sequence 21, Appl
1218	40	3.8	40	8	US-10-884-091-14	Sequence 14, Appl
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1225	40	3.8	1846	6	US-10-027-632-259214	Sequence 259214,
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c1227	40	3.8	2344	3	US-09-814-353-19093	Sequence 19093, A
c1228	40	3.8	4545	6	US-10-347-470A-29	Sequence 29, Appl
c1229	40	3.8	4545	7	US-10-322-281-585	Sequence 585, App
c1230	40	3.8	5452	6	US-10-017-161-1481	Sequence 1481, Ap
c1231	40	3.8	5452	6	US-10-292-798-1189	Sequence 1189, Ap
1232	40	3.8	77294	8	US-10-729-802-1	Sequence 1, Appli
c1233	40	3.8	77536	3	US-09-940-316B-1	Sequence 1, Appli
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1235	39.8	3.8	719	7	US-10-437-963-97276	Sequence 97276, A
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1237	39.8	3.8	775	7	US-10-767-701-1230	Sequence 1230, Ap
1238	39.8	3.8	789	7	US-10-437-963-20496	Sequence 20496, A
1239	39.8	3.8	823	8	US-10-425-115-53676	Sequence 53676, A
1240	39.8	3.8	900	8	US-10-425-115-72218	Sequence 72218, A
c1241	39.8	3.8	916	7	US-10-437-963-89595	Sequence 89595, A
1242	39.8	3.8	1296	7	US-10-437-963-99652	Sequence 99652, A
1243	39.8	3.8	1347	7	US-10-767-701-11203	Sequence 11203, A
1244	39.8	3.8	1754	7	US-10-425-114-28227	Sequence 28227, A
c1245	39.8	3.8	1969	7	US-10-437-963-100354	Sequence 100354,
1246	39.6	3.8	492	7	US-10-424-599-129863	Sequence 129863,
1247	39.6	3.8	528	7	US-10-424-599-42496	Sequence 42496, A
1250	39.6	3.8	671	7	US-10-437-963-15288	Sequence 15288, A
c1253	39.6	3.8	1590	6	US-10-156-761-763	Sequence 763, App
1254	39.6	3.8	1806	8	US-10-425-115-122005	Sequence 122005,
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1256	39.6	3.8	8867	3	US-09-932-367A-22	Sequence 22, Appl
1257	39.6	3.8	77536	3	US-09-940-316B-1	Sequence 1, Appli
c1258	39.4	3.8	263	7	US-10-021-323-16665	Sequence 16665, A
1259	39.4	3.8	301	8	US-10-425-115-86895	Sequence 86895, A
1260	39.4	3.8	573	7	US-10-767-701-4301	Sequence 4301, Ap
1261	39.4	3.8	658	7	US-10-767-701-4204	Sequence 4204, Ap
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	31	56	5.3	201	8	US-10-995-561-29266	Sequence 29266, A
	32	56	5.3	201	8	US-10-995-561-65567	Sequence 65567, A
	33	53.8	5.1	644	11	US-11-247-304-22	Sequence 22, Appl
	34	53.8	5.1	644	11	US-11-251-011-22	Sequence 22, Appl
	35	53.8	5.1	644	11	US-11-251-012-22	Sequence 22, Appl
	37	52.2	5.0	1320	11	US-11-103-195-155	Sequence 155, App
	38	52.2	5.0	1320	14	US-11-102-240-155	Sequence 155, App
	39	45.4	4.3	1170	11	US-11-096-568A-12748	Sequence 12748, A
c	40	42.4	4.0	405	14	US-11-175-690-168	Sequence 168, App
c	41	42.4	4.0	405	14	US-11-175-690-169	Sequence 169, App
	42	42.4	4.0	1629	9	US-10-501-035-167	Sequence 167, App
	43	42.2	4.0	9087	7	US-10-455-772-275	Sequence 275, App
	44	42.2	4.0	9087	7	US-10-455-772-283	Sequence 283, App
	45	42.2	4.0	9087	7	US-10-455-772-285	Sequence 285, App
	46	42.2	4.0	9087	7	US-10-455-772-287	Sequence 287, App
c	47	41.8	4.0	118063	9	US-10-330-773-156	Sequence 156, App
	48	41.2	3.9	914	10	US-10-301-480-548550	Sequence 548550,
	49	41.2	3.9	914	10	US-10-301-480-1161959	Sequence 1161959,
	50	40.8	3.9	355211	9	US-10-330-773-242	Sequence 242, App
	51	40.6	3.9	1118	14	US-11-124-367A-28	Sequence 28, Appl
	52	40.6	3.9	2736	8	US-10-858-730-38	Sequence 38, Appl
c	53	40.6	3.9	95050	8	US-10-857-780-7	Sequence 7, Appli
c	54	40.4	3.9	1753	11	US-11-096-568A-23954	Sequence 23954, A
c	55	40.4	3.9	8651	8	US-10-432-483-48	Sequence 48, Appl
	57	40	3.8	1575	6	US-09-925-065A-58444	Sequence 58444, A
	58	40	3.8	1575	9	US-10-301-480-159682	Sequence 159682,
	59	40	3.8	1575	10	US-10-301-480-773091	Sequence 773091,
	60	40	3.8	1846	9	US-10-301-480-94021	Sequence 94021, A
	61	40	3.8	1846	10	US-10-301-480-707430	Sequence 707430,
c	62	40	3.8	100000	14	US-11-124-367A-5044	Sequence 5044, Ap
c	63	40	3.8	113193	7	US-10-478-943D-1	Sequence 1, Appli
	64	39.8	3.8	6264	14	US-11-075-185-58	Sequence 58, Appl
	65	39.8	3.8	78869	14	US-11-075-185-1	Sequence 1, Appli
c	66	39.4	3.8	5153	9	US-10-501-035-110	Sequence 110, App
	67	39.2	3.7	766	6	US-09-925-065A-8156	Sequence 8156, Ap
	68	39.2	3.7	766	9	US-10-301-480-109393	Sequence 109393,
	69	39.2	3.7	766	10	US-10-301-480-722802	Sequence 722802,
c	70	39.2	3.7	70513	8	US-10-995-561-13368	Sequence 13368, A
	71	39	3.7	4396	14	US-11-000-688-41	Sequence 41, Appl
c	72	38.6	3.7	3108	8	US-10-477-507A-1	Sequence 1, Appli
	73	38.4	3.7	2164	8	US-10-750-185-41189	Sequence 41189, A
	74	38.4	3.7	2164	8	US-10-750-623-41189	Sequence 41189, A
	75	38.2	3.6	2792	8	US-10-821-234-79	Sequence 79, Appl
c	76	38.2	3.6	5382	9	US-10-501-035-116	Sequence 116, App
	77	38	3.6	1802	11	US-11-096-568A-11817	Sequence 11817, A
c	78	38	3.6	2639	11	US-11-072-512-684	Sequence 684, App
	79	37.8	3.6	469	6	US-09-925-065A-147692	Sequence 147692,
	80	37.8	3.6	491	6	US-09-925-065A-562090	Sequence 562090,
	81	37.8	3.6	499	6	US-09-925-065A-562089	Sequence 562089,
	82	37.8	3.6	606	6	US-09-925-065A-515258	Sequence 515258,
c	83	37.8	3.6	611	9	US-10-301-480-216324	Sequence 216324,
c	84	37.8	3.6	611	10	US-10-301-480-829733	Sequence 829733,
c	85	37.8	3.6	614	6	US-09-925-065A-117599	Sequence 117599,
	86	37.8	3.6	1851	11	US-11-096-568A-11082	Sequence 11082, A
c	87	37.8	3.6	191684	14	US-11-121-086-2	Sequence 2, Appli
	88	37.6	3.6	437	6	US-09-925-065A-291337	Sequence 291337,
	89	37.6	3.6	437	6	US-09-925-065A-291338	Sequence 291338,
	90	37.6	3.6	437	6	US-09-925-065A-291339	Sequence 291339,
c	91	37.6	3.6	465	6	US-09-925-065A-208188	Sequence 208188,
c	92	37.6	3.6	472	6	US-09-925-065A-578824	Sequence 578824,
c	93	37.6	3.6	475	6	US-09-925-065A-187533	Sequence 187533,
c	94	37.6	3.6	476	6	US-09-925-065A-187532	Sequence 187532,
c	95	37.6	3.6	477	10	US-10-301-480-251092	Sequence 251092,
c	96	37.6	3.6	477	10	US-10-301-480-864501	Sequence 864501,
	97	37.6	3.6	484	6	US-09-925-065A-152750	Sequence 152750,
	98	37.6	3.6	484	6	US-09-925-065A-152751	Sequence 152751,
	99	37.6	3.6	484	6	US-09-925-065A-152752	Sequence 152752,
	100	37.6	3.6	484	6	US-09-925-065A-563830	Sequence 563830,
	101	37.6	3.6	487	10	US-10-301-480-246473	Sequence 246473,
	102	37.6	3.6	487	10	US-10-301-480-246474	Sequence 246474,
	103	37.6	3.6	487	10	US-10-301-480-246475	Sequence 246475,

	104	37.6	3.6	487	10	US-10-301-480-859882 Sequence 859882,
	105	37.6	3.6	487	10	US-10-301-480-859883 Sequence 859883,
	106	37.6	3.6	487	10	US-10-301-480-859884 Sequence 859884,
c	107	37.6	3.6	488	6	US-09-925-065A-208187 Sequence 208187,
c	108	37.6	3.6	488	6	US-09-925-065A-208189 Sequence 208189,
c	109	37.6	3.6	497	6	US-09-925-065A-578827 Sequence 578827,
c	110	37.6	3.6	499	6	US-09-925-065A-578822 Sequence 578822,
c	111	37.6	3.6	500	6	US-09-925-065A-578825 Sequence 578825,
c	112	37.6	3.6	500	6	US-09-925-065A-578826 Sequence 578826,
c	113	37.6	3.6	501	6	US-09-925-065A-588413 Sequence 588413,
c	114	37.6	3.6	501	10	US-10-301-480-241898 Sequence 241898,
c	115	37.6	3.6	501	10	US-10-301-480-855307 Sequence 855307,
c	116	37.6	3.6	503	6	US-09-925-065A-158057 Sequence 158057,
c	117	37.6	3.6	503	6	US-09-925-065A-158058 Sequence 158058,
c	118	37.6	3.6	512	10	US-10-301-480-295766 Sequence 295766,
c	119	37.6	3.6	512	10	US-10-301-480-295767 Sequence 295767,
c	120	37.6	3.6	512	10	US-10-301-480-909175 Sequence 909175,
c	121	37.6	3.6	512	10	US-10-301-480-909176 Sequence 909176,
	122	37.6	3.6	1587	8	US-10-775-169-31 Sequence 31, Appl
c	123	37.6	3.6	16917	14	US-11-124-367A-5000 Sequence 5000, Ap
c	124	37.4	3.6	611	9	US-10-301-480-216323 Sequence 216323,
c	125	37.4	3.6	611	9	US-10-301-480-216325 Sequence 216325,
c	126	37.4	3.6	611	10	US-10-301-480-829732 Sequence 829732,
c	127	37.4	3.6	611	10	US-10-301-480-829734 Sequence 829734,
c	128	37.4	3.6	614	6	US-09-925-065A-117598 Sequence 117598,
c	129	37.4	3.6	614	6	US-09-925-065A-117600 Sequence 117600,
	130	37.4	3.6	1212	10	US-10-503-511-1 Sequence 1, Appli
c	131	37.4	3.6	1557	8	US-10-996-217A-6 Sequence 6, Appli
	132	37.4	3.6	2569	11	US-11-072-512-452 Sequence 452, App
	133	37.4	3.6	4770	7	US-10-496-351-3 Sequence 3, Appli
c	134	37.4	3.6	82746	7	US-10-496-351-56 Sequence 56, Appl
c	135	37.2	3.6	465	6	US-09-925-065A-208186 Sequence 208186,
c	136	37.2	3.6	467	10	US-10-301-480-295765 Sequence 295765,
c	137	37.2	3.6	467	10	US-10-301-480-909174 Sequence 909174,
c	138	37.2	3.6	476	9	US-10-301-480-3350 Sequence 3350, Ap
c	139	37.2	3.6	476	10	US-10-301-480-616759 Sequence 616759,
c	140	37.2	3.6	499	6	US-09-925-065A-578823 Sequence 578823,
c	141	37.2	3.6	503	6	US-09-925-065A-136660 Sequence 136660,
c	142	37.2	3.6	503	10	US-10-301-480-232157 Sequence 232157,
c	143	37.2	3.6	503	10	US-10-301-480-845566 Sequence 845566,
c	144	37.2	3.6	1304	11	US-11-096-568A-7863 Sequence 7863, Ap
c	145	37.2	3.6	1460	11	US-11-096-568A-20290 Sequence 20290, A
	146	37.2	3.6	2556	8	US-10-467-657-5003 Sequence 5003, Ap
	147	37.2	3.6	88421	14	US-11-205-109-1 Sequence 1, Appli
c	148	37.2	3.6	168516	14	US-11-121-086-3 Sequence 3, Appli
c	149	37	3.5	622	6	US-09-925-065A-707593 Sequence 707593,
	150	37	3.5	1278	11	US-11-096-568A-23508 Sequence 23508, A
c	155	37	3.5	12277	8	US-10-477-507A-3 Sequence 3, Appli
	156	37	3.5	113193	7	US-10-478-943D-1 Sequence 1, Appli
c	157	36.6	3.5	622	6	US-09-925-065A-707592 Sequence 707592,
	158	36.6	3.5	840	6	US-09-925-065A-7698 Sequence 7698, Ap
	159	36.6	3.5	840	9	US-10-301-480-108935 Sequence 108935,
	160	36.6	3.5	840	10	US-10-301-480-722344 Sequence 722344,
	161	36.6	3.5	1507	11	US-11-096-568A-7851 Sequence 7851, Ap
	162	36.6	3.5	1658	11	US-11-096-568A-18102 Sequence 18102, A
	163	36.6	3.5	2767	14	US-11-122-329-87 Sequence 87, Appl
	164	36.6	3.5	5015	11	US-11-245-147-166 Sequence 166, App
	165	36.4	3.5	715	8	US-10-750-185-49751 Sequence 49751, A
	166	36.4	3.5	715	8	US-10-750-623-49751 Sequence 49751, A
	167	36.4	3.5	1865	11	US-11-096-568A-25735 Sequence 25735, A
	168	36.4	3.5	2248	6	US-09-925-065A-552673 Sequence 552673,
	169	36.4	3.5	2248	6	US-09-925-065A-687666 Sequence 687666,
	170	36.4	3.5	2248	10	US-10-301-480-530623 Sequence 530623,
	171	36.4	3.5	2248	10	US-10-301-480-1144032 Sequence 1144032,
	172	36.4	3.5	4912	14	US-11-000-688-33 Sequence 33, Appl
	173	36.2	3.5	500	6	US-09-925-065A-520460 Sequence 520460,
c	174	36.2	3.5	1479	11	US-11-096-568A-10978 Sequence 10978, A
c	175	36.2	3.5	4838	11	US-11-154-293-5 Sequence 5, Appli
	176	36.2	3.5	12309	8	US-10-995-561-13450 Sequence 13450, A
	177	36.2	3.5	24054	8	US-10-995-561-13373 Sequence 13373, A
	178	36.2	3.5	25209	8	US-10-995-561-13407 Sequence 13407, A
c	179	36.2	3.5	95832	8	US-10-995-561-13273 Sequence 13273, A
c	180	36	3.4	494	6	US-09-925-065A-557904 Sequence 557904,
	181	36	3.4	496	6	US-09-925-065A-96620 Sequence 96620, A
	182	36	3.4	496	6	US-09-925-065A-133388 Sequence 133388,
	183	36	3.4	496	6	US-09-925-065A-133389 Sequence 133389,
c	184	36	3.4	512	6	US-09-925-065A-557905 Sequence 557905,
	185	36	3.4	590	6	US-09-925-065A-9412 Sequence 9412, Ap
	186	36	3.4	590	6	US-09-925-065A-9413 Sequence 9413, Ap
c	187	36	3.4	590	6	US-09-925-065A-41842 Sequence 41842, A
	188	36	3.4	590	9	US-10-301-480-110649 Sequence 110649,
	189	36	3.4	590	9	US-10-301-480-110650 Sequence 110650,
c	190	36	3.4	590	9	US-10-301-480-143080 Sequence 143080,
	191	36	3.4	590	10	US-10-301-480-724058 Sequence 724058,
	192	36	3.4	590	10	US-10-301-480-724059 Sequence 724059,
c	193	36	3.4	590	10	US-10-301-480-756489 Sequence 756489,
c	194	36	3.4	604	10	US-10-301-480-500173 Sequence 500173,
c	195	36	3.4	604	10	US-10-301-480-1113582 Sequence 1113582,
	196	36	3.4	605	6	US-09-925-065A-438985 Sequence 438985,
	197	36	3.4	808	11	US-11-096-568A-25164 Sequence 25164, A
	198	36	3.4	1325	11	US-11-096-568A-10371 Sequence 10371, A
c	199	36	3.4	1566	11	US-11-096-568A-17637 Sequence 17637, A
	200	36	3.4	2049	8	US-10-750-185-30215 Sequence 30215, A
	201	36	3.4	2049	8	US-10-750-623-30215 Sequence 30215, A
	202	36	3.4	2716	14	US-11-186-282-28 Sequence 28, Appl
c	207	35.8	3.4	1148	11	US-11-096-568A-9581 Sequence 9581, Ap
	208	35.8	3.4	1400	14	US-11-136-527-8100 Sequence 8100, Ap
	209	35.8	3.4	1428	8	US-10-509-464-4 Sequence 4, Appli
c	210	35.8	3.4	1721	11	US-11-096-568A-17949 Sequence 17949, A
	211	35.8	3.4	2018	8	US-10-750-185-63929 Sequence 63929, A
	212	35.8	3.4	2018	8	US-10-750-623-63929 Sequence 63929, A
	213	35.8	3.4	2098	14	US-11-136-527-4004 Sequence 4004, Ap
c	214	35.8	3.4	687411	9	US-10-330-773-26 Sequence 26, Appl
	215	35.6	3.4	330	11	US-11-024-980-1 Sequence 1, Appli
	217	35.6	3.4	535	11	US-11-103-195-159 Sequence 159, App
	218	35.6	3.4	535	14	US-11-102-240-159 Sequence 159, App
c	219	35.6	3.4	600	14	US-11-136-527-5048 Sequence 5048, Ap
	220	35.6	3.4	897	14	US-11-136-527-952 Sequence 952, App
	221	35.6	3.4	923	14	US-11-150-533-15 Sequence 15, Appl
	222	35.6	3.4	1224	14	US-11-117-161-1 Sequence 1, Appli
	223	35.6	3.4	1224	14	US-11-080-257-1 Sequence 1, Appli
	224	35.6	3.4	1909	11	US-11-096-568A-24544 Sequence 24544, A
	225	35.6	3.4	1928	14	US-11-012-668-15 Sequence 15, Appl
	226	35.6	3.4	2870	14	US-11-169-041-63 Sequence 63, Appl
	227	35.6	3.4	3018	7	US-10-496-351-34 Sequence 34, Appl
	228	35.6	3.4	100000	14	US-11-124-367A-5004 Sequence 5004, Ap
c	229	35.4	3.4	736	6	US-09-925-065A-72665 Sequence 72665, A
c	230	35.4	3.4	736	9	US-10-301-480-173904 Sequence 173904,
c	231	35.4	3.4	736	10	US-10-301-480-787313 Sequence 787313,
	232	35.4	3.4	838	6	US-09-925-065A-7318 Sequence 7318, Ap
	233	35.4	3.4	838	6	US-09-925-065A-7319 Sequence 7319, Ap
	234	35.4	3.4	838	6	US-09-925-065A-7320 Sequence 7320, Ap
	235	35.4	3.4	838	6	US-09-925-065A-7321 Sequence 7321, Ap
	236	35.4	3.4	838	6	US-09-925-065A-7322 Sequence 7322, Ap
	237	35.4	3.4	838	9	US-10-301-480-108555 Sequence 108555,
	238	35.4	3.4	838	9	US-10-301-480-108556 Sequence 108556,
	239	35.4	3.4	838	9	US-10-301-480-108557 Sequence 108557,
	240	35.4	3.4	838	9	US-10-301-480-108558 Sequence 108558,
	241	35.4	3.4	838	9	US-10-301-480-108559 Sequence 108559,
	242	35.4	3.4	838	10	US-10-301-480-721964 Sequence 721964,
	243	35.4	3.4	838	10	US-10-301-480-721965 Sequence 721965,
	244	35.4	3.4	838	10	US-10-301-480-721966 Sequence 721966,
	245	35.4	3.4	838	10	US-10-301-480-721967 Sequence 721967,
	246	35.4	3.4	838	10	US-10-301-480-721968 Sequence 721968,
c	247	35.4	3.4	839	10	US-10-301-480-549979 Sequence 549979,
c	248	35.4	3.4	839	10	US-10-301-480-1163388 Sequence 1163388,
	249	35.4	3.4	1046	11	US-11-096-568A-25765 Sequence 25765, A
	250	35.4	3.4	1453	11	US-11-096-568A-16714 Sequence 16714, A
	251	35.4	3.4	1499	11	US-11-096-568A-22080 Sequence 22080, A
	252	35.4	3.4	1648	11	US-11-096-568A-25288 Sequence 25288, A
c	253	35.4	3.4	4510	14	US-11-136-527-1828 Sequence 1828, Ap
	254	35.4	3.4	4614	9	US-10-893-483-46 Sequence 46, Appl
	255	35.4	3.4	5261	9	US-10-893-483-47 Sequence 47, Appl
c	256	35.4	3.4	88421	14	US-11-205-109-1 Sequence 1, Appli
c	257	35.4	3.4	153376	14	US-11-121-086-5 Sequence 5, Appli
c	258	35.2	3.4	666	6	US-09-925-065A-686089 Sequence 686089,

259	35.2	3.4	1227	11	US-11-096-568A-22676	Sequence 22676, A
c 260	35.2	3.4	1286	14	US-11-136-527-1971	Sequence 1971, Ap
c 261	35.2	3.4	1641	11	US-11-096-568A-20413	Sequence 20413, A
c 262	35.2	3.4	1866	8	US-10-955-054A-5	Sequence 5, Appli
263	35.2	3.4	2612	11	US-11-072-512-1320	Sequence 1320, Ap
264	35.2	3.4	2807	14	US-11-214-199-11	Sequence 11, Appl
265	35.2	3.4	4406	11	US-11-072-512-979	Sequence 979, App
c 266	35.2	3.4	9975	7	US-10-496-351-4	Sequence 4, Appli
267	35.2	3.4	13187	14	US-11-136-527-4095	Sequence 4095, Ap
268	35.2	3.4	82746	7	US-10-496-351-56	Sequence 56, Appl
c 269	35.2	3.4	164810	14	US-11-121-086-4	Sequence 4, Appli
270	35	3.3	944	6	US-09-925-065A-708264	Sequence 708264,
271	35	3.3	944	6	US-09-925-065A-708265	Sequence 708265,
272	35	3.3	1305	9	US-10-330-773-646	Sequence 646, App
273	35	3.3	1340	11	US-11-096-568A-10253	Sequence 10253, A
274	35	3.3	1566	14	US-11-143-980-7	Sequence 7, Appli
275	35	3.3	1864	11	US-11-096-568A-21677	Sequence 21677, A
276	35	3.3	2023	8	US-10-995-561-55	Sequence 55, Appl
277	35	3.3	2272	14	US-11-094-519A-12	Sequence 12, Appl
c 278	35	3.3	2292	8	US-10-821-234-168	Sequence 168, App
279	35	3.3	2312	7	US-10-516-635-1	Sequence 1, Appli
280	35	3.3	2312	9	US-10-921-793-55	Sequence 55, Appl
281	35	3.3	2312	9	US-10-931-198-55	Sequence 55, Appl
282	35	3.3	2312	10	US-10-942-042-55	Sequence 55, Appl
283	35	3.3	2312	11	US-11-245-147-91	Sequence 91, Appl
284	35	3.3	2312	11	US-11-245-147-240	Sequence 240, App
285	35	3.3	3376	8	US-10-750-185-33780	Sequence 33780, A
286	35	3.3	3376	8	US-10-750-623-33780	Sequence 33780, A
c 287	35	3.3	3568	8	US-10-750-185-55449	Sequence 55449, A
c 288	35	3.3	3568	8	US-10-750-623-55449	Sequence 55449, A
289	35	3.3	4663	9	US-10-912-971-1	Sequence 1, Appli
c 290	35	3.3	7006	8	US-10-821-234-218	Sequence 218, App
291	35	3.3	12591	8	US-10-995-561-13415	Sequence 13415, A
292	35	3.3	14023	8	US-10-995-561-13221	Sequence 13221, A
c 293	35	3.3	14619	14	US-11-128-061-745	Sequence 745, App
c 294	35	3.3	14619	14	US-11-128-049-745	Sequence 745, App
295	35	3.3	103471	9	US-10-330-773-645	Sequence 645, App
c 296	35	3.3	116856	14	US-11-143-980-1	Sequence 1, Appli
c 297	35	3.3	199130	8	US-10-995-561-13233	Sequence 13233, A
298	35	3.3	246960	14	US-11-121-086-8	Sequence 8, Appli
c 299	34.8	3.3	201	8	US-10-995-561-77211	Sequence 77211, A
c 300	34.8	3.3	512	8	US-10-750-185-1689	Sequence 1689, Ap
c 301	34.8	3.3	512	8	US-10-750-623-1689	Sequence 1689, Ap
c 302	34.8	3.3	673	8	US-10-750-185-45667	Sequence 45667, A
c 303	34.8	3.3	673	8	US-10-750-623-45667	Sequence 45667, A
304	34.8	3.3	675	6	US-09-925-065A-821880	Sequence 821880,
c 305	34.8	3.3	820	8	US-10-750-185-41020	Sequence 41020, A
c 306	34.8	3.3	820	8	US-10-750-623-41020	Sequence 41020, A
307	34.8	3.3	915	7	US-10-782-413-49	Sequence 49, Appl
308	34.8	3.3	1095	7	US-10-782-413-50	Sequence 50, Appl
309	34.8	3.3	1126	7	US-10-782-413-43	Sequence 43, Appl
310	34.8	3.3	1191	8	US-10-750-185-45797	Sequence 45797, A
311	34.8	3.3	1191	8	US-10-750-623-45797	Sequence 45797, A
312	34.8	3.3	1383	6	US-09-925-065A-717011	Sequence 717011,
c 313	34.8	3.3	1611	11	US-11-072-512-1094	Sequence 1094, Ap
c 314	34.8	3.3	1756	11	US-11-096-568A-15790	Sequence 15790, A
c 315	34.8	3.3	1816	14	US-11-128-061-894	Sequence 894, App
c 316	34.8	3.3	1816	14	US-11-128-049-894	Sequence 894, App
317	34.8	3.3	3200	8	US-10-645-441-13	Sequence 13, Appl
318	34.6	3.3	936	8	US-10-750-185-43199	Sequence 43199, A
319	34.6	3.3	936	8	US-10-750-623-43199	Sequence 43199, A
c 320	34.6	3.3	2063	8	US-10-750-185-56693	Sequence 56693, A
c 321	34.6	3.3	2063	8	US-10-750-623-56693	Sequence 56693, A
322	34.6	3.3	8147	7	US-10-469-469-253	Sequence 253, App
c 323	34.4	3.3	438	10	US-10-301-480-480179	Sequence 480179,
c 324	34.4	3.3	438	10	US-10-301-480-1093588	Sequence 1093588,
c 325	34.4	3.3	440	6	US-09-925-065A-414315	Sequence 414315,
c 326	34.4	3.3	591	7	US-10-381-094A-1	Sequence 1, Appli
327	34.4	3.3	918	11	US-11-096-568A-23803	Sequence 23803, A
c 328	34.4	3.3	960	8	US-10-750-185-47103	Sequence 47103, A
c 329	34.4	3.3	960	8	US-10-750-623-47103	Sequence 47103, A
c 330	34.4	3.3	1035	6	US-09-925-065A-33742	Sequence 33742, A
c 331	34.4	3.3	1035	6	US-09-925-065A-33743	Sequence 33743, A
c 332	34.4	3.3	1035	9	US-10-301-480-134980	Sequence 134980,
c 333	34.4	3.3	1035	9	US-10-301-480-134981	Sequence 134981,
c 334	34.4	3.3	1035	10	US-10-301-480-748389	Sequence 748389,
c 335	34.4	3.3	1035	10	US-10-301-480-748390	Sequence 748390,
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342	34.4	3.3	1676	11	US-11-096-568A-19912	Sequence 19912, A
343	34.4	3.3	1874	11	US-11-096-568A-10447	Sequence 10447, A
c 344	34.4	3.3	12884	8	US-10-995-561-13247	Sequence 13247, A
c 345	34.4	3.3	13884	8	US-10-995-561-13376	Sequence 13376, A
c 346	34.4	3.3	16082	8	US-10-995-561-13485	Sequence 13485, A
347	34.4	3.3	19864	8	US-10-995-561-13218	Sequence 13218, A
c 348	34.4	3.3	23894	8	US-10-995-561-13320	Sequence 13320, A
349	34.4	3.3	67467	14	US-11-124-368A-2889	Sequence 2889, Ap
c 350	34.4	3.3	100000	14	US-11-124-368A-2913	Sequence 2913, Ap
351	34.4	3.3	116856	14	US-11-143-980-1	Sequence 1, Appli
352	34.4	3.3	127722	9	US-10-330-773-278	Sequence 278, App
c 353	34.4	3.3	394468	8	US-10-995-561-13473	Sequence 13473, A
c 354	34.2	3.3	243	14	US-11-143-401-94	Sequence 94, Appl
c 355	34.2	3.3	375	6	US-09-925-065A-597213	Sequence 597213,
c 356	34.2	3.3	577	6	US-09-925-065A-67798	Sequence 67798, A
c 357	34.2	3.3	577	9	US-10-301-480-169037	Sequence 169037,
c 358	34.2	3.3	577	10	US-10-301-480-782446	Sequence 782446,
363	34.2	3.3	687	9	US-10-973-115B-445	Sequence 445, App
364	34.2	3.3	687	11	US-11-290-153-445	Sequence 445, App
365	34.2	3.3	736	14	US-11-157-049-1	Sequence 1, Appli
c 366	34.2	3.3	799	10	US-10-301-480-571949	Sequence 571949,
c 367	34.2	3.3	799	10	US-10-301-480-1185358	Sequence 1185358,
c 368	34.2	3.3	945	10	US-10-301-480-580772	Sequence 580772,
c 369	34.2	3.3	945	10	US-10-301-480-1194181	Sequence 1194181,
370	34.2	3.3	1396	14	US-11-000-688-963	Sequence 963, App
c 371	34.2	3.3	2052	6	US-09-925-065A-708127	Sequence 708127,
c 372	34.2	3.3	2052	6	US-09-925-065A-708128	Sequence 708128,
c 373	34.2	3.3	2052	6	US-09-925-065A-708129	Sequence 708129,
c 374	34.2	3.3	2829	8	US-10-467-657-5507	Sequence 5507, Ap
375	34.2	3.3	3228	8	US-10-467-657-5707	Sequence 5707, Ap
376	34.2	3.3	3368	14	US-11-136-527-2245	Sequence 2245, Ap
c 378	34.2	3.3	6723	9	US-10-501-035-168	Sequence 168, App
379	34.2	3.3	13628	14	US-11-124-368A-2933	Sequence 2933, Ap
380	34	3.2	627	11	US-11-096-568A-9424	Sequence 9424, Ap
c 381	34	3.2	670	10	US-10-301-480-542165	Sequence 542165,
c 382	34	3.2	670	10	US-10-301-480-1155574	Sequence 1155574,
c 383	34	3.2	760	6	US-09-925-065A-75126	Sequence 75126, A
c 384	34	3.2	760	9	US-10-301-480-176365	Sequence 176365,
c 385	34	3.2	760	10	US-10-301-480-789774	Sequence 789774,
386	34	3.2	982	10	US-10-301-480-548551	Sequence 548551,
387	34	3.2	982	10	US-10-301-480-1161960	Sequence 1161960,
c 388	34	3.2	1448	11	US-11-096-568A-25903	Sequence 25903, A
389	34	3.2	1623	14	US-11-094-917-52	Sequence 52, Appl
390	34	3.2	2151	11	US-11-072-512-1105	Sequence 1105, Ap
391	34	3.2	2677	14	US-11-122-329-19	Sequence 19, Appl
c 392	34	3.2	4453	14	US-11-011-332A-73	Sequence 73, Appl
393	34	3.2	7366	14	US-11-094-917-51	Sequence 51, Appl
c 394	34	3.2	8459	9	US-10-501-035-86	Sequence 86, Appl
c 395	34	3.2	20320	8	US-10-995-561-13287	Sequence 13287, A
396	34	3.2	23063	8	US-10-995-561-13447	Sequence 13447, A
397	34	3.2	76427	14	US-11-124-367A-5041	Sequence 5041, Ap
c 398	34	3.2	86765	9	US-10-501-035-146	Sequence 146, App
399	33.8	3.2	618	6	US-09-925-065A-507222	Sequence 507222,
400	33.8	3.2	1637	11	US-11-096-568A-24109	Sequence 24109, A
401	33.8	3.2	4293	7	US-10-204-639-119	Sequence 119, App
c 402	33.8	3.2	13953	14	US-11-124-368A-2930	Sequence 2930, Ap
403	33.8	3.2	44362	8	US-10-995-561-13422	Sequence 13422, A
404	33.6	3.2	201	8	US-10-995-561-55412	Sequence 55412, A
c 405	33.6	3.2	519	6	US-09-925-065A-523269	Sequence 523269,
c 406	33.6	3.2	539	6	US-09-925-065A-485294	Sequence 485294,
c 407	33.6	3.2	539	6	US-09-925-065A-485295	Sequence 485295,
408	33.6	3.2	662	8	US-10-750-185-46110	Sequence 46110, A
409	33.6	3.2	662	8	US-10-750-623-46110	Sequence 46110, A
c 410	33.6	3.2	729	8	US-10-750-185-36866	Sequence 36866, A
c 411	33.6	3.2	729	8	US-10-750-623-36866	Sequence 36866, A
412	33.6	3.2	932	11	US-11-096-568A-11936	Sequence 11936, A
413	33.6	3.2	1201	11	US-11-096-568A-22415	Sequence 22415, A
c 414	33.6	3.2	1254	11	US-11-096-568A-21266	Sequence 21266, A

c 415	33.6	3.2	1618	11	US-11-096-568A-12724	Sequence 12724, A
416	33.6	3.2	1753	11	US-11-096-568A-23954	Sequence 23954, A
417	33.6	3.2	2049	14	US-11-000-688-406	Sequence 406, App
c 418	33.6	3.2	2304	14	US-11-052-554A-538	Sequence 538, App
c 419	33.6	3.2	2647	8	US-10-821-234-101	Sequence 101, App
420	33.6	3.2	126552	14	US-11-121-086-1	Sequence 1, Appli
c 421	33.6	3.2	176760	14	US-11-121-086-51	Sequence 51, Appl
422	33.4	3.2	436	6	US-09-925-065A-625629	Sequence 625629,
423	33.4	3.2	468	6	US-09-925-065A-839681	Sequence 839681,
c 424	33.4	3.2	612	6	US-09-925-065A-922382	Sequence 922382,
425	33.4	3.2	736	11	US-11-096-568A-741	Sequence 741, App
426	33.4	3.2	792	11	US-11-253-151-1	Sequence 1, Appli
427	33.4	3.2	1201	6	US-09-925-065A-680110	Sequence 680110,
428	33.4	3.2	1230	11	US-11-096-568A-19162	Sequence 19162, A
c 429	33.4	3.2	3147	14	US-11-136-527-3218	Sequence 3218, Ap
430	33.4	3.2	5316	14	US-11-019-711-17	Sequence 17, Appl
431	33.4	3.2	46752	8	US-10-995-561-13410	Sequence 13410, A
432	33.4	3.2	415117	8	US-10-995-561-13274	Sequence 13274, A
c 433	33.2	3.2	832	10	US-10-301-480-566979	Sequence 566979,
c 434	33.2	3.2	832	10	US-10-301-480-1180388	Sequence 1180388,
c 435	33.2	3.2	916	8	US-10-750-185-40162	Sequence 40162, A
c 436	33.2	3.2	916	8	US-10-750-623-40162	Sequence 40162, A
437	33.2	3.2	919	11	US-11-096-568A-1963	Sequence 1963, Ap
438	33.2	3.2	930	10	US-10-301-480-547487	Sequence 547487,
439	33.2	3.2	930	10	US-10-301-480-1160896	Sequence 1160896,
440	33.2	3.2	1113	8	US-10-055-877-70	Sequence 70, Appl
c 441	33.2	3.2	1140	11	US-11-096-568A-16700	Sequence 16700, A
442	33.2	3.2	1219	8	US-10-055-877-68	Sequence 68, Appl
443	33.2	3.2	1296	8	US-10-525-710-23	Sequence 23, Appl
444	33.2	3.2	1296	11	US-11-079-463-872	Sequence 872, App
445	33.2	3.2	1980	11	US-11-096-568A-20888	Sequence 20888, A
c 446	33.2	3.2	2389	14	US-11-000-688-600	Sequence 600, App
447	33.2	3.2	2457	14	US-11-037-243-52	Sequence 52, Appl
c 448	33.2	3.2	2537	11	US-11-096-568A-23981	Sequence 23981, A
449	33.2	3.2	3710	14	US-11-136-527-2494	Sequence 2494, Ap
450	33.2	3.2	7006	8	US-10-821-234-218	Sequence 218, App
451	33.2	3.2	7265	7	US-10-782-413-66	Sequence 66, Appl
452	33.2	3.2	7893	14	US-11-186-731-3	Sequence 3, Appli
453	33.2	3.2	8106	14	US-11-186-731-1	Sequence 1, Appli
454	33.2	3.2	9222	7	US-10-496-351-2	Sequence 2, Appli
455	33.2	3.2	23907	14	US-11-186-731-6	Sequence 6, Appli
456	33.2	3.2	24120	14	US-11-186-731-4	Sequence 4, Appli
457	33.2	3.2	61718	8	US-10-995-561-13326	Sequence 13326, A
c 458	33.2	3.2	90508	9	US-10-330-773-701	Sequence 701, App
c 459	33.2	3.2	172543	14	US-11-121-086-6	Sequence 6, Appli
c 460	33	3.2	201	8	US-10-995-561-77306	Sequence 77306, A
c 461	33	3.2	336	11	US-11-201-825-18	Sequence 18, Appl
462	33	3.2	446	6	US-09-925-065A-491415	Sequence 491415,
463	33	3.2	457	8	US-10-802-796-591	Sequence 591, App
464	33	3.2	457	11	US-11-221-284-591	Sequence 591, App
465	33	3.2	577	6	US-09-925-065A-884361	Sequence 884361,
c 466	33	3.2	596	11	US-11-096-568A-26867	Sequence 26867, A
c 467	33	3.2	596	14	US-11-108-172-931	Sequence 931, App
c 468	33	3.2	691	10	US-10-301-480-567099	Sequence 567099,
c 469	33	3.2	691	10	US-10-301-480-1180508	Sequence 1180508,
c 470	33	3.2	712	11	US-11-051-720-502	Sequence 502, App
c 471	33	3.2	786	11	US-11-201-825-6	Sequence 6, Appli
472	33	3.2	818	11	US-11-096-568A-1293	Sequence 1293, Ap
473	33	3.2	1102	14	US-11-019-711-43	Sequence 43, Appl
474	33	3.2	1102	14	US-11-019-711-45	Sequence 45, Appl
c 475	33	3.2	1221	14	US-11-075-185-53	Sequence 53, Appl
476	33	3.2	1258	8	US-10-997-437A-1	Sequence 1, Appli
c 477	33	3.2	1495	11	US-11-096-568A-5865	Sequence 5865, Ap
c 478	33	3.2	1540	6	US-09-925-065A-673062	Sequence 673062,
c 479	33	3.2	1540	6	US-09-925-065A-673063	Sequence 673063,
480	33	3.2	1733	14	US-11-080-991-85	Sequence 85, Appl
481	33	3.2	1759	14	US-11-000-688-21	Sequence 21, Appl
c 482	33	3.2	1802	8	US-10-821-234-191	Sequence 191, App
c 483	33	3.2	1847	8	US-10-750-185-49039	Sequence 49039, A
c 484	33	3.2	1847	8	US-10-750-623-49039	Sequence 49039, A
485	33	3.2	1869	14	US-11-147-360-3	Sequence 3, Appli
c 486	33	3.2	1903	11	US-11-051-720-49	Sequence 49, Appl
487	33	3.2	1938	7	US-10-784-004-501	Sequence 501, App
488	33	3.2	1938	7	US-10-784-004-503	Sequence 503, App
489	33	3.2	1938	7	US-10-784-004-984	Sequence 984, App
490	33	3.2	1964	14	US-11-128-061-433	Sequence 433, App
491	33	3.2	1964	14	US-11-128-049-433	Sequence 433, App
c 492	33	3.2	1968	11	US-11-096-568A-18774	Sequence 18774, A
493	33	3.2	2009	11	US-11-096-568A-12701	Sequence 12701, A
c 494	33	3.2	2064	11	US-11-096-568A-23036	Sequence 23036, A
c 495	33	3.2	2231	14	US-11-183-914-24	Sequence 24, Appl
c 496	33	3.2	2364	11	US-11-051-720-50	Sequence 50, Appl
c 497	33	3.2	2539	14	US-11-136-527-215	Sequence 215, App
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499	33	3.2	3129	8	US-10-821-234-292	Sequence 292, App
c 500	33	3.2	3132	6	US-09-925-065A-709758	Sequence 709758,
c 501	33	3.2	3132	6	US-09-925-065A-709759	Sequence 709759,
502	33	3.2	4387	11	US-11-036-196-1684	Sequence 1684, Ap
503	33	3.2	4387	11	US-11-224-663-519	Sequence 519, App
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506	33	3.2	13242	8	US-10-995-561-13441	Sequence 13441, A
c 507	33	3.2	14172	14	US-11-075-185-2	Sequence 2, Appli
c 508	33	3.2	16643	8	US-10-995-561-13302	Sequence 13302, A
c 509	33	3.2	18238	8	US-10-995-561-13386	Sequence 13386, A
510	33	3.2	32847	9	US-10-330-773-744	Sequence 744, App
c 511	33	3.2	181172	14	US-11-121-086-41	Sequence 41, Appl
512	33	3.2	191091	14	US-11-121-086-60	Sequence 60, Appl
c 513	33	3.2	201309	11	US-11-114-798-51	Sequence 51, Appl
c 514	33	3.2	1694969	7	US-10-506-454-1690	Sequence 1690, Ap
c 515	32.8	3.1	404	10	US-10-301-480-299339	Sequence 299339,
c 516	32.8	3.1	404	10	US-10-301-480-912748	Sequence 912748,
517	32.8	3.1	558	14	US-11-147-047-15	Sequence 15, Appl
518	32.8	3.1	576	6	US-09-925-065A-811393	Sequence 811393,
519	32.8	3.1	692	14	US-11-157-049-11	Sequence 11, Appl
c 520	32.8	3.1	949	10	US-10-301-480-559714	Sequence 559714,
c 521	32.8	3.1	949	10	US-10-301-480-1173123	Sequence 1173123,
c 522	32.8	3.1	1225	11	US-11-096-568A-8727	Sequence 8727, Ap
c 523	32.8	3.1	1296	11	US-11-096-568A-23592	Sequence 23592, A
c 524	32.8	3.1	1327	8	US-10-750-185-48886	Sequence 48886, A
c 525	32.8	3.1	1327	8	US-10-750-623-48886	Sequence 48886, A
526	32.8	3.1	1452	11	US-11-096-568A-21486	Sequence 21486, A
527	32.8	3.1	1606	11	US-11-096-568A-22323	Sequence 22323, A
c 528	32.8	3.1	2127	8	US-10-750-185-34757	Sequence 34757, A
c 529	32.8	3.1	2127	8	US-10-750-623-34757	Sequence 34757, A
530	32.8	3.1	2135	11	US-11-072-512-1181	Sequence 1181, Ap
531	32.8	3.1	2294	14	US-11-094-519A-21	Sequence 21, Appl
532	32.8	3.1	2526	11	US-11-072-512-270	Sequence 270, App
c 533	32.8	3.1	4617	14	US-11-052-554A-530	Sequence 530, App
c 534	32.8	3.1	5218	14	US-11-186-284-168	Sequence 168, App
535	32.8	3.1	6277	14	US-11-136-527-707	Sequence 707, App
c 536	32.8	3.1	6360	14	US-11-056-470-2	Sequence 2, Appli
537	32.8	3.1	14172	14	US-11-075-185-2	Sequence 2, Appli
c 538	32.8	3.1	44920	9	US-10-330-773-887	Sequence 887, App
539	32.8	3.1	1694969	7	US-10-506-454-1690	Sequence 1690, Ap
c 540	32.6	3.1	201	8	US-10-995-561-77214	Sequence 77214, A
541	32.6	3.1	490	6	US-09-925-065A-252080	Sequence 252080,
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543	32.6	3.1	499	10	US-10-301-480-945076	Sequence 945076,
544	32.6	3.1	572	6	US-09-925-065A-448012	Sequence 448012,
545	32.6	3.1	573	10	US-10-301-480-507701	Sequence 507701,
546	32.6	3.1	573	10	US-10-301-480-1121110	Sequence 1121110,
547	32.6	3.1	591	6	US-09-925-065A-922412	Sequence 922412,
548	32.6	3.1	591	6	US-09-925-065A-946994	Sequence 946994,
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550	32.6	3.1	601	10	US-10-301-480-1094076	Sequence 1094076,
551	32.6	3.1	608	6	US-09-925-065A-921124	Sequence 921124,
552	32.6	3.1	615	6	US-09-925-065A-414941	Sequence 414941,
553	32.6	3.1	621	7	US-10-943-508A-91	Sequence 91, Appl
c 554	32.6	3.1	788	14	US-11-084-085-38	Sequence 38, Appl
555	32.6	3.1	795	7	US-10-496-351-50	Sequence 50, Appl
556	32.6	3.1	854	10	US-10-301-480-592319	Sequence 592319,
557	32.6	3.1	854	10	US-10-301-480-1205728	Sequence 1205728,
558	32.6	3.1	864	10	US-10-301-480-592320	Sequence 592320,
559	32.6	3.1	864	10	US-10-301-480-1205729	Sequence 1205729,
c 560	32.6	3.1	983	11	US-11-096-568A-16080	Sequence 16080, A

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c	562	32.6	3.1	1233	14	US-11-136-527-2827	Sequence 2827, Ap
c	563	32.6	3.1	1233	14	US-11-136-527-6923	Sequence 6923, Ap
	564	32.6	3.1	1254	11	US-11-096-568A-21218	Sequence 21218, A
c	565	32.6	3.1	1425	11	US-11-096-568A-9062	Sequence 9062, Ap
	566	32.6	3.1	1445	11	US-11-096-568A-19594	Sequence 19594, A
c	567	32.6	3.1	1591	6	US-09-925-065A-9042	Sequence 9042, Ap
c	568	32.6	3.1	1591	9	US-10-301-480-110279	Sequence 110279,
c	569	32.6	3.1	1591	10	US-10-301-480-723688	Sequence 723688,
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	571	32.6	3.1	1608	6	US-09-925-065A-37514	Sequence 37514, A
	572	32.6	3.1	1608	9	US-10-301-480-138751	Sequence 138751,
	573	32.6	3.1	1608	9	US-10-301-480-138752	Sequence 138752,
	574	32.6	3.1	1608	10	US-10-301-480-752160	Sequence 752160,
	575	32.6	3.1	1608	10	US-10-301-480-752161	Sequence 752161,
	576	32.6	3.1	1611	11	US-11-051-724-31	Sequence 31, Appl
c	577	32.6	3.1	1673	6	US-09-925-065A-94923	Sequence 94923, A
c	578	32.6	3.1	1673	9	US-10-301-480-196165	Sequence 196165,
c	579	32.6	3.1	1673	10	US-10-301-480-809574	Sequence 809574,
	580	32.6	3.1	1725	11	US-11-096-568A-12404	Sequence 12404, A
c	581	32.6	3.1	1864	11	US-11-096-568A-22086	Sequence 22086, A
	582	32.6	3.1	2001	11	US-11-096-568A-12396	Sequence 12396, A
c	583	32.6	3.1	2092	14	US-11-136-527-1902	Sequence 1902, Ap
	584	32.6	3.1	2600	6	US-09-925-065A-92367	Sequence 92367, A
	585	32.6	3.1	2600	6	US-09-925-065A-92368	Sequence 92368, A
	586	32.6	3.1	2600	9	US-10-301-480-193609	Sequence 193609,
	587	32.6	3.1	2600	9	US-10-301-480-193610	Sequence 193610,
	588	32.6	3.1	2600	10	US-10-301-480-807018	Sequence 807018,
	589	32.6	3.1	2600	10	US-10-301-480-807019	Sequence 807019,
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	591	32.6	3.1	3408	8	US-10-858-730-40	Sequence 40, Appl
	592	32.6	3.1	5582	14	US-11-000-688-386	Sequence 386, App
	593	32.6	3.1	11905	7	US-10-496-351-57	Sequence 57, Appl
	594	32.6	3.1	13377	14	US-11-124-368A-2882	Sequence 2882, Ap
	595	32.6	3.1	29871	8	US-10-995-561-13387	Sequence 13387, A
	596	32.6	3.1	100864	9	US-10-330-773-239	Sequence 239, App
c	597	32.6	3.1	321019	8	US-10-995-561-13204	Sequence 13204, A
c	598	32.4	3.1	306	14	US-11-124-368A-64	Sequence 64, Appl
c	599	32.4	3.1	395	6	US-09-925-065A-212255	Sequence 212255,
	600	32.4	3.1	443	6	US-09-925-065A-235419	Sequence 235419,
	601	32.4	3.1	448	6	US-09-925-065A-656497	Sequence 656497,
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	603	32.4	3.1	448	10	US-10-301-480-931632	Sequence 931632,
	604	32.4	3.1	483	6	US-09-925-065A-172812	Sequence 172812,
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	606	32.4	3.1	489	10	US-10-301-480-877879	Sequence 877879,
c	607	32.4	3.1	505	6	US-09-925-065A-932922	Sequence 932922,
c	608	32.4	3.1	516	6	US-09-925-065A-795966	Sequence 795966,
c	609	32.4	3.1	516	6	US-09-925-065A-851226	Sequence 851226,
	610	32.4	3.1	534	6	US-09-925-065A-547996	Sequence 547996,
	611	32.4	3.1	534	10	US-10-301-480-525946	Sequence 525946,
	612	32.4	3.1	534	10	US-10-301-480-1139355	Sequence 1139355,
	613	32.4	3.1	585	6	US-09-925-065A-124445	Sequence 124445,
	614	32.4	3.1	585	6	US-09-925-065A-124446	Sequence 124446,
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c	616	32.4	3.1	595	10	US-10-301-480-222123	Sequence 222123,
c	617	32.4	3.1	595	10	US-10-301-480-835531	Sequence 835531,
c	618	32.4	3.1	595	10	US-10-301-480-835532	Sequence 835532,
c	619	32.4	3.1	602	6	US-09-925-065A-788901	Sequence 788901,
c	620	32.4	3.1	606	6	US-09-925-065A-502039	Sequence 502039,
c	621	32.4	3.1	980	10	US-10-301-480-609927	Sequence 609927,
c	622	32.4	3.1	980	10	US-10-301-480-1223336	Sequence 1223336,
	623	32.4	3.1	1019	11	US-11-096-568A-2921	Sequence 2921, Ap
	624	32.4	3.1	1095	8	US-10-986-501-93	Sequence 93, Appl
c	625	32.4	3.1	1144	9	US-10-501-035-139	Sequence 139, App
	626	32.4	3.1	1233	11	US-11-096-568A-26398	Sequence 26398, A
c	627	32.4	3.1	1323	9	US-10-330-773-857	Sequence 857, App
c	628	32.4	3.1	1349	8	US-10-750-185-27534	Sequence 27534, A
c	629	32.4	3.1	1349	8	US-10-750-623-27534	Sequence 27534, A
	630	32.4	3.1	1357	11	US-11-096-568A-9643	Sequence 9643, Ap
	631	32.4	3.1	1365	11	US-11-096-568A-18849	Sequence 18849, A
	632	32.4	3.1	1487	9	US-10-515-547-1	Sequence 1, Appli
	633	32.4	3.1	1573	11	US-11-096-568A-24540	Sequence 24540, A
	634	32.4	3.1	1646	6	US-09-925-065A-92790	Sequence 92790, A
	635	32.4	3.1	1646	9	US-10-301-480-194032	Sequence 194032,
	636	32.4	3.1	1646	10	US-10-301-480-807441	Sequence 807441,
c	637	32.4	3.1	1689	11	US-11-036-196-1593	Sequence 1593, Ap
c	638	32.4	3.1	1748	14	US-11-136-527-253	Sequence 253, App
c	639	32.4	3.1	1759	11	US-11-096-568A-21990	Sequence 21990, A
	640	32.4	3.1	1770	8	US-10-821-234-642	Sequence 642, App
	641	32.4	3.1	1872	14	US-11-210-316-27	Sequence 27, Appl
c	642	32.4	3.1	1994	14	US-11-000-688-727	Sequence 727, App
	643	32.4	3.1	2032	8	US-10-909-125-1741	Sequence 1741, Ap
	644	32.4	3.1	2113	11	US-11-072-512-477	Sequence 477, App
	649	32.4	3.1	2162	11	US-11-150-463-1	Sequence 1, Appli
	650	32.4	3.1	2171	8	US-10-955-054A-185	Sequence 185, App
	651	32.4	3.1	2255	9	US-10-517-696-38	Sequence 38, Appl
	652	32.4	3.1	2357	8	US-10-947-249-99	Sequence 99, Appl
c	653	32.4	3.1	2556	8	US-10-533-355-12	Sequence 12, Appl
c	654	32.4	3.1	2947	14	US-11-136-527-144	Sequence 144, App
c	655	32.4	3.1	2951	14	US-11-136-527-2838	Sequence 2838, Ap
	656	32.4	3.1	3305	14	US-11-017-550-68	Sequence 68, Appl
c	657	32.4	3.1	3345	11	US-11-072-512-533	Sequence 533, App
c	658	32.4	3.1	5519	14	US-11-136-527-2383	Sequence 2383, Ap
c	659	32.4	3.1	10524	14	US-11-075-185-37	Sequence 37, Appl
	660	32.4	3.1	12391	14	US-11-017-550-67	Sequence 67, Appl
	661	32.4	3.1	14055	7	US-10-496-351-1	Sequence 1, Appli
c	662	32.4	3.1	22343	9	US-10-330-773-856	Sequence 856, App
	663	32.4	3.1	46202	9	US-10-330-773-884	Sequence 884, App
	664	32.4	3.1	54985	14	US-11-124-367A-5047	Sequence 5047, Ap
c	665	32.4	3.1	78869	14	US-11-075-185-1	Sequence 1, Appli
c	666	32.4	3.1	147700	8	US-10-857-780-3	Sequence 3, Appli
c	667	32.4	3.1	161994	14	US-11-112-908-57	Sequence 57, Appl
	668	32.2	3.1	152	8	US-10-995-561-10458	Sequence 10458, A
	669	32.2	3.1	152	8	US-10-995-561-10470	Sequence 10470, A
c	670	32.2	3.1	233	8	US-10-514-863-6	Sequence 6, Appli
	671	32.2	3.1	465	6	US-09-925-065A-124697	Sequence 124697,
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c	673	32.2	3.1	479	6	US-09-925-065A-479706	Sequence 479706,
c	674	32.2	3.1	479	6	US-09-925-065A-479707	Sequence 479707,
	675	32.2	3.1	570	6	US-09-925-065A-232257	Sequence 232257,
	676	32.2	3.1	573	10	US-10-301-480-315600	Sequence 315600,
	677	32.2	3.1	573	10	US-10-301-480-929009	Sequence 929009,
c	678	32.2	3.1	612	6	US-09-925-065A-922381	Sequence 922381,
c	679	32.2	3.1	794	10	US-10-301-480-603533	Sequence 603533,
c	680	32.2	3.1	794	10	US-10-301-480-1216942	Sequence 1216942,
c	681	32.2	3.1	799	10	US-10-301-480-575355	Sequence 575355,
c	682	32.2	3.1	799	10	US-10-301-480-1188764	Sequence 1188764,
c	683	32.2	3.1	905	8	US-10-750-185-27138	Sequence 27138, A
c	684	32.2	3.1	905	8	US-10-750-623-27138	Sequence 27138, A
	685	32.2	3.1	980	11	US-11-096-568A-15774	Sequence 15774, A
c	686	32.2	3.1	991	8	US-10-750-185-39786	Sequence 39786, A
c	687	32.2	3.1	991	8	US-10-750-623-39786	Sequence 39786, A
	688	32.2	3.1	1017	14	US-11-112-908-487	Sequence 487, App
	689	32.2	3.1	1255	11	US-11-096-568A-15721	Sequence 15721, A
	690	32.2	3.1	1334	11	US-11-096-568A-23619	Sequence 23619, A
	691	32.2	3.1	1423	8	US-10-391-414-4	Sequence 4, Appli
c	692	32.2	3.1	1425	11	US-11-096-568A-17437	Sequence 17437, A
	693	32.2	3.1	1530	11	US-11-096-568A-19330	Sequence 19330, A
	694	32.2	3.1	1608	6	US-09-925-065A-37515	Sequence 37515, A
	695	32.2	3.1	1608	9	US-10-301-480-138753	Sequence 138753,
	696	32.2	3.1	1608	10	US-10-301-480-752162	Sequence 752162,
	697	32.2	3.1	1632	8	US-10-750-185-39675	Sequence 39675, A
	698	32.2	3.1	1632	8	US-10-750-623-39675	Sequence 39675, A
c	699	32.2	3.1	1735	6	US-09-925-065A-84372	Sequence 84372, A
c	700	32.2	3.1	1735	9	US-10-301-480-185612	Sequence 185612,
c	701	32.2	3.1	1735	10	US-10-301-480-799021	Sequence 799021,
	702	32.2	3.1	1830	14	US-11-000-688-978	Sequence 978, App
c	703	32.2	3.1	1919	11	US-11-096-568A-20665	Sequence 20665, A
c	704	32.2	3.1	1939	11	US-11-072-512-1437	Sequence 1437, Ap
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	706	32.2	3.1	2013	11	US-11-096-568A-23969	Sequence 23969, A
	707	32.2	3.1	2038	6	US-09-925-065A-2329	Sequence 2329, Ap
	708	32.2	3.1	2038	6	US-09-925-065A-2330	Sequence 2330, Ap
	709	32.2	3.1	2038	6	US-09-925-065A-2331	Sequence 2331, Ap
	710	32.2	3.1	2038	9	US-10-301-480-103566	Sequence 103566,

	711	32.2	3.1	2038	9	US-10-301-480-103567 Sequence 103567,
	712	32.2	3.1	2038	9	US-10-301-480-103568 Sequence 103568,
	713	32.2	3.1	2038	10	US-10-301-480-716975 Sequence 716975,
	714	32.2	3.1	2038	10	US-10-301-480-716976 Sequence 716976,
	715	32.2	3.1	2038	10	US-10-301-480-716977 Sequence 716977,
	716	32.2	3.1	2148	11	US-11-072-512-179 Sequence 179, App
c	717	32.2	3.1	2584	8	US-10-821-234-836 Sequence 836, App
c	718	32.2	3.1	2782	12	US-11-112-944-25 Sequence 25, Appl
	719	32.2	3.1	2895	14	US-11-019-711-37 Sequence 37, Appl
	720	32.2	3.1	2898	8	US-10-955-054A-14 Sequence 14, Appl
c	721	32.2	3.1	3081	8	US-10-514-863-1 Sequence 1, Appli
	722	32.2	3.1	3453	8	US-10-955-054A-176 Sequence 176, App
	723	32.2	3.1	3490	14	US-11-122-329-110 Sequence 110, App
	724	32.2	3.1	5102	8	US-10-775-169-230 Sequence 230, App
	725	32.2	3.1	5102	9	US-10-501-035-5 Sequence 5, Appli
	726	32.2	3.1	5128	14	US-11-169-041-36 Sequence 36, Appl
	727	32.2	3.1	5210	14	US-11-136-527-2911 Sequence 2911, Ap
c	728	32.2	3.1	14055	7	US-10-496-351-1 Sequence 1, Appli
c	729	32.2	3.1	23606	8	US-10-995-561-13465 Sequence 13465, A
	730	32.2	3.1	31737	14	US-11-122-329-97 Sequence 97, Appl
c	731	32.2	3.1	96256	8	US-10-775-169-352 Sequence 352, App
	732	32.2	3.1	100000	14	US-11-124-368A-2883 Sequence 2883, Ap
c	733	32.2	3.1	127340	14	US-11-112-908-35 Sequence 35, Appl
c	734	32.2	3.1	128978	8	US-10-775-169-345 Sequence 345, App
	735	32.2	3.1	155515	14	US-11-112-908-42 Sequence 42, Appl
	736	32.2	3.1	159660	14	US-11-112-908-43 Sequence 43, Appl
	737	32.2	3.1	177623	14	US-11-112-908-41 Sequence 41, Appl
	738	32	3.1	201	14	US-11-124-367A-6745 Sequence 6745, Ap
	739	32	3.1	201	14	US-11-124-367A-16101 Sequence 16101, A
	740	32	3.1	500	6	US-09-925-065A-107346 Sequence 107346,
	741	32	3.1	504	9	US-10-301-480-207215 Sequence 207215,
	742	32	3.1	504	10	US-10-301-480-820624 Sequence 820624,
c	743	32	3.1	527	6	US-09-925-065A-9832 Sequence 9832, Ap
c	744	32	3.1	527	9	US-10-301-480-111069 Sequence 111069,
c	745	32	3.1	527	10	US-10-301-480-724478 Sequence 724478,
	746	32	3.1	568	6	US-09-925-065A-544122 Sequence 544122,
c	747	32	3.1	574	6	US-09-925-065A-767460 Sequence 767460,
c	748	32	3.1	624	6	US-09-925-065A-299825 Sequence 299825,
c	749	32	3.1	642	10	US-10-301-480-376385 Sequence 376385,
c	750	32	3.1	642	10	US-10-301-480-989794 Sequence 989794,
c	751	32	3.1	724	11	US-11-096-568A-9838 Sequence 9838, Ap
c	752	32	3.1	773	6	US-09-925-065A-928173 Sequence 928173,
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	754	32	3.1	963	8	US-10-858-730-182 Sequence 182, App
	755	32	3.1	1114	11	US-11-096-568A-16674 Sequence 16674, A
	756	32	3.1	1386	11	US-11-096-568A-25805 Sequence 25805, A
	757	32	3.1	1420	14	US-11-136-527-1819 Sequence 1819, Ap
	758	32	3.1	1741	11	US-11-096-568A-13489 Sequence 13489, A
	759	32	3.1	1875	11	US-11-096-568A-10308 Sequence 10308, A
c	760	32	3.1	2352	14	US-11-052-554A-541 Sequence 541, App
	761	32	3.1	2539	14	US-11-136-527-215 Sequence 215, App
c	762	32	3.1	2554	11	US-11-227-543-22 Sequence 22, Appl
c	763	32	3.1	2745	14	US-11-052-554A-544 Sequence 544, App
	764	32	3.1	3108	8	US-10-477-507A-1 Sequence 1, Appli
	765	32	3.1	3240	14	US-11-052-554A-529 Sequence 529, App
c	766	32	3.1	3456	14	US-11-136-527-155 Sequence 155, App
	767	32	3.1	3656	8	US-10-947-249-198 Sequence 198, App
c	768	32	3.1	3925	7	US-10-784-004-1190 Sequence 1190, Ap
	769	32	3.1	5300	14	US-11-000-688-563 Sequence 563, App
c	770	32	3.1	5706	14	US-11-052-554A-519 Sequence 519, App
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c	773	32	3.1	6604	11	US-11-134-587B-1 Sequence 1, Appli
	774	32	3.1	12277	8	US-10-477-507A-3 Sequence 3, Appli
	775	32	3.1	27936	14	US-11-124-367A-5042 Sequence 5042, Ap
	776	32	3.1	44920	9	US-10-330-773-887 Sequence 887, App
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	778	32	3.1	170285	14	US-11-112-908-58 Sequence 58, Appl
c	779	32	3.1	180531	11	US-11-114-798-57 Sequence 57, Appl
c	780	32	3.1	390183	9	US-10-330-773-937 Sequence 937, App
c	781	31.8	3.0	396	10	US-10-301-480-279690 Sequence 279690,
c	782	31.8	3.0	396	10	US-10-301-480-893099 Sequence 893099,
c	783	31.8	3.0	402	6	US-09-925-065A-189925 Sequence 189925,
c	784	31.8	3.0	500	10	US-10-301-480-274807 Sequence 274807,
c	785	31.8	3.0	500	10	US-10-301-480-888216 Sequence 888216,
c	786	31.8	3.0	502	6	US-09-925-065A-184479 Sequence 184479,
c	787	31.8	3.0	513	6	US-09-925-065A-819194 Sequence 819194,
	788	31.8	3.0	528	10	US-10-301-480-471734 Sequence 471734,
	789	31.8	3.0	528	10	US-10-301-480-1085143 Sequence 1085143,
c	790	31.8	3.0	533	6	US-09-925-065A-133455 Sequence 133455,
	791	31.8	3.0	534	6	US-09-925-065A-404820 Sequence 404820,
c	792	31.8	3.0	540	10	US-10-301-480-229457 Sequence 229457,
c	793	31.8	3.0	540	10	US-10-301-480-842866 Sequence 842866,
	794	31.8	3.0	571	10	US-10-301-480-575534 Sequence 575534,
	795	31.8	3.0	571	10	US-10-301-480-1188943 Sequence 1188943,
c	796	31.8	3.0	621	6	US-09-925-065A-773337 Sequence 773337,
c	797	31.8	3.0	644	6	US-09-925-065A-67610 Sequence 67610, A
c	798	31.8	3.0	644	9	US-10-301-480-168849 Sequence 168849,
c	799	31.8	3.0	644	10	US-10-301-480-782258 Sequence 782258,
c	800	31.8	3.0	658	6	US-09-925-065A-922210 Sequence 922210,
	801	31.8	3.0	969	8	US-10-750-185-54360 Sequence 54360, A
	802	31.8	3.0	969	8	US-10-750-623-54360 Sequence 54360, A
	803	31.8	3.0	995	8	US-10-750-185-58013 Sequence 58013, A
	804	31.8	3.0	995	8	US-10-750-623-58013 Sequence 58013, A
c	805	31.8	3.0	999	11	US-11-096-568A-9639 Sequence 9639, Ap
	806	31.8	3.0	1141	11	US-11-096-568A-24652 Sequence 24652, A
	807	31.8	3.0	1232	11	US-11-096-568A-23938 Sequence 23938, A
c	808	31.8	3.0	1290	11	US-11-172-740-819 Sequence 819, App
c	809	31.8	3.0	1330	8	US-10-750-185-64812 Sequence 64812, A
c	810	31.8	3.0	1330	8	US-10-750-623-64812 Sequence 64812, A
c	811	31.8	3.0	1481	11	US-11-096-568A-19615 Sequence 19615, A
c	812	31.8	3.0	1526	14	US-11-124-368A-40 Sequence 40, Appl
c	813	31.8	3.0	1542	11	US-11-096-568A-9647 Sequence 9647, Ap
	814	31.8	3.0	1585	11	US-11-096-568A-22319 Sequence 22319, A
c	815	31.8	3.0	1621	8	US-10-750-185-56891 Sequence 56891, A
c	816	31.8	3.0	1621	8	US-10-750-623-56891 Sequence 56891, A
	817	31.8	3.0	1655	8	US-10-995-561-392 Sequence 392, App
c	818	31.8	3.0	1735	14	US-11-124-368A-41 Sequence 41, Appl
	819	31.8	3.0	2136	11	US-11-072-512-618 Sequence 618, App
	820	31.8	3.0	2142	14	US-11-080-991-15 Sequence 15, Appl
	821	31.8	3.0	2210	14	US-11-121-438-11 Sequence 11, Appl
	822	31.8	3.0	3464	9	US-10-511-989-21 Sequence 21, Appl
	823	31.8	3.0	4464	9	US-10-511-989-23 Sequence 23, Appl
c	824	31.8	3.0	4745	8	US-10-909-125-837 Sequence 837, App
	825	31.8	3.0	5003	8	US-10-995-561-391 Sequence 391, App
	826	31.8	3.0	5601	9	US-10-511-989-185 Sequence 185, App
c	827	31.8	3.0	5648	11	US-11-036-196-1694 Sequence 1694, Ap
	828	31.8	3.0	5910	9	US-10-501-035-19 Sequence 19, Appl
c	829	31.8	3.0	11905	7	US-10-496-351-57 Sequence 57, Appl
c	830	31.8	3.0	12507	14	US-11-136-527-2447 Sequence 2447, Ap
	831	31.8	3.0	28516	9	US-10-330-773-447 Sequence 447, App
c	832	31.8	3.0	48203	8	US-10-995-561-13378 Sequence 13378, A
	833	31.8	3.0	103665	9	US-10-330-773-680 Sequence 680, App
	834	31.8	3.0	151870	8	US-10-995-561-13199 Sequence 13199, A
c	835	31.8	3.0	175603	9	US-10-330-773-531 Sequence 531, App
c	836	31.8	3.0	196200	14	US-11-121-086-9 Sequence 9, Appli
c	837	31.8	3.0	246960	14	US-11-121-086-8 Sequence 8, Appli
	838	31.8	3.0	348101	9	US-10-330-773-122 Sequence 122, App
c	839	31.6	3.0	443	6	US-09-925-065A-854738 Sequence 854738,
	840	31.6	3.0	494	10	US-10-301-480-475996 Sequence 475996,
	841	31.6	3.0	494	10	US-10-301-480-1089405 Sequence 1089405,
	842	31.6	3.0	496	6	US-09-925-065A-409548 Sequence 409548,
c	843	31.6	3.0	568	6	US-09-925-065A-544122 Sequence 544122,
c	844	31.6	3.0	573	6	US-09-925-065A-785578 Sequence 785578,
c	845	31.6	3.0	589	10	US-10-301-480-599463 Sequence 599463,
c	846	31.6	3.0	589	10	US-10-301-480-1212872 Sequence 1212872,
c	847	31.6	3.0	605	6	US-09-925-065A-780157 Sequence 780157,
c	848	31.6	3.0	615	6	US-09-925-065A-792798 Sequence 792798,
	849	31.6	3.0	649	6	US-09-925-065A-48480 Sequence 48480, A
	850	31.6	3.0	649	9	US-10-301-480-149718 Sequence 149718,
	851	31.6	3.0	649	10	US-10-301-480-763127 Sequence 763127,
	852	31.6	3.0	697	8	US-10-623-155-17 Sequence 17, Appl
	853	31.6	3.0	732	14	US-11-147-047-14 Sequence 14, Appl
	854	31.6	3.0	735	8	US-10-524-647-101 Sequence 101, App
	855	31.6	3.0	735	9	US-10-524-972-85 Sequence 85, Appl
c	856	31.6	3.0	770	10	US-10-301-480-554742 Sequence 554742,

c 857	31.6	3.0	770	10	US-10-301-480-1168151	Sequence 1168151,
c 858	31.6	3.0	847	10	US-10-301-480-548392	Sequence 548392,
c 859	31.6	3.0	847	10	US-10-301-480-1161801	Sequence 1161801,
c 860	31.6	3.0	849	11	US-11-096-568A-26007	Sequence 26007, A
c 861	31.6	3.0	861	10	US-10-301-480-548391	Sequence 548391,
c 862	31.6	3.0	861	10	US-10-301-480-1161800	Sequence 1161800,
c 863	31.6	3.0	899	6	US-09-925-065A-38122	Sequence 38122, A
c 864	31.6	3.0	899	6	US-09-925-065A-38123	Sequence 38123, A
c 865	31.6	3.0	899	6	US-09-925-065A-38124	Sequence 38124, A
c 866	31.6	3.0	899	9	US-10-301-480-139360	Sequence 139360,
c 867	31.6	3.0	899	9	US-10-301-480-139361	Sequence 139361,
c 868	31.6	3.0	899	9	US-10-301-480-139362	Sequence 139362,
c 869	31.6	3.0	899	10	US-10-301-480-752769	Sequence 752769,
c 870	31.6	3.0	899	10	US-10-301-480-752770	Sequence 752770,
c 871	31.6	3.0	899	10	US-10-301-480-752771	Sequence 752771,
c 872	31.6	3.0	961	10	US-10-301-480-536580	Sequence 536580,
c 873	31.6	3.0	961	10	US-10-301-480-1149989	Sequence 1149989,
874	31.6	3.0	981	10	US-10-301-480-587798	Sequence 587798,
875	31.6	3.0	981	10	US-10-301-480-1201207	Sequence 1201207,
876	31.6	3.0	1072	11	US-11-096-568A-20417	Sequence 20417, A
877	31.6	3.0	1188	6	US-09-925-065A-67064	Sequence 67064, A
878	31.6	3.0	1188	9	US-10-301-480-168303	Sequence 168303,
879	31.6	3.0	1188	10	US-10-301-480-781712	Sequence 781712,
c 880	31.6	3.0	1315	8	US-10-750-185-35432	Sequence 35432, A
c 881	31.6	3.0	1315	8	US-10-750-623-35432	Sequence 35432, A
c 882	31.6	3.0	1472	6	US-09-925-065A-711806	Sequence 711806,
883	31.6	3.0	1524	6	US-09-925-065A-62647	Sequence 62647, A
884	31.6	3.0	1524	6	US-09-925-065A-62648	Sequence 62648, A
885	31.6	3.0	1524	6	US-09-925-065A-62649	Sequence 62649, A
886	31.6	3.0	1524	6	US-09-925-065A-62650	Sequence 62650, A
887	31.6	3.0	1524	9	US-10-301-480-163885	Sequence 163885,
888	31.6	3.0	1524	9	US-10-301-480-163886	Sequence 163886,
889	31.6	3.0	1524	9	US-10-301-480-163887	Sequence 163887,
890	31.6	3.0	1524	9	US-10-301-480-163888	Sequence 163888,
891	31.6	3.0	1524	10	US-10-301-480-777294	Sequence 777294,
892	31.6	3.0	1524	10	US-10-301-480-777295	Sequence 777295,
893	31.6	3.0	1524	10	US-10-301-480-777296	Sequence 777296,
894	31.6	3.0	1524	10	US-10-301-480-777297	Sequence 777297,
899	31.6	3.0	1670	9	US-10-973-115B-325	Sequence 325, App
900	31.6	3.0	1670	11	US-11-290-153-325	Sequence 325, App
c 901	31.6	3.0	1692	11	US-11-096-568A-20613	Sequence 20613, A
902	31.6	3.0	1746	11	US-11-096-568A-26082	Sequence 26082, A
903	31.6	3.0	1772	11	US-11-096-568A-21812	Sequence 21812, A
c 904	31.6	3.0	1834	14	US-11-046-255A-3	Sequence 3, Appli
c 905	31.6	3.0	1845	11	US-11-096-568A-25561	Sequence 25561, A
c 906	31.6	3.0	2062	6	US-09-925-065A-40195	Sequence 40195, A
c 907	31.6	3.0	2062	6	US-09-925-065A-40196	Sequence 40196, A
c 908	31.6	3.0	2062	6	US-09-925-065A-40197	Sequence 40197, A
c 909	31.6	3.0	2062	6	US-09-925-065A-40198	Sequence 40198, A
c 910	31.6	3.0	2062	9	US-10-301-480-141433	Sequence 141433,
c 911	31.6	3.0	2062	9	US-10-301-480-141434	Sequence 141434,
c 912	31.6	3.0	2062	9	US-10-301-480-141435	Sequence 141435,
c 913	31.6	3.0	2062	9	US-10-301-480-141436	Sequence 141436,
c 914	31.6	3.0	2062	10	US-10-301-480-754842	Sequence 754842,
c 915	31.6	3.0	2062	10	US-10-301-480-754843	Sequence 754843,
c 916	31.6	3.0	2062	10	US-10-301-480-754844	Sequence 754844,
c 917	31.6	3.0	2062	10	US-10-301-480-754845	Sequence 754845,
918	31.6	3.0	2094	11	US-11-096-568A-24017	Sequence 24017, A
919	31.6	3.0	2268	14	US-11-037-243-23	Sequence 23, Appl
c 920	31.6	3.0	2376	8	US-10-955-054A-179	Sequence 179, App
c 921	31.6	3.0	2388	8	US-10-821-234-252	Sequence 252, App
c 922	31.6	3.0	2500	11	US-11-245-147-210	Sequence 210, App
937	31.6	3.0	2669	11	US-11-288-493-65	Sequence 65, Appl
938	31.6	3.0	2782	12	US-11-112-944-25	Sequence 25, Appl
939	31.6	3.0	3624	9	US-10-755-092-6	Sequence 6, Appli
c 940	31.6	3.0	3850	5	US-09-889-325-3	Sequence 3, Appli
c 941	31.6	3.0	3850	5	US-09-889-325-3	Sequence 3, Appli
942	31.6	3.0	3900	14	US-11-091-883-411	Sequence 411, App
c 943	31.6	3.0	4259	14	US-11-091-883-312	Sequence 312, App
c 944	31.6	3.0	4259	14	US-11-091-883-392	Sequence 392, App
945	31.6	3.0	4381	14	US-11-136-527-2390	Sequence 2390, Ap
946	31.6	3.0	5562	14	US-11-180-074-3	Sequence 3, Appli
947	31.6	3.0	6990	14	US-11-000-688-609	Sequence 609, App
948	31.6	3.0	7351	9	US-10-893-483-101	Sequence 101, App
949	31.6	3.0	9975	7	US-10-496-351-4	Sequence 4, Appli
c 950	31.6	3.0	11070	14	US-11-075-185-34	Sequence 34, Appl
951	31.6	3.0	12927	9	US-10-893-483-102	Sequence 102, App
952	31.6	3.0	24770	9	US-10-893-483-96	Sequence 96, Appl
c 953	31.6	3.0	25740	8	US-10-995-561-13439	Sequence 13439, A
954	31.6	3.0	38449	8	US-10-995-561-13358	Sequence 13358, A
955	31.6	3.0	65885	8	US-10-995-561-13490	Sequence 13490, A
c 956	31.6	3.0	76427	14	US-11-124-367A-5041	Sequence 5041, Ap
957	31.6	3.0	175673	14	US-11-121-086-55	Sequence 55, Appl
958	31.6	3.0	228006	9	US-10-330-773-119	Sequence 119, App
c 959	31.6	3.0	1691140	14	US-11-091-018-1	Sequence 1, Appli
960	31.4	3.0	201	8	US-10-995-561-63861	Sequence 63861, A
c 961	31.4	3.0	201	8	US-10-995-561-64231	Sequence 64231, A
c 962	31.4	3.0	547	6	US-09-925-065A-133454	Sequence 133454,
c 963	31.4	3.0	548	10	US-10-301-480-229456	Sequence 229456,
c 964	31.4	3.0	548	10	US-10-301-480-842865	Sequence 842865,
965	31.4	3.0	552	10	US-10-301-480-337119	Sequence 337119,
966	31.4	3.0	552	10	US-10-301-480-950528	Sequence 950528,
967	31.4	3.0	582	6	US-09-925-065A-258514	Sequence 258514,
968	31.4	3.0	583	6	US-09-925-065A-7125	Sequence 7125, Ap
969	31.4	3.0	583	9	US-10-301-480-108362	Sequence 108362,
970	31.4	3.0	583	10	US-10-301-480-721771	Sequence 721771,
971	31.4	3.0	600	14	US-11-136-527-7000	Sequence 7000, Ap
972	31.4	3.0	600	14	US-11-136-527-7338	Sequence 7338, Ap
c 973	31.4	3.0	604	6	US-09-925-065A-863279	Sequence 863279,
c 974	31.4	3.0	668	6	US-09-925-065A-816986	Sequence 816986,
975	31.4	3.0	838	11	US-11-096-568A-21286	Sequence 21286, A
976	31.4	3.0	849	11	US-11-096-568A-26007	Sequence 26007, A
977	31.4	3.0	953	10	US-10-301-480-569649	Sequence 569649,
978	31.4	3.0	953	10	US-10-301-480-1183058	Sequence 1183058,
979	31.4	3.0	987	10	US-10-301-480-531062	Sequence 531062,
980	31.4	3.0	987	10	US-10-301-480-1144471	Sequence 1144471,
981	31.4	3.0	999	8	US-10-750-185-44043	Sequence 44043, A
982	31.4	3.0	999	8	US-10-750-623-44043	Sequence 44043, A
c 983	31.4	3.0	1017	5	US-09-978-360A-279	Sequence 279, App
984	31.4	3.0	1114	5	US-09-978-360A-210	Sequence 210, App
985	31.4	3.0	1152	14	US-11-147-360-1	Sequence 1, Appli
986	31.4	3.0	1250	5	US-09-978-360A-333	Sequence 333, App
c 987	31.4	3.0	1277	11	US-11-096-568A-16527	Sequence 16527, A
988	31.4	3.0	1326	11	US-11-096-568A-24259	Sequence 24259, A
c 989	31.4	3.0	1331	8	US-10-750-185-56538	Sequence 56538, A
c 990	31.4	3.0	1331	8	US-10-750-623-56538	Sequence 56538, A
991	31.4	3.0	1332	11	US-11-230-180-1	Sequence 1, Appli
992	31.4	3.0	1332	11	US-11-195-205-5	Sequence 5, Appli
c 993	31.4	3.0	1345	11	US-11-096-568A-26357	Sequence 26357, A
994	31.4	3.0	1498	11	US-11-096-568A-20286	Sequence 20286, A
995	31.4	3.0	1583	11	US-11-096-568A-18054	Sequence 18054, A
996	31.4	3.0	1597	11	US-11-096-568A-16386	Sequence 16386, A
997	31.4	3.0	1873	8	US-10-750-185-37088	Sequence 37088, A
998	31.4	3.0	1873	8	US-10-750-623-37088	Sequence 37088, A
c 999	31.4	3.0	1991	14	US-11-136-527-3242	Sequence 3242, Ap
c1000	31.4	3.0	2052	11	US-11-072-512-207	Sequence 207, App
1001	31.4	3.0	2066	11	US-11-072-512-56	Sequence 56, Appl
1002	31.4	3.0	2302	8	US-10-510-507-2	Sequence 2, Appli
1003	31.4	3.0	2316	14	US-11-080-991-59	Sequence 59, Appl
1004	31.4	3.0	2455	9	US-10-203-486-22	Sequence 22, Appl
1005	31.4	3.0	2456	14	US-11-169-041-32	Sequence 32, Appl
1006	31.4	3.0	2520	9	US-10-511-538-78	Sequence 78, Appl
c1007	31.4	3.0	2725	8	US-10-750-185-37614	Sequence 37614, A
c1008	31.4	3.0	2725	8	US-10-750-623-37614	Sequence 37614, A
1009	31.4	3.0	3569	14	US-11-136-527-2904	Sequence 2904, Ap
c1014	31.4	3.0	3990	14	US-11-052-554A-520	Sequence 520, App
1015	31.4	3.0	4895	8	US-10-993-514-1	Sequence 1, Appli
1016	31.4	3.0	11070	14	US-11-075-185-34	Sequence 34, Appl
1017	31.4	3.0	13187	14	US-11-136-527-3585	Sequence 3585, Ap
1018	31.4	3.0	14603	8	US-10-995-561-13361	Sequence 13361, A
1019	31.4	3.0	18394	8	US-10-995-561-13367	Sequence 13367, A
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1021	31.4	3.0	47460	14	US-11-124-368A-2877	Sequence 2877, Ap
1022	31.4	3.0	100000	14	US-11-124-367A-5086	Sequence 5086, Ap
1023	31.4	3.0	160226	14	US-11-121-086-29	Sequence 29, Appl
c1024	31.4	3.0	168656	14	US-11-112-908-59	Sequence 59, Appl

c1025	31.4	3.0	169725	14	US-11-121-086-63	Sequence 63, Appl
c1026	31.4	3.0	170285	14	US-11-112-908-58	Sequence 58, Appl
c1027	31.4	3.0	175023	14	US-11-121-086-18	Sequence 18, Appl
1028	31.4	3.0	200628	14	US-11-121-086-62	Sequence 62, Appl
1029	31.4	3.0	215974	9	US-10-330-773-500	Sequence 500, App
1030	31.2	3.0	201	14	US-11-124-367A-16065	Sequence 16065, A
c1031	31.2	3.0	482	11	US-11-096-568A-13624	Sequence 13624, A
1032	31.2	3.0	510	6	US-09-925-065A-615415	Sequence 615415,
1033	31.2	3.0	615	7	US-10-496-351-38	Sequence 38, Appl
1034	31.2	3.0	624	10	US-10-301-480-596460	Sequence 596460,
1035	31.2	3.0	624	10	US-10-301-480-1209869	Sequence 1209869,
c1036	31.2	3.0	630	6	US-09-925-065A-603	Sequence 603, App
c1037	31.2	3.0	630	6	US-09-925-065A-604	Sequence 604, App
c1038	31.2	3.0	630	9	US-10-301-480-101840	Sequence 101840,
c1039	31.2	3.0	630	9	US-10-301-480-101841	Sequence 101841,
c1040	31.2	3.0	630	10	US-10-301-480-715249	Sequence 715249,
c1041	31.2	3.0	630	10	US-10-301-480-715250	Sequence 715250,
1042	31.2	3.0	638	6	US-09-925-065A-756296	Sequence 756296,
1043	31.2	3.0	638	6	US-09-925-065A-826395	Sequence 826395,
1044	31.2	3.0	649	6	US-09-925-065A-48479	Sequence 48479, A
1045	31.2	3.0	649	9	US-10-301-480-149717	Sequence 149717,
1046	31.2	3.0	649	10	US-10-301-480-763126	Sequence 763126,
c1047	31.2	3.0	717	6	US-09-925-065A-59650	Sequence 59650, A
c1048	31.2	3.0	717	9	US-10-301-480-160888	Sequence 160888,
c1049	31.2	3.0	717	10	US-10-301-480-774297	Sequence 774297,
1050	31.2	3.0	786	11	US-11-182-480-21	Sequence 21, Appl
1051	31.2	3.0	786	11	US-11-182-408-21	Sequence 21, Appl
1052	31.2	3.0	1011	7	US-10-455-772-453	Sequence 453, App
1053	31.2	3.0	1243	8	US-10-750-185-64769	Sequence 64769, A
1054	31.2	3.0	1243	8	US-10-750-623-64769	Sequence 64769, A
1055	31.2	3.0	1422	11	US-11-096-568A-16647	Sequence 16647, A
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1057	31.2	3.0	1466	11	US-11-096-568A-23350	Sequence 23350, A
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1062	31.2	3.0	1738	11	US-11-040-218-10	Sequence 10, Appl
1063	31.2	3.0	1770	11	US-11-040-218-6	Sequence 6, Appli
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c1065	31.2	3.0	1864	11	US-11-096-568A-14807	Sequence 14807, A
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c1067	31.2	3.0	2023	8	US-10-995-561-55	Sequence 55, Appl
1068	31.2	3.0	2066	7	US-10-455-772-445	Sequence 445, App
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1072	31.2	3.0	2104	11	US-11-224-663-654	Sequence 654, App
1073	31.2	3.0	2104	11	US-11-224-525-654	Sequence 654, App
1074	31.2	3.0	2122	14	US-11-136-527-3463	Sequence 3463, Ap
1075	31.2	3.0	2200	7	US-10-455-772-449	Sequence 449, App
1076	31.2	3.0	2234	7	US-10-469-469-317	Sequence 317, App
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1078	31.2	3.0	2502	11	US-11-256-548-5	Sequence 5, Appli
1079	31.2	3.0	2514	11	US-11-051-720-1610	Sequence 1610, Ap
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1081	31.2	3.0	2706	11	US-11-051-720-1611	Sequence 1611, Ap
1082	31.2	3.0	2871	11	US-11-051-720-1609	Sequence 1609, Ap
1083	31.2	3.0	2928	8	US-10-750-185-51636	Sequence 51636, A
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1089	31.2	3.0	5181	11	US-11-242-459-42	Sequence 42, Appl
c1090	31.2	3.0	5679	14	US-11-075-185-36	Sequence 36, Appl
c1091	31.2	3.0	12591	8	US-10-995-561-13415	Sequence 13415, A
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c1097	31.2	3.0	162173	14	US-11-121-086-72	Sequence 72, Appl
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1099	31.2	3.0	188682	14	US-11-112-908-23	Sequence 23, Appl
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c1107	31	3.0	542	10	US-10-301-480-1046978	Sequence 1046978,
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c1112	31	3.0	575	10	US-10-301-480-950529	Sequence 950529,
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1116	31	3.0	600	14	US-11-120-308-33	Sequence 33, Appl
c1117	31	3.0	604	6	US-09-925-065A-863280	Sequence 863280,
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1122	31	3.0	672	14	US-11-136-527-4984	Sequence 4984, Ap
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c1132	31	3.0	826	10	US-10-301-480-739200	Sequence 739200,
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c1202	31	3.0	2898	14	US-11-000-463-613	Sequence 613, App
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1205	31	3.0	3112	11	US-11-036-196-1500	Sequence 1500, Ap
1206	31	3.0	3112	11	US-11-224-663-4	Sequence 4, Appli
1207	31	3.0	3112	11	US-11-224-525-4	Sequence 4, Appli
1208	31	3.0	3113	14	US-11-136-527-2039	Sequence 2039, Ap
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c1210	31	3.0	3148	7	US-10-784-004-981	Sequence 981, App
1219	31	3.0	4104	9	US-10-973-115B-449	Sequence 449, App
1220	31	3.0	4104	11	US-11-290-153-449	Sequence 449, App
1221	31	3.0	4255	8	US-10-453-372-863	Sequence 863, App
1222	31	3.0	4708	14	US-11-136-527-3301	Sequence 3301, Ap
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1224	31	3.0	4835	8	US-10-453-372-881	Sequence 881, App
1225	31	3.0	5000	8	US-10-453-372-865	Sequence 865, App
1226	31	3.0	5000	8	US-10-453-372-883	Sequence 883, App
1227	31	3.0	5172	8	US-10-453-372-859	Sequence 859, App
1228	31	3.0	5180	11	US-11-036-196-2042	Sequence 2042, Ap
1229	31	3.0	5464	14	US-11-136-527-3219	Sequence 3219, Ap
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1231	31	3.0	6786	14	US-11-069-834-59	Sequence 59, Appl
1232	31	3.0	72352	9	US-10-330-773-43	Sequence 43, Appl
1233	31	3.0	90120	9	US-10-330-773-390	Sequence 390, App
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1246	30.8	2.9	575	10	US-10-301-480-596459	Sequence 596459,
1247	30.8	2.9	575	10	US-10-301-480-1209868	Sequence 1209868,
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1251	30.8	2.9	600	8	US-10-750-185-4833	Sequence 4833, Ap
1252	30.8	2.9	600	8	US-10-750-623-4505	Sequence 4505, Ap
1253	30.8	2.9	600	8	US-10-750-623-4833	Sequence 4833, Ap
1254	30.8	2.9	605	6	US-09-925-065A-757106	Sequence 757106,
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c1259	30.8	2.9	642	10	US-10-301-480-989793	Sequence 989793,
c1260	30.8	2.9	674	6	US-09-925-065A-534903	Sequence 534903,
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c1262	30.8	2.9	695	10	US-10-301-480-535166	Sequence 535166,
c1263	30.8	2.9	695	10	US-10-301-480-1148324	Sequence 1148324,
c1264	30.8	2.9	695	10	US-10-301-480-1148575	Sequence 1148575,
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1267	30.8	2.9	751	10	US-10-301-480-754912	Sequence 754912,
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c1269	30.8	2.9	807	9	US-10-301-480-137226	Sequence 137226,
c1270	30.8	2.9	807	10	US-10-301-480-750635	Sequence 750635,
c1271	30.8	2.9	876	10	US-10-301-480-579677	Sequence 579677,
c1272	30.8	2.9	876	10	US-10-301-480-1193086	Sequence 1193086,
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c1274	30.8	2.9	943	8	US-10-750-185-26745	Sequence 26745, A
c1275	30.8	2.9	943	8	US-10-750-623-26745	Sequence 26745, A
1276	30.8	2.9	948	8	US-10-750-185-41688	Sequence 41688, A
1277	30.8	2.9	948	8	US-10-750-623-41688	Sequence 41688, A
c1278	30.8	2.9	999	10	US-10-301-480-596283	Sequence 596283,
c1279	30.8	2.9	999	10	US-10-301-480-1209692	Sequence 1209692,
1280	30.8	2.9	1014	11	US-11-228-659-10	Sequence 10, Appl
1281	30.8	2.9	1103	11	US-11-096-568A-26079	Sequence 26079, A
c1282	30.8	2.9	1160	9	US-10-714-887-341	Sequence 341, App
c1283	30.8	2.9	1280	7	US-10-965-103-37	Sequence 37, Appl
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c1285	30.8	2.9	1280	11	US-11-221-284-4	Sequence 4, Appli
1286	30.8	2.9	1398	8	US-10-821-234-698	Sequence 698, App
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1296	30.8	2.9	1696	11	US-11-096-568A-10890	Sequence 10890, A
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1302	30.8	2.9	2058	14	US-11-065-943-57	Sequence 57, Appl
1303	30.8	2.9	2190	8	US-10-947-249-104	Sequence 104, App
1304	30.8	2.9	2246	11	US-11-072-512-822	Sequence 822, App
c1314	30.8	2.9	2465	11	US-11-210-471-9	Sequence 9, Appli
1315	30.8	2.9	2490	8	US-10-512-109-26	Sequence 26, Appl
1316	30.8	2.9	2515	14	US-11-136-527-2896	Sequence 2896, Ap
c1317	30.8	2.9	2891	11	US-11-072-512-1190	Sequence 1190, Ap
1318	30.8	2.9	3126	14	US-11-019-711-3	Sequence 3, Appli
c1319	30.8	2.9	3183	6	US-09-925-065A-724593	Sequence 724593,
1320	30.8	2.9	3383	14	US-11-000-688-200	Sequence 200, App
c1321	30.8	2.9	3959	7	US-10-965-103-38	Sequence 38, Appl
1322	30.8	2.9	4246	14	US-11-059-814-19	Sequence 19, Appl
1323	30.8	2.9	4595	11	US-11-228-659-8	Sequence 8, Appli
1324	30.8	2.9	5099	14	US-11-124-367A-115	Sequence 115, App
1325	30.8	2.9	5100	14	US-11-108-528-79	Sequence 79, Appl
1326	30.8	2.9	5135	14	US-11-124-367A-114	Sequence 114, App
1327	30.8	2.9	5204	14	US-11-019-711-7	Sequence 7, Appli
1328	30.8	2.9	5562	7	US-10-204-639-95	Sequence 95, Appl
1329	30.8	2.9	10800	14	US-11-019-711-5	Sequence 5, Appli
1330	30.8	2.9	10809	14	US-11-019-711-1	Sequence 1, Appli
c1331	30.8	2.9	11438	8	US-10-821-234-224	Sequence 224, App
1332	30.8	2.9	12507	14	US-11-136-527-2447	Sequence 2447, Ap
c1333	30.8	2.9	52787	9	US-10-330-773-331	Sequence 331, App
1334	30.8	2.9	73404	14	US-11-124-368A-2914	Sequence 2914, Ap
1335	30.8	2.9	100000	14	US-11-124-368A-2873	Sequence 2873, Ap
c1336	30.8	2.9	124285	9	US-10-893-483-105	Sequence 105, App
c1337	30.8	2.9	126552	14	US-11-121-086-1	Sequence 1, Appli
1338	30.8	2.9	156297	14	US-11-121-086-65	Sequence 65, Appl
1339	30.8	2.9	157224	14	US-11-112-908-51	Sequence 51, Appl
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